

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:13:38 ; Search time 5086.94 Seconds
(without alignments)
10984.434 Million cell updates/sec

Title: US-09-467-368-1

Perfect score: 983

Sequence: 1 TCGCCCCGACGCTTGCAAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_scs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	983	100.0	983	6	AR044575 Sequence
2	983	100.0	983	6	AR157660 Sequence
3	845.2	86.0	2460	15	TLU35436 Thermomyc
4	585	59.5	588	6	AX244978 Sequence
5	262.4	26.7	89019	15	BX842624 Neurospor
6	243.6	24.8	786	15	TRU24191
7	240.6	24.5	1039	15	HIXYL1
8	239	24.3	1123	6	I65436
9	239	24.3	1123	6	BD006885
10	232.6	23.7	841	15	AY156910
11	228.2	23.2	672	15	AY320048
12	214.6	21.8	2202	15	AF246830
13	214.4	21.8	928	15	TVI012718
14	213	21.7	912	15	AK110604
15	211.4	21.5	696	15	AY648860
16	206.2	21.0	678	15	AY536639
17	205	20.9	1195	6	E28868
18	205	20.9	1195	6	E28869

19	204.4	20.8	816	15	AF490982	AF490982 Aspergill
20	204.4	20.8	843	15	AY551187	AY551187 Aspergill
21	203.4	20.7	576	1	SOL292317	AJ292317 Streptomy
22	203.4	20.7	2208	15	CEMXB2	D49851 Chaetomium
23	203	20.7	696	6	CQ786060	CQ786060 Sequence
24	202.2	20.6	300800	1	SC0939112	AL939112 Streptomy
25	200.8	20.4	3173	1	AB110644	AB110644 Streptomy
26	200.2	20.4	1623	15	APB14BXYL	Z68891 A.pisi endo
27	199.8	20.3	1767	1	SPXYL1	X98518 Streptomyce
28	199.6	20.3	851	6	A62443	A62443 Sequence 5
29	199.6	20.3	4398	1	STMXLNB	M64552 Streptomyce
30	199.4	20.3	1640	15	CCIXYLANAS	L13596 Cochliobous
31	199.2	20.3	1008	1	AF194025	AF194025 Streptomy
32	198.4	20.2	949	15	AJ863566	AJ863566 Gibberell
33	197.2	20.1	1375	1	AFI508952	AJ508952 Nonomurae
34	197.2	20.1	1375	6	AR274543	AR274543 Sequence
35	197.2	20.1	1375	6	AR369734	AR369734 Sequence
36	197.2	20.1	1375	6	AR441840	AR441840 Sequence
37	196.8	20.0	687	15	AY575961	AY575961 Gibberell
38	194.8	19.8	2015	15	CEMXA1	D49850 Chaetomium
39	194.6	19.8	695	15	CNS01CPS	AL15832 Botrytis
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43	190	19.3	3204	1	AY795559	AY795559 Thermobif
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45	188.2	19.1	514	6	E28872	E28872 Xylanase ge

ALIGNMENTS

RESULT 1	AR044575	983 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR044575	Sequence 1 from patent US 5817500.			
DEFINITION	AR044575				
ACCESSION	AR044575				
VERSION	AR044575.1	GI:5966040			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 983)				
AUTHORS	Hansen, P., Kamp, P., Mullertz, A. and Knap, I. Helmer.				
TITLE	Animal feed additives				
JOURNAL	Patent: US 5817500-A 1 06-OCT-1998;				
FEATURES	Location/Qualifiers				
source	1..983				
ORIGIN	/organism="Unknown"				
	/mol_type="unassigned DNA"				

Query Match	100.0%;	Score 983;	DB 6;	Length 983;
Best Local Similarity	100.0%;	Pred. No. 7.8e-223;		
Matches 983;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TCGCCCCGACGCTTGCAATCCTTGACGATGATGCTTACCCCGTTGCCCTTGC	60	
DB	1	TCGCCCCGACGCTTGCAATCCTTGACGATGATGCTTACCCCGTTGCCCTTGC	60	
QY	61	GCTTAGCCCGACGCTGGGGCCCTTGCCCTTCCCGCAGGGAATGCCACGAGCTCGAAAAG	120	
DB	61	GCTTAGCCCGACGCTGGGGCCCTTGCCCTTCCCGCAGGGAATGCCACGAGCTCGAAAAG	120	
QY	121	CGACAGACACCCCACTCGGAGGGCTGGACGATGTTATTACTATTCTGTGGAGT	180	
DB	121	CGACAGACACCCCACTCGGAGGGCTGGACGATGTTATTACTATTCTGTGGAGT	180	
QY	181	GACGCTGAGCGCAGGCGACGATACCACTGGAAGCGCGACCTACGAGATCAGCTGG	240	
DB	181	GACGCTGAGCGCAGGCGACGATACCACTGGAAGCGCGACCTACGAGATCAGCTGG	240	
QY	241	GAGATGGCGGTAACTCGTGGTGAAAGGCTGGAACCCCGGCTGAACGCAAGAGCC	300	

Db	241	GGAGATGGCGGTACCTCGTCGGTGGAAAGGCGTGAACCCCGCCTGAACGCAAGAGCC	300
Qy	301	ATCCACTTTGAGGGTGTTTACCAAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGG	360
Db	301	ATCCACTTTGAGGGTGTTTACCAAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGG	360
Qy	361	ACCCGCAACCCGCTGTCGAGTATTACATCGTCGAGAACTTTGGCACTTATGATCCTTCC	420
Db	361	ACCCGCAACCCGCTGTCGAGTATTACATCGTCGAGAACTTTGGCACTTATGATCCTTCC	420
Qy	421	TCCGCTGCTACCGATCTAGGACTGTGAGTGCAGCGTAGCATCTATCGACTCGGCAAG	480
Db	421	TCCGCTGCTACCGATCTAGGACTGTGAGTGCAGCGTAGCATCTATCGACTCGGCAAG	480
Qy	481	ACCACTCGCGTCAACGACCTAGCATCGACGCGCAACCAACCTTGAACCAATACTGTGCG	540
Db	481	ACCACTCGCGTCAACGACCTAGCATCGACGCGCAACCAACCTTGAACCAATACTGTGCG	540
Qy	541	GTCCGCGAGGACAAGCGCAACGCGGTACCGTCCAGACGGGCTGCCACTTCAGCGCCTGG	600
Db	541	GTCCGCGAGGACAAGCGCAACGCGGTACCGTCCAGACGGGCTGCCACTTCAGCGCCTGG	600
Qy	601	GCTCGCGCTGTTTGAATGTCAACGGTGACCACTAATCAAGATCGTTGCAACGGAAGGC	660
Db	601	GCTCGCGCTGTTTGAATGTCAACGGTGACCACTAATCAAGATCGTTGCAACGGAAGGC	660
Qy	661	TACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAGACGTAACTTGG	720
Db	661	TACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAGACGTAACTTGG	720
Qy	721	TGCTGATCTCGCAGGCAACAGCAAGAAATGTCGTCAAGATGTGCCGTTGAAGTATTCA	780
Db	721	TGCTGATCTCGCAGGCAACAGCAAGAAATGTCGTCAAGATGTGCCGTTGAAGTATTCA	780
Qy	781	ATCAGCATATCTGTCTGCCCTTGCGAGTGATACCTTTGAGGAAGCTGTGGAAGCTTTGTGC	840
Db	781	ATCAGCATATCTGTCTGCCCTTGCGAGTGATACCTTTGAGGAAGCTGTGGAAGCTTTGTGC	840
Qy	841	GAGCCTGGCCAGGATCAGTAGTTCCTTTGCGGTGTTTGTCTCCCTATTCTCGTGAAGAAA	900
Db	841	GAGCCTGGCCAGGATCAGTAGTTCCTTTGCGGTGTTTGTCTCCCTATTCTCGTGAAGAAA	900
Qy	901	TTGTTATTGCTTCTGTTGTTAGTACATAGCCGAGCAATTGAGGCTCACGCTTGGGAA	960
Db	901	TTGTTATTGCTTCTGTTGTTAGTACATAGCCGAGCAATTGAGGCTCACGCTTGGGAA	960
Qy	961	AAAAAAAAAAAAAAAAAAAAA	983
Db	961	AAAAAAAAAAAAAAAAAAAAA	983

RESULT 2
AR157660
LOCUS AR157660 983 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6245546.
ACCESSION AR157660
VERSION AR157660.1 GI:16218623
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 983)
AUTHORS Hansen, P., Kamp,., Wagner, P., Mullertz, A. and Knap, I., Helmer.
TITLE Animal feed additives
JOURNAL Patent: US 6245546-A 1 12-JUN-2001;
FEATURES
source 1..983
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 983; DB 6; Length 983;

Best Local Similarity 100.0%; Pred. No. 7.8e-223;
Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TGGCCCCGACGTCTTCAATCCTTGACGTAGTGTCCGCTTTACCCCGCTGCCCCCTGGCG	60
Db	1	TGGCCCCGACGTCTTCAATCCTTGACGTAGTGTCCGCTTTACCCCGCTGCCCCCTGGCG	60
Qy	61	GCCTTAGCCCGGACTGGGGCCCTGGCCTTCCCGGACAGGAATGCGACGGAGCTCGAAAAG	120
Db	61	GCCTTAGCCCGGACTGGGGCCCTGGCCTTCCCGGACAGGAATGCGACGGAGCTCGAAAAG	120
Qy	121	CGACAGACAACCCCAACTCGGAGGGCTGGCAAGATGTTATTACTATTCTGTGTGAGT	180
Db	121	CGACAGACAACCCCAACTCGGAGGGCTGGCAAGATGTTATTACTATTCTGTGTGAGT	180
Qy	181	GACGGTGAGCGCAGGCCACGTACACCAACCTGGAAGCGGCACTACGAGATCAGCTGG	240
Db	181	GACGGTGAGCGCAGGCCACGTACACCAACCTGGAAGCGGCACTACGAGATCAGCTGG	240
Qy	241	GGAGATGGCGGTAACTCGTCGGTGGAAAAGGCTGAAACCCCGCCTGAACGCAAGAGCC	300
Db	241	GGAGATGGCGGTAACTCGTCGGTGGAAAAGGCTGAAACCCCGCCTGAACGCAAGAGCC	300
Qy	301	ATCCACTTTGAGGGTGTTTACCAAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGG	360
Db	301	ATCCACTTTGAGGGTGTTTACCAAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGG	360
Qy	361	ACCCGCAACCCGCTGCTGAGTATTACATCGTCGAGAACTTTGGSCACTATGATCCTTCC	420
Db	361	ACCCGCAACCCGCTGCTGAGTATTACATCGTCGAGAACTTTGGSCACTATGATCCTTCC	420
Qy	421	TCCGCTGCTACCGATCTAGGAAGTGTGAGTGCAGCGTAGCATCTATCGACTCGGCAAG	480
Db	421	TCCGCTGCTACCGATCTAGGAAGTGTGAGTGCAGCGTAGCATCTATCGACTCGGCAAG	480
Qy	481	ACCACTCGCGTCAACGCACTTAGCATCGACGGCAACCAACCTTGAACCAATACTGTGCG	540
Db	481	ACCACTCGCGTCAACGCACTTAGCATCGACGGCAACCAACCTTGAACCAATACTGTGCG	540
Qy	541	GTCCGCCAGGACAAGCGCAACAGCGGTACCGTCCAGACGGGCTGCCACTTCAGCGCCTGG	600
Db	541	GTCCGCCAGGACAAGCGCAACAGCGGTACCGTCCAGACGGGCTGCCACTTCAGCGCCTGG	600
Qy	601	GCTCGCGCTGTTTGAATGTCAACGGTGACCACTAATCAAGATCGTTGCAACGGAAGGC	660
Db	601	GCTCGCGCTGTTTGAATGTCAACGGTGACCACTAATCAAGATCGTTGCAACGGAAGGC	660
Qy	661	TACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAGACGTAACTTGG	720
Db	661	TACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAGACGTAACTTGG	720
Qy	721	TGCTGATCTCGCAGGCAACAGCAAGAAATGTCAGATGTGCCGCTTGAAGTATTCA	780
Db	721	TGCTGATCTCGCAGGCAACAGCAAGAAATGTCAGATGTGCCGCTTGAAGTATTCA	780
Qy	781	ATCAGCATATCTGTCTGCCCTTGCGAGTGATACCTTTGAGGAAGCTGTGGAAGCTTTGTGC	840
Db	781	ATCAGCATATCTGTCTGCCCTTGCGAGTGATACCTTTGAGGAAGCTGTGGAAGCTTTGTGC	840
Qy	841	GAGCCTGGCCAGGATCAGTAGTTCCTTTGCGGTGTTTGTCTCCCTATTCTCGTGAAGAAA	900
Db	841	GAGCCTGGCCAGGATCAGTAGTTCCTTTGCGGTGTTTGTCTCCCTATTCTCGTGAAGAAA	900
Qy	901	TTGTTATTGCTTCTGTTGTTAGTACATAGCCGAGCAATTGAGGCTCACGCTTGGGAA	960
Db	901	TTGTTATTGCTTCTGTTGTTAGTACATAGCCGAGCAATTGAGGCTCACGCTTGGGAA	960
Qy	961	AAAAAAAAAAAAAAAAAAAAA	983
Db	961	AAAAAAAAAAAAAAAAAAAAA	983

RESULT 3

TLU35436 TLU35436 2460 bp DNA linear PLN 15-NOV-2001
LOCUS Thermomyces lanuginosus endo-beta-1,4-D-xylanase precursor (xynA)
DEFINITION gene, complete cds.
ACCESSION U35436
VERSION U35436.1 GI:2737877
KEYWORDS
SOURCE Thermomyces lanuginosus
ORGANISM Thermomyces lanuginosus
REFERENCE 1 (bases 1 to 2460)
AUTHORS Schlachter,A., Holzmann,K., Hayn,M., Steiner,W. and Schwab,H.
TITLE Cloning and characterization of the gene for the thermostable
xylanase XynA from Thermomyces lanuginosus
JOURNAL J. Biotechnol. 49 (1-3), 211-218 (1996)
PUBMED 8879171
REFERENCE 2 (bases 1 to 2460)
AUTHORS Schlacher,A., Holzmann,K., Hayn,M., Steiner,W. and Schwab,H.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1995) Institute of Biotechnology, SFB
Biocatalysis, TU-Graz, Petersgasse 12, Graz 8010, Austria
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/strain="DSM 5826"
/db_xref="taxon:5541"
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969..976
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ORIGIN
Query Match 86.0%; Score 845.2; DB 15; Length 2460;
Best Local Similarity 89.8%; Pred. No. 4.7e-190;
Matches 963; Conservative 0; Mismatches 3; Indels 106; Gaps 1;
QY 1 TCGGCGCCGAGCTTGCAATCCTTGAGTGATGTCGGCTTTACCCCGTTGCCCTTGG 60
DB 1035 TCGGCGCCGAGCTTGCAATCCTTGAGTGATGTCGGCTTTACCCCGTTGCCCTTGG 1094
QY 61 GCCTTAGCCGCACTGGGGCCCTTGCCCGGACGGAATGCCACGAGCTGAAAAAG 120
DB 1095 GCCTTAGCCGCACTGGGGCCCTTGCCCGGACGGAATGCCACGAGCTGAAAAAG 1154
QY 121 CGACAGACAACCCCAACTCGAGGGCTGGCAGATGTTATTACTATTCTGTGAGT 180

DB 1155 CGACAGACAACCCCAACTCGAGGGCTGGCAGATGTTATTACTATTCTGTGAGT 1214
QY 181 GACGGTGAAGCGCAGGCCACGTACACCAACCTGGAAGCGGCACCTACGAGATCAGCTGG 240
DB 1215 GACGGTGAAGCGCAGGCCACGTACACCAACCTGGAAGCGGCACCTACGAGATCAGCTGG 1274
QY 241 GGAGATGGCGGTAACTCGTCGGTGAAGGGCTGGAACCCCGCCTGAACGA----- 294
DB 1275 GGAGATGGCGGTAACTCGTCGGTGAAGGGCTGGAACCCCGCCTGAACGAGGTAC 1334
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QY 315 TGTTTACCAAGCCAAACGGGACACAGCTACCTTGGCGTCAAGGTGGAACCCGCAACCCGCT 374
DB 1455 TGTTTACCAAGCCAAACGGGACACAGCTACCTTGGCGTCTACGGTTGGAACCCGCAACCCGCT 1514
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QY 435 TCTAGGAATGTGAGTGCAGCGGTAGCATCTATGCACTCGGCAAGACCACTCGGTCAA 494
DB 1575 TCTAGGAATGTGAGTGCAGCGGTAGCATCTATGCACTCGGCAAGACCACTCGGTCAA 1634
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QY 675 CTATGCTCGCATCACCGTGTGCTGACGTTGGGCTAAAGCTAACCTGTGTGATCTCGCGA 734
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QY 795 CTGCCCTTGCAGTGATACTTTGGAGGACTGTGAGAACTTTGTCGAGCCTGGCCAGGA 854
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QY 855 TCAGTAGTTGCTTTGCGGTTTGTCTCCCTATTCTCGTGAATAATTGTATTTGCTTGG 914
DB 1995 TCAGTAGTTGCTTTGCGGTTTGTCTCCCTATTCTCGTGAATAATTGTATTTGCTTGG 2054
QY 915 TTGTCTAGTGTACATAGCCGAGCAATTGAGGCTTCAGCCTTGGAATAAAAA 966
DB 2055 TTGTCTAGTGTACATAGCCGAGCAATTGAGGCTTCAGCCTTGGAATAATA 2106
RESULT 4
AX244978 588 bp DNA linear PAT 28-SEP-2001
LOCUS AX244978
DEFINITION Sequence 9 from Patent WO0166711.
ACCESSION AX244978
VERSION AX244978.1 GI:15859703
KEYWORDS
SOURCE Thermomyces lanuginosus
ORGANISM Thermomyces lanuginosus

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source
1	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomycetes.	Sibbesen, O. and Sorensen, J. F.	Xylanase variants having altered sensitivity to xylanase inhibitors	Patent: WO 0166711-A 9 13-SEP-2001;	DANISCO A/S (DK)
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				/mol_type="unassigned DNA"	
				/db_xref="taxon:5541"	
ORIGIN					
Query Match	59.5%;	Score 585;	DB 6;	length 588;	
Best Local Similarity	100.0%;	Pred. No. 3.3e-128;			
Matches 585;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	124	CAGACAACCCCACTCGAGGGCTGGCAGATGTTATTACTATTCTGTGGAGTGC	183		
DB	4	CAGACAACCCCACTCGAGGGCTGGCAGATGTTATTACTATTCTGTGGAGTGC	63		
QY	184	GGTGAGCGCAGGCCACGTACCAACTGGAAGCGGCACTTACGATCAGCTGGGA	243		
DB	64	GGTGAGCGCAGGCCACGTACCAACTGGAAGCGGCACTTACGATCAGCTGGGA	123		
QY	244	GATGCGGTAACTCTGTCGTGTAAGGGCTGGAAACCCGGCTGAACGCAAGCCATC	303		
DB	124	GATGCGGTAACTCTGTCGTGTAAGGGCTGGAAACCCGGCTGAACGCAAGCCATC	183		
QY	304	CACCTTGAAGGGTGTATACCAAGCCAAACGGCAACAGCTACTTGGCTCTACCGTTGACC	363		
DB	184	CACCTTGAAGGGTGTATACCAAGCCAAACGGCAACAGCTACTTGGCTCTACCGTTGACC	243		
QY	364	CGCAACCCGCTGTCGAGTATTACATGTCGAGAACTTTGGCACTTATGATCCTTCTCC	423		
DB	244	CGCAACCCGCTGTCGAGTATTACATGTCGAGAACTTTGGCACTTATGATCCTTCTCC	303		
QY	424	GGTGCTAACCGATCTAGGAACGTGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACC	483		
DB	304	GGTGCTAACCGATCTAGGAACGTGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACC	363		
QY	484	ACTGCGTCAACGCACCTAGCATGACGGCAACCCAAACCTTGCACCACTACTGTCGCTC	543		
DB	364	ACTGCGTCAACGCACCTAGCATGACGGCAACCCAAACCTTGCACCACTACTGTCGCTC	423		
QY	544	CGCCAGGACAAAGCGCACACCGGTAACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGCT	603		
DB	424	CGCCAGGACAAAGCGCACACCGGTAACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGCT	483		
QY	604	CGCGCTGTTTGAATGTCAACCGGTACCACTACTACAGATGTTGCCAAGGAGGCTAC	663		
DB	484	CGCGCTGTTTGAATGTCAACCGGTACCACTACTACAGATGTTGCCAAGGAGGCTAC	543		
QY	664	TTACAGACGGCTATGCTGCGATCAACCGTGTGCTGACGTGGGCTAA	708		
DB	544	TTACAGACGGCTATGCTGCGATCAACCGTGTGCTGACGTGGGCTAA	588		
RESULT 5					
LOCUS	BX842624	89019 bp	DNA	linear	PLN 17-APR-2005
DEFINITION	Neurospora crassa DNA linkage group I BAC clone B10D6.				
ACCESSION	BX842624				
VERSION	BX842624.1	GI:38566913			
KEYWORDS					
SOURCE	Neurospora crassa				
ORGANISM	Neurospora crassa				
REFERENCE	Schulte, U., Algn, V., Hoheisel, J., Brandt, P., Fartmann, B.,				
AUTHORS	Holland, R., Nyakatura, G., Mewes, H.W. and Mannhaupt, G.				
JOURNAL	Unpublished				

REFERENCE AUTHORS TITLE JOURNAL	COMMENT	FEATURES source
2 (bases 1 to 89019) German Neurospora genome,project. Direct Submission Submitted (26-NOV-2003) MIPS, Institut fuer Bioinformatik, GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail: G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, E-mail: ulrich.schulte@uni-duesseldorf.de BAC clone 10D6 (strain OR74A) is available at the Fungal Genetic Stock Center, http://www.fgsc.net Sequencing was performed by MWG Biotech AG, Ebersberg, Germany, http://www.mwgdna.com Information on performance of analysis and a more detailed annotation of this entry and other sequences can be viewed at: http://mips.gsf.de/proj/neurospora .	1. 89019 /organism="Neurospora crassa" /mol_type="genomic DNA" /db_xref="taxon:5141" /chromosome="I" 232. .2121 /gene="B10D6.010" complement(join(232. .1210,1265. .1881,1942. .2121)) /gene="B10D6.010" complement(join(232. .1210,1265. .1881,1942. .2121)) /gene="B10D6.010" /codon_start=1 /product="hypothetical protein" /protein_id="CAE76217.1" /db_xref="GI:38566914" /translation="MSFPFSLGFAPRSLTFPSSNVKAIATASIALSVKLLINAVA PSOADEEYGRGAPDQTAQDAELKHTSATSTDNSTADSMTDNKSDFTEVTPAKD IQLNKDVEISDDNDVIQGVNGTATADTEINIDTKEPCTSOHNDIQEIAIHAIPISTE KGIAHNNSNGVRSYRHGFVVDIVVEVETPSKQHSVRSCHSIPMBIIEVDVPSAQ ATVIASPIINSDKTAMPVDEEDTIISSDAAPNKKAEBAILHHAREESTATNPSSESKQT VNTESPSTVPGTPDVTDSVLEIDDAQVTPICTKLEENDVLTPTAVRTTIDHARS TWYDFSHLSPEQLDNLFTIIVIDRPNGVSYAQLSCGWWYRMDKEDNPVMTQEEYED LLAMPASFKKDKEDTKLPLPTIVLTDEEGNEFPABEIMYSVDAVEVNGLTPTNKEA EQQTQVKPITPTTVERIPSKWYLTNPSSESVDLATATVIDRPNGIAYVQPHGGL MYRLDEADNALMTQGEYEDLLAMPDSYKVKQEVKLPPVVLVTDEEGNEFLAEBDD MSFATYHGTVETQDSASEAIIITD" complement(232. .1210) /gene="B10D6.010" /number=1 complement(1211. .1264) /gene="B10D6.010" /number=1 complement(1265. .1881) /gene="B10D6.010" /number=2 complement(1882. .1941) /gene="B10D6.010" /number=2 complement(1942. .2121) /gene="B10D6.010" /number=3 2918. .4077 /gene="B10D6.020" complement(join(2918. .3032,3509. .3850,3914. .4077)) /gene="B10D6.020" complement(join(2918. .3032,3509. .3850,3914. .4077)) /gene="B10D6.020" /codon_start=1 /product="hypothetical protein" /protein_id="CAE76218.1" /db_xref="GI:38566915" /db_xref="UniProt/TREMBL:Q7SDC5" /translation="MANNPGKVGREGASETLNEQADIWVDKPVDKDWLNAPTDLDEB DLYSPQLVELSKLERFLDDLVPTTPRAPISWRLLIEHVITIKYIKIRKREKKK IFEAMVRETLGLDKDTSVDNTAYTNGVKLVEMTIQFALDVKLEMQRLSQSLAAGSS	

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QY	147	CTGCGACGATGGTTATTACTATTCTCGTTCGAGTGCACGCTGGAGCCGACGCATAC	206
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DEFINITION	Sequence 3 from patent US 5667990.		PAT 07-OCT-1997
ACCESSION	165436		

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VERSION      165436.1      GI:2482006
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ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 1123)
AUTHORS      Berka, R. Michael., Yoder, W., Takagi, S. and Boominathan, K. Chettier.
TITLE        Aspergillus expression system
JOURNAL      Patent: US 5667990-A 3 16-SEP-1997;
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ACCESSION	BD006885		linear
VERSION	BD006885.1	GI:18635256	
KEYWORDS	JP 2001025393-A/2.		
SOURCE	Humicola insolens		
ORGANISM	Humicola insolens		

REFERENCE 1 (bases 1 to 1123)
AUTHORS Berka,R.M., Yoder,W., Takagi,S. and Boominazan,C.C.
TITLE Aspergillus expression system
JOURNAL Patent: JP 2001025393-A 2 30-JAN-2001;
NOVO NORDISK BIOTECH INC

COMMENT OS Humicola insolens
PN JP 2001025393-A/2
PD 30-JAN-2001
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Query Match 24.3%; Score 239; DB 6; Length 1123;
Best Local Similarity 64.4%; Pred. No. 6.2e-46;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

OY 87 CTTCCCGCAGGGAATGCCAGAGCTGGAAGAAAGCAGACAGACACCCCACTCGAGGG 146
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ACCESSION AY156910
VERSION AY156910.1 GI:26514829
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REFERENCE 1 (bases 1 to 841)
AUTHORS Min,S.Y., Kim,B.G. and Ahn,J.-H.
TITLE Purification, Characterization, and cDNA Cloning of Xylanase from Fungus Trichoderma Strain SY
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 841)
AUTHORS Min,S.Y., Kim,B.G. and Ahn,J.-H.
TITLE Direct Submission
JOURNAL Submitted (30-SEP-2002) Forest and Environmental Science, Konkuk University, 1 Hwayang-Dong, Kwangjin-Gu, Seoul 143-701, South Korea

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CDS

ORIGIN

Query Match 23.7%; Score 232.6; DB 15; Length 841;
Best Local Similarity 60.2%; Pred. No. 2e-44;
Matches 404; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

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ORIGIN

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OY		222	C A C C T A C G A G A T C A G C T G E G G A G A T G G C G G T A A C C T C G T C G T G A A A G G S C T G A A C C C	281
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RESULT	13
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LOCUS	TW1012718
DEFINITION	Trichoderma viride mRNA for endo-1,4-beta-xylanase.
ACCESSION	AJ012718
VERSION	AJ012718.1 GI:6434132
	928 bp mRNA linear PLN 15-APR-2005

KEYWORDS	endo-1,4-beta-xylanase.
SOURCE	Trichoderma viride
ORGANISM	Trichoderma viride Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma; Trichoderma viride species complex.
REFERENCE	1
AUTHORS	Furman-Matarasso, N., Cohen, E. and Avni, A.
TITLE	Mutations in the Active Site of the Ethylene Inducing Xylanase Elicitor Inhibits the b-1-4-Endoxylanase Activity But Not the Elicitation Activity
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 928)
AUTHORS	Avni, A.
TITLE	Direct Submission
JOURNAL	Submitted (10-NOV-1998) Avni A., Plant Sciences, Tel-Aviv University, Tel-Aviv University, Tel-Aviv, 69978, ISRAEL
FEATURES	Location/Qualifiers
Source	1. .928

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RESULT 14	AK110604	LOCUS	DEFINITION
	AK110604	912 bp	mRNA linear PLN 24-JUL-2003
		Oryza sativa (japonica cultivar-group)	cdna clone:002-168-G08, full
		insert sequence.	

ACCESSION	AK110604
VERSION	AK110604.1
KEYWORDS	FLI_CDNA; oligo capping.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1
AUTHORS The Rice Full-length cDNA Consortium, National Institute of

Agrobiological Sciences Rice Full-length cDNA Project Team:
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shieniki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y.

TITLE	JOURNAL
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice	Science 301 (5631), 376-379 (2003)

**JOURNAL
PUBMED
REFERENCE
AUTHORS**

REFERENCE
AUTHORS

2 (bases 1 to 912)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,

Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, S., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ocomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akanura, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba,
305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
Tel: 81-29-838-7007, Fax: 81-29-838-7007)

COMMENT This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: http://cdna01.dna.affrc.go.jp/cDNA/NIRAS_Rice_Full-Length_cDNA_Project_Team/Kikuchi,S.,Satcho,K.,Nagata,T.,Kawagashira,N.,Doi,K.,Kishimoto,N.,Yazaki,J.,Ishikawa,M.,Yamada,H.,Ooka,H.,Hotta,I.,Kojima,K.,Namiki,T.,Ohmeda,E.,Yahagi,W.,Suzuki,K.,Li,C.,Ohtsuki,K.,Shishiki,T.and Yamamoto,M.

Fais Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, U., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Iu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nilkura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Oca, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES	Location/Qualifiers
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Best Local Similarity	62.8%;	Pred. No. 9.4e-40;		
Matches 365; Conservative	0;	Mismatches 210;	Indels 6;	Gaps 2;

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QY 232 ATCAGCTGGGAGATGCGGTAACTCGTGGTGAAAAGGCTGAACCCCGGCTGAAC 291
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:07:17 ; Search time 615.413 Seconds
(without alignments)
10645.530 Million cell updates/sec

Title: US-09-467-368-1

Perfect score: 983

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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	224.6	22.8	666	10	ABQ80362
8	223	22.7	705	10	ABQ80364
9	205	20.9	1195	2	AAZ28864
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21	187.8	19.1	1273	2	AAQ90388	Aa990388 Xylanase
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25	181.8	18.5	1281	2	AAT71585	Aat71585 Chaetomi
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ALIGNMENTS

RESULT 1	
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AC	AAAT40742;
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DT	21-MAY-1997 (first entry)
XX	
DE	Xylanase coding sequence.
XX	
KW	Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermoascus;
KW	Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia;
KW	Byssoschlamus; Paecilomyces; animal feed additive; in-vivo breakdown;
KW	plant cell wall; growth rate; feed conversion; BS.
XX	
OS	Thermomyces lanuginosus.
XX	
FH	Key
FT	CDS
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DR	WPI; 1996-454790/45.
DR	P-PSDB; AAWO1112.
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PT	Fungal xylanase preps. for use as animal feed additives - and DNA
PT	construct for producing recombinant Thermomyces xylanase.
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PS	Claim 5; Page 45-46; 69pp; English.
XX	

CC This sequence represents the coding sequence for the xylanase from
CC Thermomyces lanuginosus strain DSM 4109. The encoded xylanase, and
CC xylanases derived from Humicola, Thermoascus, Chaetomium, Mucor,
CC Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssoschlamus or
CC Paecilomyces strains can be used in the monocomponent xylanase
CC preparations of the invention. The xylanase preparations and the
CC recombinant Thermomyces xylanase are useful as animal feed additives,
CC which promote in-vivo breakdown of plant cell wall material and thus
CC improve digestibility, growth rate and/or feed conversion
XX
SQ Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 983; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 5.1e-255;
Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGCCCCGACGCTTGTGCAATCCTTGACGATGATGGTGGCTTTACCCCGTTGCCCTTGGC 60
DB 1 TCGGCCCGACGCTTGTGCAATCCTTGACGATGATGGTGGCTTTACCCCGTTGCCCTTGGC 60
QY 61 GCCTTAGCCGCGACTGGGGCCCTTCCCGGACGGGAATGCCACGGAGCTGAAAAAG 120
DB 61 GCCTTAGCCGCGACTGGGGCCCTTCCCGGACGGGAATGCCACGGAGCTGAAAAAG 120
QY 121 CGACAGACAACCCCACTCGGAGGCTGGCAGCATGTTATTACTATTCTGCTGGAGT 180
DB 121 CGACAGACAACCCCACTCGGAGGCTGGCAGCATGTTATTACTATTCTGCTGGAGT 180
QY 181 GACGGTGAAGCGCAGGCCACGTACCAACCTGGAAGCGGCACCTACGAGATCAGCTGG 240
DB 181 GACGGTGAAGCGCAGGCCACGTACCAACCTGGAAGCGGCACCTACGAGATCAGCTGG 240
QY 241 GGAGATGGCGGTAACTCTGTCGGTGAAGAGGGCTGGAACCCCGGCTGAACCGAAGCC 300
DB 241 GGAGATGGCGGTAACTCTGTCGGTGAAGAGGGCTGGAACCCCGGCTGAACCGAAGCC 300
QY 301 ATCCACTTTGAGGGGTGTTTACCGACCAACGGCAACAGCTTCTGCGGTCTACGGTTGG 360
DB 301 ATCCACTTTGAGGGGTGTTTACCGACCAACGGCAACAGCTTCTGCGGTCTACGGTTGG 360
QY 361 ACCCGCAACCCGCTGTGAGTATTATCATCTGTGAGAACTTTGGACCTATGATCCTTCC 420
DB 361 ACCCGCAACCCGCTGTGAGTATTATCATCTGTGAGAACTTTGGACCTATGATCCTTCC 420
QY 421 TCCGGTGTACCGATCTAGAACTGTGAGTGCAGCGGTAGCATCTATGACTCGGCAAG 480
DB 421 TCCGGTGTACCGATCTAGAACTGTGAGTGCAGCGGTAGCATCTATGACTCGGCAAG 480
QY 481 ACCACTCGCTCAACGCACCTAGCATGACGGCACCCCAACCTTGACCAATATGCTGC 540
DB 481 ACCACTCGCTCAACGCACCTAGCATGACGGCACCCCAACCTTGACCAATATGCTGC 540
QY 541 GTCCGCCAGGACAAGCGCACCAAGCGGTACCGTCCAGACGGGCTGCCACTTGACGCTTGG 600
DB 541 GTCCGCCAGGACAAGCGCACCAAGCGGTACCGTCCAGACGGGCTGCCACTTGACGCTTGG 600
QY 601 GCTCGCGCTGGTTGAATGTCAACGCTGACCACTACTACAGATCGTTGCAACGGAGGGC 660
DB 601 GCTCGCGCTGGTTGAATGTCAACGCTGACCACTACTACAGATCGTTGCAACGGAGGGC 660
QY 661 TACTTCAGACGGCTATGCTCGCATCAACCGTTGCTGACGTGGCTTAAGACGTAACCTGG 720
DB 661 TACTTCAGACGGCTATGCTCGCATCAACCGTTGCTGACGTGGCTTAAGACGTAACCTGG 720
QY 721 TGGTATCTCGCAGGCAACAGCCCAAGATGTCTCAGATGTCCGGTTGAAGTATTCA 780
DB 721 TGGTATCTCGCAGGCAACAGCCCAAGATGTCTCAGATGTCCGGTTGAAGTATTCA 780
QY 781 ATCAGCATATCTGTCTGCCCTTGCGAGTGAATACTTTGAGGACTGTGGAACCTTTGTGC 840
DB 781 ATCAGCATATCTGTCTGCCCTTGCGAGTGAATACTTTGAGGACTGTGGAACCTTTGTGC 840
QY 841 GAGCCTGGCCAGGATCAGTAGTGTGCTTGGCGGTGTTTGTCTCCTATTCTCGTGAAAAA 900

DB 841 GAGCCTGGCCAGGATCAGTAGTGTGCTTGGCGGTGTTTGTCTCCCTATTCTCGTGAAAAA 900
QY 901 TTGTTATTGCTTCTGTTGTCTAGTGATACATAGCCGACATTTGAGGCTCAGCTTGGAA 960
DB 901 TTGTTATTGCTTCTGTTGTCTAGTGATACATAGCCGACATTTGAGGCTCAGCTTGGAA 960
QY 961 AAAAAAAAAAAAAAAAAAAAAA 983
DB 961 AAAAAAAAAAAAAAAAAAAAAA 983

RESULT 2
AAT43010
ID AAT43010 standard; cDNA; 983 BP.
XX
AC AAT43010;
XX
DT 16-OCT-2003 (revised)
DT 22-FEB-1997 (first entry)
XX
DE Endo-1,4-beta-D-xylanase gene.
XX
KW Endo-1,4-beta-D-xylanase; xylanase; Thermomyces lanuginosus;
KW Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae; yeast;
KW flour; baking; dough; ss.
XX
OS Thermomyces lanuginosus; (strain DSM 4109).
XX
FH Key Location/Qualifiers
FT 5'UTR 1..30
FT CDS /*tag= a
FT 31..708
FT /product= "Endo-1,4-beta-D-xylanase"
FT /note= "EC-3.2.1.8"
FT 709..983
FT 3'UTR /*tag= c
XX
PN WO9632472-A1.
XX
PD 17-OCT-1996.
XX
PF 11-APR-1996; 96WO-DK000171.
XX
PR 11-APR-1995; 95DK-00000435.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Jorgensen OB, Si JQ, Jakobsen TS;
XX
DR WPI; 1996-477123/47.
XX
DR P-PSDB; AAM05187.
XX
PT Bread improving additive contg. xylanase from Thermomyces - and opt.
PT alpha-amylase, increases volume, improves anti-staling properties etc.
XX
PS Claim 7; Page 30-31; 41pp; English.
XX

CC The sequence encodes an endo-1,4-beta-D-xylanase from Thermomyces
CC lanuginosus (Humicola lanuginosa), which may be used as a bread-
CC improving additive. The enzyme may be expressed recombinantly from a
CC plasmid pYES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed),
CC and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour,
CC optionally along with other enzymes (amylase, maltogenase, lipase,
CC cellulase, hemicellulase, pentosanase, glucose-oxidase, laccase,
CC protease and/or peroxidase). The enzyme combines particularly well with
CC amylolytic enzymes, and may be used to improve baking properties of flour
CC and/or dough, by increasing volume and improving texture, flavour, crumb
CC softness, freshness and anti-staling properties, while improving dough
CC machinability and stability. (Updated on 16-OCT-2003 to standardise OS
CC field)
XX

SQ Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 983; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 5.1e-255;
Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGCCCCGACGTCTTGCAATCCTTGAGTGTGTCGGCTTACCCCGTTGCCCTTGGC 60
DB 1 TCGGCCCGACGCTTGCAATCCTTGAGTGTGTCGGCTTACCCCGTTGCCCTTGGC 60
QY 61 GCCTTAGCCCGCACTGGGGCCCTGGCTTCCCGGCAAGGAATGCCAGAGCTCGAAAAAG 120
DB 61 GCCTTAGCCCGCACTGGGGCCCTGGCTTCCCGGCAAGGAATGCCAGAGCTCGAAAAAG 120
QY 121 CGACAGAACACCCCACTCGGAGGCTGGCACGATGGTTATTACTATTCTCGTGGAGAGT 180
DB 121 CGACAGAACACCCCACTCGGAGGCTGGCACGATGGTTATTACTATTCTCGTGGAGAGT 180
QY 181 GACGGTGAAGCGCAGCGCACGTAACAACCTGMAAGCGGCACTACGAGATCAGCTGG 240
DB 181 GACGGTGAAGCGCAGCGCACGTAACAACCTGMAAGCGGCACTACGAGATCAGCTGG 240
QY 241 GAGATGCGCGGTAACTCGTCGGTGAAGGGCTGMAACCCCGCTGAACGCAAGAGCC 300
DB 241 GAGATGCGCGGTAACTCGTCGGTGAAGGGCTGMAACCCCGCTGAACGCAAGAGCC 300
QY 301 ATGCACCTTGAGGGGTGTTACCAAGCAACGGCAACAGTACCTTGCGGTCTACCGTTGG 360
DB 301 ATGCACCTTGAGGGGTGTTACCAAGCAACGGCAACAGTACCTTGCGGTCTACCGTTGG 360
QY 361 ACCCGCAACCCCGCTGTCGAGTATTAATCGTCGAACTTTGGCACTATGATCCTTCC 420
DB 361 ACCCGCAACCCCGCTGTCGAGTATTAATCGTCGAACTTTGGCACTATGATCCTTCC 420
QY 421 TCCGGTGTACCGATCTAGGAAGTGTGAGTGCAGCGGTAGCATCTATCGACTGGCAAG 480
DB 421 TCCGGTGTACCGATCTAGGAAGTGTGAGTGCAGCGGTAGCATCTATCGACTGGCAAG 480
QY 481 ACCACTCGCGTCAACGCACTAGCATCGACGGCAACCAACCTTGACCAATATCTGTCG 540
DB 481 ACCACTCGCGTCAACGCACTAGCATCGACGGCAACCAACCTTGACCAATATCTGTCG 540
QY 541 GTCCGCGAGGACAAGCGCACCGGTACCGTCCAGACGGGCTGCCACTTCCAGCGCTGG 600
DB 541 GTCCGCGAGGACAAGCGCACCGGTACCGTCCAGACGGGCTGCCACTTCCAGCGCTGG 600
QY 601 GCTCGCGCTGTTGAATGTCAACGGGTGACCACTACTACAGATCGTTGCAACGGAGGGC 660
DB 601 GCTCGCGCTGTTGAATGTCAACGGGTGACCACTACTACAGATCGTTGCAACGGAGGGC 660
QY 661 TACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGAGCTGGGCTAAGACGTAACTGG 720
DB 661 TACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGAGCTGGGCTAAGACGTAACTGG 720
QY 721 TGGTGAATCTCGGAGGCAACGCAAGATGTGTGATGTGCCGTTGAAGGTATTCA 780
DB 721 TGGTGAATCTCGGAGGCAACGCAAGATGTGTGATGTGCCGTTGAAGGTATTCA 780
QY 781 ATCAGCATATCTGTCTGCCCTTGCGAGTGATACTTTGAGGAAGTGTGAGAACTTTGTGC 840
DB 781 ATCAGCATATCTGTCTGCCCTTGCGAGTGATACTTTGAGGAAGTGTGAGAACTTTGTGC 840
QY 841 GAGCCTGGCCAGGATCAGTAGTTGCTTTGCGGTGTTTGTCTCCCTATTCTCGTGAATAAA 900
DB 841 GAGCCTGGCCAGGATCAGTAGTTGCTTTGCGGTGTTTGTCTCCCTATTCTCGTGAATAAA 900
QY 901 TTGTTATGCTTCTGTTCTAGTGAATAGCCGAGCAATTGAGGCTCACGCTTGGGAA 960
DB 901 TTGTTATGCTTCTGTTCTAGTGAATAGCCGAGCAATTGAGGCTCACGCTTGGGAA 960
QY 961 AAAAAAAAAAAAAAAAAAAAAA 983
DB 961 AAAAAAAAAAAAAAAAAAAAAA 983

RESULT 3
AAS13813
ID AAS13813 standard; DNA; 588 BP.

XX AAS13813;
AC AAS13813;
XX 18-DEC-2001 (first entry)
DT 18-DEC-2001 (first entry)
XX DNA encoding Thermomyces lanuginosus xylanase A.
DE Xylanase A; plant cell wall; baking; cereal; starch production; wood;
KW wood pulp bleaching; hemicellulose; arabinoxylan; foodstuff; bread; ds.
XX Thermomyces lanuginosus.
OS
XX WO200166711-A1.
PN
XX 13-SEP-2001.
PD 13-SEP-2001.
XX 08-MAR-2001; 2001WO-IB000426.
PF 08-MAR-2001; 2001WO-IB000426.
XX 08-MAR-2000; 2000GB-00005585.
PR 08-MAR-2000; 2000GB-00005585.
XX 27-JUN-2000; 2000GB-00015751.
XX (DANI-) DANISCO AS.
PA (DANI-) DANISCO AS.
XX Sibbensen O, Sorensen JF;
PI Sibbensen O, Sorensen JF;
XX WPI; 2001-596834/67.
XX
XX Novel variant xylanase polypeptide or its fragment useful for degrading
PT or modifying plant cell wall, comprises amino acid modifications such
PT that the polypeptide has altered sensitivity to xylanase inhibitor.
XX
XX Disclosure; Page 64; 70pp; English.
XX
XX The invention relates to a variant xylanase polypeptide (I) or its
XX fragment having xylanase activity, comprising one or more amino acid
XX modifications such that (I) or its fragment has an altered sensitivity to
XX a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or
XX its coding sequence (II) is useful for degrading or modifying plant cell
XX wall or for processing a plant material by contacting the plant cell wall
XX or plant material with (I) or (II). (I) is useful for modifying plant
XX materials, and in baking, processing cereals, starch production,
XX processing wood and enhancing the bleaching of wood pulp. (I) is useful
XX for altering the viscosity derived from the presence of hemicellulose or
XX arabinoxylan in a solution or system comprising plant cell wall material.
XX (I) is useful for preparing a foodstuff such as bread, pretzels,
XX tortillas, cakes, cookies, biscuits or crackers. The present sequence
XX represents the coding sequence of Thermomyces lanuginosus xylanase A as
XX described in the method of the invention.
XX
SQ Sequence 588 BP; 131 A; 178 C; 168 G; 111 T; 0 U; 0 Other;

Query Match 59.5%; Score 585; DB 5; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 CAGACAAACCCCACTCGAGGGCTGGACGATGTTATTACTATTCTGCTGAGTGAC 183
DB 4 CAGACAAACCCCACTCGAGGGCTGGACGATGTTATTACTATTCTGCTGAGTGAC 63
QY 184 GGTGAGCGCAGGCGCACGTAACAACCTGGAAGCGGCACTACGAGATCAGCTGGGA 243
DB 64 GGTGAGCGCAGGCGCACGTAACAACCTGGAAGCGGCACTACGAGATCAGCTGGGA 123
QY 244 GATGCGGTAACTCGTCGGTGAAGAGGCTGGAACCCCGCTGAACGCAAGACCATC 303
DB 124 GATGCGGTAACTCGTCGGTGAAGAGGCTGGAACCCCGCTGAACGCAAGACCATC 183
QY 304 CACTTGAGGGGTGTTACCAAGCAACGCAACAGCTACCTTGCGTACGGTTGACC 363

FH Key Location/Qualifiers
FT CDS 126..809
/*tag= a
XX PN WO9515390-A1.
XX PD 08-JUN-1995.
XX PF 29-NOV-1994; 94WO-US013612.
XX PR 01-DEC-1993; 93US-00160591.
XX PA (NOVO) NOVO NORDISK BIOTECH INC.
XX PI Berka RM, Yoder W, Takagi S, Boomnathan K;
XX DR WPI, 1995-215270/28.
XX DR P-PSDB; AAR75421.
XX PT Aspergillus foetidus cells expressing heterologous enzyme - partic.
XX PT fungal lipase or xylanase, provide high yields without significant prodn.
XX PT of protease or mycotoxin.
XX PS Disclosure; Page 35-36; 47pp; English.
XX CC A DNA fragment (AAQ74098) encoding H. insolens xylanase (AAR75421) was
XX CC isolated from PYES (DSM 6995) and inserted into pHD414 (contg. the TAKA
XX CC promoter and AMG terminator) to form pAXX40-1-1-1. This plasmid and
XX CC pJal77 (impairing hygromycin B resistance) were used to transform
XX CC protoplasts of A. foetidus NO953. The xylanase yield was 0.12 g/l.
XX CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
XX CC correct OS field.)
SQ Sequence 1123 BP; 249 A; 342 C; 293 G; 239 T; 0 U; 0 Other;

Query Match 24.3%; Score 239; DB 2; Length 1123;
Best Local Similarity 64.4%; Pred. No. 5.4e-54;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

OY 87 CTTCCCGGCGAAGGATGCCACGAGCTCGAAAAGCGACAGCAACCCCACTCGAGGG 146
DB 197 CGTTCCTCGGAGCAACTCGACGGCCCTTCAGGCTCGACAGGTGACCCCAACGGCGAGGG 256
OY 147 CTGGCAGATGGTTATTACTATTCTGTGTGAGTGACGGTGGAGCGACGACCTAC 206
DB 257 CTGGCAACAAGGCTACTTCTACTCGGTGGTCCGACGGCGAGAGCCAGGTTCACTAC 316
OY 207 CAACCTGGAAGCGCGACCTACGAGATCAGCTGGGAGATGGCGGTAACTCGTCGGTGG 266
DB 317 CAACCTCGAGGGCAGCCGCTACCAAGTCAGATGGCGTAACCCGCAACTTCGTGCGTGG 376
OY 267 AAAGGCTGGAACCCCGCCTGAACGCAAGACCATCCACTTTGAGGGTGTACAGCC 326
DB 377 TAAAGGTTGGAACCCGGG--AAACCGCCGCAAGATCACTACGGCGGCTACTTCAACCC 433
OY 327 AAACGGCAACGCTACCTTGGCGGTCTACGGTTGACCCGCAACCCGCTGTGAGTATTA 386
DB 434 CCAGGGCAAGGCTACCTGACCGCTTACGGCTGACCCGCAACCCGCTGTGAGTACTA 493
OY 387 CATCGTCGAGAATTGTCACCTATGATCTCGGCAAGACCACTCGCGTCAACGCACTAGCAT 446
DB 494 TGTATCATGAGTCGTACGACGATCAATCCCGCAGCGACGCTCAGTACAAGGCGACATT 553
OY 447 CGAGTGCAGCGGTAGCATCTATGATCGGCAAGACCACTCGCGTCAACGCACTAGCAT 506
DB 554 CTATACCGAGCGCGATCAGTATGACATCTTGTGAGCAACCGCTACAACCAAGCCAGCAT 613
OY 507 CGACGGCAACCAAACTTCGACCAATACTGTGCGTCCGCGAGGAGCAAGCCGCAAGCGG 566
DB 614 CGACGGCAACCGGAGCGTTCAGCAGTACTGTCTATCCGCAAGAAAGCGGTGCGAGG 673
OY 567 TACCGTCCAGACGGGCTGCCACTTTCAGCGCCTGGGCTCGCGCTGTTGAATGTCAACGG 626

DB 674 CTGGTCAACATGCAGAACCACTTCAACGCGTGGCAGCAGCAAGGATGCCGT---CGG 730
OY 627 TGACCACTACTACAGATCGTTGCAACGGAGGCTACTTCAAGCAGCGCTATGCTGCAT 686
DB 731 CCAGCACTACTACCAAGGTGTCGCGCACCGAGGCTACCAAGACAGTGGCGAGTCCGACAT 790
OY 687 CACCGTT 693
DB 791 CTATGTT 797

RESULT 6

AAQ94952
ID AAQ94952 standard; DNA; 1123 BP.
XX AC AAQ94952;
XX DT 25-MAR-2003 (revised)
XX DT 02-DEC-1995 (first entry)
XX DE Humicola insolens xylanase.
XX KM Xylanase; DSM 6995; ss.
XX OS Humicola insolens.
XX FH Key Location/Qualifiers
FT CDS 126..806
FT /*tag= a

PN WO9515391-A2.
XX PD 08-JUN-1995.
XX PF 29-NOV-1994; 94WO-US013613.
XX PR 01-DEC-1993; 93US-00161675.
XX PA (NOVO) NOVO NORDISK BIOTECH INC.

PI Berka RM, Yoder W, Takagi S, Boomnathan K;
XX DR WPI; 1995-215271/28.
XX DR P-PSDB; AAR78231.
XX PT Aspergillus japonicus-type cells expressing heterologous protein - esp.
XX PT fungal enzyme, provide high yields without significant prodn. of protease
XX PT or mycotoxin.
XX PS Example; Page 39-40; 50pp; English.

XX CC A strain of B. coli contg. the approx. 1,100 bp xylanase HindIII/ XbaI
XX CC cDNA fragment in PYES is deposited in DSM as DSM 6995. The xylanase cDNA
XX CC fragment is isolated from one of the clones. The sequence of the xylanase
XX CC gene and protein are given in AAQ94952 and AAR78231 and the gene is
XX CC deposited as DSM 6995. (Updated on 25-MAR-2003 to correct PN field.)
SQ Sequence 1123 BP; 249 A; 342 C; 293 G; 239 T; 0 U; 0 Other;

Query Match 24.3%; Score 239; DB 2; Length 1123;
Best Local Similarity 64.4%; Pred. No. 5.4e-54;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

OY 87 CTTCCCGGCGAAGGATGCCACGGAAGCTCGAAAAGCGACAGCAACCCCACTCGAGGG 146
DB 197 CGTTCCTCGGAGCAACTCGACGGCCCTTCAGGCTCGACAGGTGACCCCAACGGCGAGGG 256
OY 147 CTGGCAGATGGTTATTACTATTCTGTGTGAGTGAACGGTGGAGCGCAAGCCAGCTACAC 206
DB 257 CTGGCAACAAGGCTACTTCTACTCGTGTGTGTCGACGCGGAGGCGCAAGTTCACTAC 316
OY 207 CAACCTGGAAGGCGGACCTTACGAGATCAGCTGGGAGATGGCGGTAACTCGTGGTGG 266

Db 317 CAACCTCGAGGGGACGCCGCTTACCAAGTCAGATGGCGGTAAACCCGGCAACTTCGTCGGTGG 376
Qy 267 AAAGGGCTGGAAACCCCGGCTTGAACGAAGCCATCCATTGGAGGTGTTTACCAGCC 326
Db 377 TAAAGGTTGGAACCCGGG--AAACGGCCGACGATCACTACGGCGGCTACTTCAACCC 433
Qy 327 AAACGGCAACAGCTACCTTGGCGGTCTACGGTTGACCCGCAACCCGCTGTGAGTATTTA 386
Db 434 CCAGGGCAACGGCTACCTGGCCGTCTACGGCTGACCCGCAACCCGCTGTGAGTACTTA 493
Qy 387 CATCGTCGAGAATTGTCACCTATGATCTTCTCCGGTGTCTACCGATCTAGGAATGT 446
Db 494 TGTCACTGAGTGTGACGCGACGTACATCCCGCAGCGAGGCTCAGTACAAGGGCACAATT 553
Qy 447 CGAGTCCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACTAGCAT 506
Db 554 CTATATCCGACGGCGATCAGTATGACATCTTTGTGAGCACCCGCTTACAACCAAGCCAGCAT 613
Qy 507 CGACGGCAACCAACCTTCGACCAATACTGTGTCGGTCCGCCAGGACCAAGCCGACAGCCG 566
Db 614 CGACGGCACCCGGACGTTCCAGCAGTACTGTCTATCCGCAAGAACAAAGCCGTGCGAAG 673
Qy 567 TACCGTCAGACGGGCTGCGCACTTCGACGCGCTGGGCTCGGCTGTTGAATGTCAACGG 626
Db 674 CTGGTCAACATGACGAACCACTTCAACGCGTGGCAGACGACGGAATGCCGT--CGG 730
Qy 627 TGACCACTACTACAGATCGTTGCAACGGAAGGCTACTTCAGCAGCGGCTATGCTGCAT 686
Db 731 CCAGCACTACTACAGTGTGTCGCCACCGAGGCTACCAAGACAGTGGCGAGTCCGACAT 790
Qy 687 CACCGTT 693
Db 791 CTATGTT 797

RESULT 7
ABQ80362
ID ABQ80362 standard; cDNA; 666 BP.
XX
AC ABQ80362;
XX
DT 11-AUG-2003 (first entry)
XX
DE A. fumigatus AfXYL1 cDNA.
XX
KW Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KW glyceride; starch; maltodextrin; oxidated phenolic compound;
KW polygalacturonic acid chain; xylan; xyloligomer; food; feed; beverage;
KW textile; tea liquor; cleaning ability; ss.

XX Aspergillus fumigatus.
XX
FH Key Location/Qualifiers
FT CDS 1..666
FT /*tag= a
FT /product= "Xylanase 1"
XX
PN WO2003012071-A2.
XX
PD 13-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024842.
XX
PR 03-AUG-2001; 2001US-0309870P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Jiang B, Storms R, Roemer T, Busshey H;
XX
DR WPI; 2003-332729/31.

DR P-PSDB; ABB80185.
XX
PT Novel isolated Aspergillus fumigatus polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.
XX
PS Claim 2; Page 163-64; 169pp; English.

CC The sequences given in ABQ80319-66 encode enzymatic proteins derived from
CC A. fumigatus. The resulting proteins display the catalytic activity of an
CC enzyme such as tannase, cellulase, glucose oxidase, glucoamylase,
CC phytase, beta-galactosidase, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidases are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrase or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylases are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC laccase are useful for modulating the amount of oxidated phenolic
CC compounds in a composition. Compositions comprising polygalacturonases
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanases are useful for modulating the amount of xylan or xyloligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A.fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers
CC for attachment to a nucleic acid array for examination of expression
CC patterns, and to raise anti-protein antibodies. The polypeptide having
CC tannase activity increases the yield of tea liquor from tea leaves,
CC improves the colour, flavour and health benefits of tea products,
CC particularly an instant tea product. The polypeptide having cellulase
CC activity enhances cleaning ability of detergent compositions

XX
SQ Sequence 666 BP; 142 A; 199 C; 192 G; 133 T; 0 U; 0 Other;

Query Match 22.8%; Score 224.6; DB 10; Length 666;
Best Local Similarity 61.5%; Pred. No. 3.4e-50;
Matches 413; Conservative 0; Mismatches 249; Indels 9; Gaps 3;

Qy 31 ATGTCGCTTACCCCGTTGCCCTTGCGGCTTAGCCGCGACTGGGGCCCTGGCCTTC 90
Db 1 ATGTCATATTCTTCTCTCGTTCTGCTGCCCTCCACCGTTGCTGGCGTACTACCA 60
Qy 91 CCGG--CAGGAATGCCAGGAGCTCGAAAAGCGACAGACAACCCCAACTCGAGGGC 147
Db 61 CCGGCTCGGAGCATATAGTTAGCTAGCCAAAGCGGAGCTCACAGCTCTCAGACTGGC 120
Qy 148 TGGCAGATGTTATTACTATTCCTGTGAGTGAAGGTGGAAGCGACAGCTACACC 207
Db 121 ACGAATAACGGCTACTACTACTCTTCTGACCGACGGCGGCGGCAAGTACCTACACC 180
Qy 208 AACCTGGAAGCGGACCTTACGAGATCACTGGGGAGATGGCGGTAACTCGTGGTGA 267
Db 181 AACGGCAATGGCGGCGCAATATCAGGTGACTGGAACAACCTGCGGCACTTTGTGCTGGG 240
Qy 268 AAGGCTGGAACCCCGGCTGAAAGCAAGCCATTCATTGAGGGTGTATTACAGCCA 327
Db 241 AAGGCTGGAACCCGGCC--AGCGAAGAAAGCGGTCACTTACAGCGGCTCTGGGAGACC 297

QY 328 AACGGCAACAGCTACCTTGCGGTCTACGGTTGGACCCGCAACCCGCTGCTCGATATTAC 387
DB 298 AGCGMAACGGCTAAGCTCTCCGTTACGGCTGGACGACAGTCGCTGGTGAATTCTAC 357
QY 388 ATCGTCGAACTTTGGCACTATGATCTTCTCCGCTGCTACCGATAGAACTGTC 447
DB 358 ATCGTGAGAGTTACGGCTCTATGACCCCTCCACGGAGCCACCATCTCGCACCGTC 417
QY 448 GAGTCGACGGTAGCATCTATGACTCGGCAAGACCACTCGGTCACAGCACTAGCATC 507
DB 418 GAGAGCGACGGGCCACGTACACCTCTACAGACGACGGGACGAATGCGCCGTCCATC 477
QY 508 GACGGCACCCAACTTCGACCAATAGTGGTCCGCCAGGACAAGCGCACCGCGT 567
DB 478 CAGGGCACGGCTACTTTTGACCAAGTACTGCTCGGTTCCGACTTCGCAACCGGACAGTGA 537
QY 568 ACCGTCGACGCGGCTGCCACTTGCAGCGCTGGGCTCGCGCTGTTGAATGTCAACGCT 627
DB 538 ACTGTACGACGAGAAACCACTTGATGCGTGAGAAATGCGGCTCTCAATT--GGGG 594
QY 628 GACCACTACTACGATCGTTGCAACGAGGGCTACTTACAGACGCGCTATGCTCGCATC 687
DB 595 AACTTGACTATATGATTGTTGCGACGAGGGGTACCAAGACGCGCTCTGCTACTATC 654
QY 688 ACCGTTGCTGA 698
DB 655 ACTGTTCTTA 665

RESULT 8

ABQ80364 ID ABQ80364 standard; cDNA; 705 BP.

AC ABQ80364;

DT 11-AUG-2003 (first entry)

DE A. fumigatus AfXYL2 cDNA.

KM Gene, enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
KM beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KM polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KM glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KM glyceride; starch; maltodextrin; oxidated phenolic compound;
KM polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
KM textile; tea liquor; cleaning ability; ss.

XX Aspergillus fumigatus.

XX Key Location/Qualifiers

FT CDS 1..705

FT /*tag= a

PN WO2003012071-A2.

PD 13-FEB-2003.

PF 05-AUG-2002; 2002WO-US024842.

PR 03-AUG-2001; 2001US-0309870P.

PA (ELIT-) ELITRA PHARM INC.

PI Jlang B, Storms R, Roemer T, Bussey H;

DR WPI, 2003-332729/31.

DR P-PSDB, ABB80186.

PT Novel isolated Aspergillus fumigatus polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.

PS Claim 2; Page 165-66; 169pp; English.

XX The sequences given in ABQ80319-66 encode enzymatic proteins derived from
CC A. fumigatus. The resulting proteins display the catalytic activity of an
CC enzyme such as tannase, cellulase, glucose oxidase, glucoamylase,
CC phytase, beta-galactosidase, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds comprising cellulase are
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidase are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrase or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylases are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC laccase are useful for modulating the amount of oxidated phenolic
CC compounds in a composition. Compositions comprising polygalacturonases
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A.fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers
CC for attachment to a nucleic acid array for examination of expression
CC patterns, and to raise anti-protein antibodies. The polypeptide having
CC tannase activity increases the yield of tea liquor from tea leaves,
CC improves the colour, flavour and health benefits of tea products,
CC particularly an instant tea product. The polypeptide having cellulase
CC activity enhances cleaning ability of detergent compositions

XX SQ Sequence 705 BP; 151 A; 227 C; 183 G; 144 T; 0 U; 0 Other;

Query Match 22.7%; Score 223; DB 10; Length 705;
Best Local Similarity 60.5%; Pred. No. 9.4e-50;
Matches 411; Conservative 0; Mismatches 250; Indels 18; Gaps 2;

QY 29 TGATGTCGCTTTACCCCGTTGCCCTTGCGGCTTAAGCCGCACTGGGCGCTGGCCT 88
DB 23 TGCTGGCGTCTCCGCCATGAGCTCTGCTGCCCGCTCGAACCCGAGCACTCGT 82
QY 89 TCCCGGCAAGGAAATGCAACGAGCTCGAAAAGCGACAGCAACCCCACTCGAGGGCT 148
DB 83 TCAATGAGACTGCTCTTCATGAGTTGCTGAGCGCGCGCGCAACCCCAAGCTCCACGGCT 142
QY 149 GGCACGATGTTATTACTATTCTGTTGAGTGAAGTGAAGCGGAGGCCACGTACACCA 208
DB 143 GGAACAAGGCTACTACTACTCTTCTGACTGATGCGCGCGGAGGTGACTACACCA 202
QY 209 ACCTGAGGCGGCACTACGATCAGCTGGGAGATGGCGGTAACTCGTGGTGA 268
DB 203 ATGGCGCGGTGCTCGTACTCCGTCACTGAGGAAGTGGGCAACTTGTGGTGA 262
QY 269 AGGCTGGAACCC-----CGGCTGAACGCAAGAGCCATCACTTGAGG 313
DB 263 AGGCTGGAACCTTGAAGCGGTAGTACCGAGCTTTAAGTGAACCATCACTACGAG 322
QY 314 GTGTTACAGCCAAACGCAACAGTACCTTGCGGTCTACGTTGAGCCGCAACCCGC 373
DB 323 GCAGTTCAACCCCAAGCGGCAATGCTACCTGGTCTACGGCTGAGCAACCAACCCCT 382
QY 374 TGGTCAGTATTATCATCGTCAAGAACTTGGCACTATGATCCTTCCGCTGCTACCG 433

Db 383 TGATTGAGTACTACGTTGTTGAGTGTATGTACATACACCCCGGACGGCGGTACT 442
Qy 434 ATCTAGGAAGTGTGAGTGGACGGTACATCTATCGACTGGCAAGACCACCTGGCTCA 493
Db 443 TCAGGGGCACTGTCAACACCGAGGTGGCACTTACAACATCTACACGGCGGTCTGCTACA 502
Qy 494 ACGCACCCTAGCATGACGGGCAACCACTTCGACCAATACTGTCGGTCCGCGAGACA 553
Db 503 ATGCTCCCTCCATCGAAGGCAACCACTTCACCCAGTACTGTCGTGCGCACTCCA 562
Qy 554 AGCGACCAAGCGGTACCGTCCAGACGGGCTGCACTTCGACGCTGGGCTCGCGTGGTT 613
Db 563 AGCGTACCGGCGCACTGTCAACCATGGCAACCACTTCACGCGCTGGAGCAAGTGGGCA 622
Qy 614 TGAATGTCAACGGTGACCACTACTACAGATCGTTGCAACGAGGGCTACTTCAGCAGCG 673
Db 623 TGAA--CCTGGGAACCTCAACAATACAGATTGTGCGCACTGAGGGTTACCAAGACAGCG 679
Qy 674 GCTATGCTCGCATCACCGT 692
Db 680 GATCTGCTTCATCACTGT 698

RESULT 9
AAZ28864
ID AAZ28864 standard; DNA; 1195 BP.

AC AAZ28864;

XX 27-AUG-2003 (revised)
DT 01-FEB-2000 (first entry)

DE Streptomyces olivaceoviridis xylanase (XynG) gene.

KM Xylanase; plasmid; expression; E.coli; xylo-oligosaccharide; xylan;
KW pulp-bleaching; ds.

XX Streptomyces olivaceoviridis.

OS
FH Key Location/Qualifiers
FT CDS 298..993
FT /*tag= a
FT /gene= "XynG"
FT /product= "xylanase"
FT sig_peptide 298..417
FT /*tag= b
FT 418..990
FT /*tag= c
FT /note= "mature peptide is claimed"

XX JP11266873-A.

PN
XX 05-OCT-1999.

PD
XX 20-MAR-1998; 98JP-00090702.

PF
XX 20-MAR-1998; 98JP-00090702.

PR
XX 20-MAR-1998; 98JP-00090702.

XX (NORQ) NORINSUISANSHO SHOKUHIN SOGO.

PA (SEIB-) SEIBUTSUKAI TOKUTEI SANGYO GIUTTSU.

XX WPI, 1999-613780/53.

DR P-PSDB; AAY44183.

XX A xylanase gene, contiguous with a vector and a transformant - used for
PT pulp-bleaching.

XX Claim 1; Page 5-6; 10pp; Japanese.

CC This sequence corresponds to a degenerate sequence encoding a xylanase
CC precursor from Streptomyces olivaceoviridis. The sequence can be inserted
CC into the plasmid pQE60 to generate plasmid FERM P-16713 for expression in
CC e.g. E.coli. The xylanase is useful for the preparation of xylo-

CC oligosaccharide from xylan and for pulp-bleaching. (Updated on 27-AUG-
CC 2003 to correct OS field.)
XX
SQ Sequence 1195 BP; 230 A; 457 C; 333 G; 174 T; 0 U; 1 Other;
Query Match 20.9%; Score 205; DB 2; Length 1195;
Best Local Similarity 62.9%; Pred. No. 8.5e-45;
Matches 354; Conservative 0; Mismatches 200; Indels 9; Gaps 2;

Qy 130 ACCCCCACTCGAGGGCTGGCAAGATGTTATTAATTCCTGTGAGTGAAGGTGGA 189
Db 430 ACCACCAACCAAGACCGGCAACCAACAGGGTTCTACTACTCTTCTGACCGACGGCGC 489
Qy 190 GCGCAGGCCACGTACACCAACCTGGAAGCGGCACTACGAGATCAGCTGGGAGATGGC 249
Db 490 GGTTCGCTCTGATGACCCCTGAACCTCCGGGCACTACAGCACTCTGTGAGCAAACTGC 549
Qy 250 GGTAACTCTGTCGGTGGAAAGGGCTGAAACCCCGGCTGAAAGCAAGAGCCATCCATT 309
Db 550 GGAACTTCGTGCGCCGCAAGGGCTGGAAGCAAGCGGAGCGC--AGGAACGTGCAGTAC 606
Qy 310 GAGGTGTTTACAGCCAAACGCAACAGCTACCTTCGGGTCTACGGTTGAACCGCAAC 369
Db 607 TCGGCAAGCTTCTACCGGTCGGCAACAGGCTACCTGCGCTGTACGGGTGACTTGAAC 666
Qy 370 CCGTGTGAGTATTAATCATCGTTCGAGAACTTTGGCACTATGATCTTCTCCGGTGCT 429
Db 667 CCGTGTGAGTATTAATCATCGTTCGAGAACTTTGGCACTATGATCTTCTCCGGTGCT 429
Qy 430 ACCGATCTAGGAAGTGTGAGTGGCAAGGTAGCATCTATCGACTCGGCAAGCACTCGC 489
Db 721 ACGTACAAAGGCAAGGTGACCAAGCGGCAAGGTAGCATCTATCGACTCGGCAAGCACTCGC 780
Qy 490 GTCAACGCACTTAGCATGACGCGCAACCAACCTTCGACCAATACTGTCGTCGCCAG 549
Db 781 TACAAGCGCCCTCTCGTGAAGGCAACCAAGACCTTCAACCACTGAGCGTCCGCGAG 840
Qy 550 GACAAGCGCAACGCGGTACCGTCCAGACGGGCTGCACTTCGACGCGTGGCTCGCGCT 609
Db 841 TCCAAGCGGACCGGCGCAACCATCAACCGGCAACCACTTCGACGCGTGGCGCTAC 900
Qy 610 GGTGTAATGTCAACGCGTACCACTACTACAGATCGTTGCAACGAGGGCTACTTCAGC 669
Db 901 GGCATGCACTGGGCAAGCTTCAGCTACTACATGATCATGGCCACCGAGGGCTACAGAGC 960
Qy 670 AGCGGTATGCTCGCATCACCGT 692
Db 961 AGCGGTCTCTCAACCTCACCGT 983

RESULT 10
AAZ28865
ID AAZ28865 standard; DNA; 1195 BP.

AC AAZ28865;

XX 27-AUG-2003 (revised)
DT 01-FEB-2000 (first entry)

DE Streptomyces olivaceoviridis xylanase (XynG) gene.

KM Xylanase; plasmid; expression; E.coli; xylo-oligosaccharide; xylan;
KW pulp-bleaching; ds.

XX Streptomyces olivaceoviridis.

OS
FH Key Location/Qualifiers
FT CDS 298..993
FT /*tag= a
FT /gene= "XynG"
FT /product= "xylanase"
FT sig_peptide 298..417
FT /*tag= b

PT mat_peptide 418. .990
FT /*tag= C
PT /note= "mature peptide is claimed"
XX Jp11266873-A.
XX 05-OCT-1999.
XX 20-MAR-1998; 98UP-00090702.
XX 20-MAR-1998; 98UP-00090702.
XX 20-MAR-1998; 98UP-00090702.
XX (NORQ) NORINSUISANSHO SHOKUHIN SOGO.
PA (SEIB-) SEIBUTSUKAI TOKUTEI SANGYO GIJUTSU.
XX WPI; 1999-613780/53.
DR P-PSDB; AAY4183.
XX
PT A xylanase gene, contiguous with a vector and a transformant - used for
PT pulp-bleaching.
PS Claim 4; Page 6-7; 10pp; Japanese.
XX
XX This sequence corresponds to the complete sequence encoding a xylanase
CC precursor from Streptomyces olivaceoviridis. The sequence can be inserted
CC into the plasmid pQE60 to generate plasmid PERM P-16713 for expression in
CC e.g. E.coli. The xylanase is useful for the preparation of xylol-
CC oligosaccharide from xylan and for pulp-bleaching. (Updated on 27-AUG-
CC 2003 to correct OS field.)
XX
SQ Sequence 1195 BP; 230 A; 457 C; 333 G; 175 T; 0 U; 0 Other;

Query Match 20.9%; Score 205; DB 2; Length 1195;
Best Local Similarity 62.9%; Pred. No. 8.5e-45;
Matches 354; Conservative 0; Mismatches 200; Indels 9; Gaps 2;
QY 130 ACCCCCACTCGAGGGCTGGACGATGTTATTCTCTGTGAGTGACGGTGA 189
DB 430 ACCACCAACGACCGGACCAACAACGGGTTCTACTCTCTTCTGACCGACGGGCGC 489
QY 190 GCGCAGGCCAGTACCAACCTGAGAGGGGCACTACGAGATCACTGGGAGATGCG 249
DB 490 GGTTCGTCTGATGACCTCGAAGCTCGGCGGCACTACGACACTCTGTGACGACTGC 549
QY 250 GGTACCTCGTGGTGAAGGGCTGGAACCCCGGCTGACGCAAGACCATCTT 309
DB 550 GGGAACTTCGTCCGGCGCAAGGGCTGAGCAACGGCGGACGC---AGGAACGTGCACTAC 606
QY 310 GAGGTTTACAGCCAAACGGCAACAGTACCTTGGGCTTACGGTGTGACCCGCAAC 369
DB 607 TCGGGCAGCTTCTAACCCGTCGGCAACGGCTACCTGGCGCTGTACGGGTGACCTGCAAC 666
QY 370 CCGCTGTCGATTTACATCGTGCAGAACTTTGGCACCTATGATCTTCTCCGGTCT 429
DB 667 CCGCTGTCGATTTACATCGTGCAGAACTTTGGCACCTATGATCTTCTCCGGTCT 429
QY 430 ACCGATCTAGGAAGTGTGAGTGCAGCGGTAGCATCTATGACTCGGCAAGACCATGCGC 489
DB 721 ACGTACAAGGGGACCGGTACCAAGCGGCGGCAAGTACGACGTCTACGACGACGGG 780
QY 490 GTCAACGCACTAGCATGACGCGCAACCAACCTTGCACCAATACTGTGCTCCGCGCAG 549
DB 781 TACAACGCCCCCTCCGTGGAAGGCAACCAACCTTCAACCAAGTACGAGCGTCCGCGCAG 840
QY 550 GACAAGCGCACCGCGGTACCGTCCAGACGGGCTGCACTTGCAGCGCTGGGCTCCGCGCT 609
DB 841 TCCAAGCGGACCGCGGCAACCATCAACCGGCAACCACTTGCAGCGCTGGGCGCGCTAC 900
QY 610 GGTGATGATGTAACGGGTACCACTACTACGATGTTGCAACGAGGGCTACTTCAAC 669
DB 901 GGCATGCACTGGGCACTTCACTACTATGATCATGCGCAACGAGGGCTACCAAGAC 960
QY 670 AGCGGTATGCTGCATCACCGT 692

Db 961 AGCGGCTCTCCAACTCAGCGT 983
RESULT 11
ADK70798
ID ADK70798 standard; DNA; 576 BP.
XX
AC ADK70798;
XX
DT 06-MAY-2004 (first entry)
XX
DE Streptomyces olivaceoviridis xylan enzyme encoding DNA SEQ ID NO:1.
XX Streptomyces olivaceoviridis; xylan enzyme; enzyme; feed additive;
KW animal feed; gene; db.
XX
OS Streptomyces olivaceoviridis.
XX
FH Key Location/Qualifiers
FT CDS 1..576
FT /*tag= a
FT /product= "xylan enzyme"
XX
XX CN1405304-A.
PN 26-MAR-2003.
XX
PD 14-SEP-2001; 2001CN-00142163.
PF 14-SEP-2001; 2001CN-00142163.
XX
PR 14-SEP-2001; 2001CN-00142163.
XX
XX (FODD-) FODDER INST CHINESE ACAD AGRIC SCI.
PA Yao B, Fan Y, Zhang H;
XX
XX WPI; 2003-514374/49.
DR P-PSDB; ADK70799.
XX
PT Heat-resisting, antiprotease acidic-neutral xylanase and its gene.
PS Claim 3; SEQ ID NO 1; 21pp; Chinese.
XX
XX The present sequence encodes the Streptomyces olivaceoviridis xylan
CC enzyme. The xylan enzyme has good heat stability, high activity under
CC acidic and neutral pH. The xylan enzyme can be used as a feed additive
CC and can be widely used in animal feed.
XX
SQ Sequence 576 BP; 125 A; 207 C; 165 G; 79 T; 0 U; 0 Other;
Query Match 20.7%; Score 203.4; DB 10; Length 576;
Best Local Similarity 62.7%; Pred. No. 1.7e-44;
Matches 353; Conservative 0; Mismatches 201; Indels 9; Gaps 2;
QY 130 ACCCCCACTCGAGGGCTGGACGATGTTATTCTCTGTGAGTGACGGTGA 189
DB 13 ACCACCAACGACCGGACCAACAACGGGTTCTACTCTCTTCTGACCGACGGGCGC 72
QY 190 GCGCAGGCCAGTACCAACCTGGAAGGGGCACTACGAGATCAGCTGGGAGATGCG 249
DB 73 GGTTCGTCTGATGACCTCGAAGCTCCGGCGCACTACGACACTCTGTGACGAACTGC 132
QY 250 GGTACCTTCGTGGTGAAGGGCTGGAACCCCGGCTGAAACGCAAGACCATCTT 309
DB 133 GGGAACTTCGCGCGGCAAGGGCTGGAACCGGCGGACGC---AGGAACGTGCACTAC 189
QY 310 GAGGTTTACAGCCAAACGGCAACAGTACCTTGGGCTTACGTTGACCGCGCAAC 369
DB 190 TCGGCACTTCTAACCCGTCGGCAACGGCTACCTGCGCTGTACGGGTGACCTGCAAC 249
QY 370 CCGCTGTCGATTTACATCGTGCAGAACTTTGGCACTATGATCTTCTCCGGTCT 429
DB 250 CCGCTGTCGATTTACATCGTGCAGAACTTTGGCACTATGATCTTCTCCGGTCT 429

QY 430 ACCGATCTAGGAATGTGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACCACTCGC 489
DB 304 ACGTACAAGGGCAGCGTCAACAGCGCGCGGCGACGTACGACGTCTACAGACGACGCGG 363
QY 490 GTCAACGCACTTAGCATGACGCGCAACCAACCTTCGACCAATATCTGTCGGTCCGCGAG 549
DB 364 TACAACGCCCCCTCCGTGAAGGCAACCAAGACTTCAACCAAGTACTGAGCGTCCGCGAG 423
QY 550 GACAAGCGCAACGCGGTACCGCTCGACAGGGGCTGCACCTTCGACCGCTGGGCTCGCGCT 609
DB 424 TCCAAGCGGACCGGCGGCGACCATCAACCGGCAACCACTTCGACCGCTGGGCGCGCTAC 483
QY 610 GGTGGAATGTCAACGGGTGACCACTACTACCAAGATCGTTGCAACGAGGGCTACTTCAGC 669
DB 484 GGATGCAACTGGGCAAGCTTCAAGCTACTATGATCTCTGCCACCGAGGGGCTACCAAGAC 543
QY 670 AGCGGCTATGCTCGCATCACCGT 692
DB 544 AGCGGCTCTCTCAACATCACGGT 566

RESULT 12
ADL23221
ID ADL23221 standard; cDNA; 696 BP.

XX ADL23221;
XX 20-MAY-2004 (first entry)
XX A. niger (hemi)cellulase NBE021 coding sequence.
XX ss; gene; A. niger; (hemi)cellulase; filamentous fungus; dough; bread;
KW biscuit; elasticity; stability; stickiness; extensibility; machinability;
KM crumb structure; softness; flavour.
XX Aspergillus niger.

XX Key Location/Qualifiers
FT CDS 1..696
FT /*tag= a
FT /product= "(Hemi)cellulase NBE021"

MO2004018662-A2.

04-MAR-2004.

15-AUG-2003; 2003WO-EP009147.

PR 19-AUG-2002; 2002EP-00102152.
PR 19-AUG-2002; 2002EP-00102160.
PR 19-AUG-2002; 2002EP-00102161.
PR 30-AUG-2002; 2002EP-00102245.
PR 03-SEP-2002; 2002EP-00102279.
PR 03-SEP-2002; 2002EP-00102298.

XX (STAM) DSM IP ASSETS BV.

PI Folkers U, Fritz A, Gerhard B, Klugbauer S, Spreafico F;
PI Wagner C, Boer DL, Meima RB;

DR WPI; 2004-226842/21.

DR P-PSDB; ADL23222.

XX Novel hemicellulase NBE012, NBE021, NBE022, NBE064, NBE075 or NBE092
PT derived from Aspergillus niger, useful for preparing dough and/or baked
PT product.

XX Disclosure; SEQ ID NO 5; 92pp; English.

CC This sequence encodes an A. niger (hemi)cellulase NBE021. The
CC (hemi)cellulase coding sequences of the invention are derived from a
CC filamentous fungus, preferably Aspergillus niger. The (hemi)cellulase is

CC useful in producing dough, which is useful for preparing a baked product
CC such as bread, biscuits from the dough. Fragments of the (hemi)cellulase
CC DNA are useful as probes and primers for detecting the expression of
CC (hemi)cellulase mRNA in a biological sample such as a tissue. They are
CC also useful as query sequences to identified other family members or
CC related sequences. Anti-(hemi)cellulase antibodies are useful for
CC qualitative or quantitative determination of a polypeptide in a
CC biological sample. These antibodies are also useful in diagnosing
CC organism is infected with Aspergillus. The dough prepared by using the
CC inventive (hemi)cellulase has increased strength, elasticity, stability,
CC reduced stickiness, improved extensibility and machinability. The
CC prepared baked product has improved crumb structure, softness and
CC flavour. The (hemi)cellulase has higher specificity towards the
CC substrate, is less antigenic and produces less undesirable side
CC activities.

XX Sequence 696 BP; 143 A; 221 C; 192 G; 140 T; 0 U; 0 Other;

Query Match 20.7%; Score 203; DB 12; Length 696;
Best Local Similarity 59.7%; Pred. No. 2.4e-44;
Matches 398; Conservative 0; Mismatches 260; Indels 9; Gaps 3;

QY 31 ATGCTCGCTTTACCCCGCTTCCCTTGGCGCTTAGCCCGGACTGGGGCCCTGCTTC 90
DB 1 ATGCTCGCTTACTCTGCTCTTCTCTCTGCTCTTTCGGCTGCTCGAGCGCGCTCTC 60
QY 91 CCGGCAAGGAATGCC--ACGAGCTCGAAAAGCGACAGACAACCCCACTCGAGGGC 147
DB 61 CCAATGGCAAGGCCCTGCTGACATGGCCAAAGCGCACTTACTTCTCCGCGAAGGC 120
QY 148 TGGCAGATGTTATTACTTATCTCTGCTGAGTGACGCTGAGCGGACGCTACACC 207
DB 121 GAGAGCAACGCTACTTCTTCTCTTCTGACCAACGCTGAGGGCGACGCTACACACC 180
QY 208 AACCTGGAAGCGCGCACCTACAGATCAGCTGGGAGATGGCGTAACTCGCTGGA 267
DB 181 AACGGCAGCGCTGTGAATACACCGTTGAGTGACCACTGTGTGACTTTGTGGCCGGC 240
QY 268 AAGGCTGAACCCCGCTGAAGCAAGACCATCACTTTGAGGTTTACAGCCA 327
DB 241 AAGGTTGAACCCCGGC--AGTCTCAGGCGCTTACCTACAGCGATCATGGGAAACC 297
QY 328 AACGGCAACGCTACCTTGGCGTCTACGGTTGGACCCGCAACCCGCTGCTGATTTAC 387
DB 298 GACGCCAACGCTTACCTGCTCTTACGGTTGGACCACTCCCTTGTGCAATTTTAT 357
QY 388 ATCTGAGAACTTTGGCACCTATGATCTCTCTCCGCTGCTACCGATCTAGGAATGTC 447
DB 358 ATCTGACAAAGTACGGTATTAAGACCCCTCTCTGCTGACCGAGCTCGGACCGTC 417
QY 448 GAGTGCAGCGTAGCATCTATGACTCGGCAAGACCACTCGCTCAACGCACTAGCATC 507
DB 418 GACAGCGACGACGGAACCTACAGATCTACCAAGACCACTCGTGAGAGCGCGACTGATC 477
QY 508 GACGGCAACCAACCTTGAACCAATACTGTCGGTCCGCCAGACAAGCGCACGCGGT 567
DB 478 GAAGGCACTGCCAACCCTTCAAGCACTACTGTCCTGCGCACTGAAGGCCGATTTGGTGA 537
QY 568 ACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCTCGGCTGTTGATGTCAACGT 627
DB 538 ACCGTACCAACGCAAGAACCACTTGCATGCTGGGAGAACCTTGTCTGAGCT---GGGT 594
QY 628 GACCACTACTACCAAGATCGTTGCAACGAGGGCTACTTCAAGCAAGCGGCTATGTCGATC 687
DB 595 ACCTTCACTACATGATCGTTGCAACGAGGATACGAGAGCAAGCGGCTGTCACCATC 654
QY 688 ACCGTTG 694
DB 655 ACCGTTG 661

RESULT 13
ADJ35015

ID ADJ35015 standard; DNA; 1008 BP.
XX
AC ADJ35015;
XX
DT 22-APR-2004 (first entry)
XX
DE DNA encoding xylanase from an environmental sample seq id 231.
XX
KW antibacterial; fungicide; thermostable xylanase activity;
KW dough conditioning; beverage production; nutritional supplement;
KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
KW fungal infection; coccidiosis; gene; ds.
XX
OS Unidentified.
XX PN WO2003106654-A2.
XX PD 24-DEC-2003.
XX PF 16-JUN-2003; 2003WO-US019153.
XX PR 14-JUN-2002; 2002US-0389299P.
XX PA (DIVE-) DIVERSA CORP.
XX PI Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D,
PI Esteghlalian A;
XX
DR WPI; 2004-099016/10.
DR P-PSDB; ADJ35016.
XX
PT Novel xylanase recombinant polypeptide useful for improving textile
PT texture, treating paper, eliminating microorganisms.
XX
PS Claim 1; SEQ ID NO 231; 570bp; English.
XX
CC The invention describes an isolated or recombinant polypeptide (I),
CC having 50% or more identity to 190 300-1200 residue amino acid sequences
CC (S1), given in the specification, over a region of 100 or more residues
CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
CC dough conditioning; beverage production; as a nutritional supplement in
CC animal feed; reducing lignin in a wood or a wood product; and for
CC eliminating and protecting animals from a microorganism comprising xylan.
CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
CC acid encoding a polypeptide having a xylanase activity which involves
CC amplification of a template nucleic acid with a primer pair capable of
CC amplifying (II) or its subsequence. (I) is useful for treating and
CC preventing bacterial infection and fungal infection e.g. coccidiosis.
CC This sequence encodes xylanase protein isolated from an environmental
CC sample.
SQ Sequence 1008 BP; 192 A; 362 C; 331 G; 123 T; 0 U; 0 Other;
Query Match 20.6%; Score 202.2; DB 12; Length 1008;
Best Local Similarity 59.1%; Pred. No. 4.5e-44;
Matches 386; Conservative 0; Mismatches 258; Indels 9; Gaps 2;
QY GCCGCGACTGGGGCCCTGGCCCTCCCGGCGAGGGAATGCCAGGAGCTGAAAAGCGACAG 126
DB 73 GTGCGCTGGCGGCGCTGCGCGCGCTGATGCTGCGGGCACCGCCAGGCGCACAGGTC 132
QY 127 ACAACCCCACTCGAGGCGTGCACGATGTTATTACTATTCTCTGTGAGTGAAGCGT 186
DB 133 GTACGACCAACAGAGAGGCGCAACAACGCTACTACTACTCTGTTCTGACCGACAGC 192
QY 187 GAGCGGAGGCGACGTACACCAACTGGAAGCGGCACTTACGAGATCAGTGGGAGAT 246
DB 193 CAGGCAACGCTCTCATGAACATGGGCTCCGGCGGTACGTACAGACACCTCGTGGCGAAC 252
QY 247 GCGGTAACTCTGCTGTGAAAGGGCTGGAACCCCGCTGAACGCAAGCATCCAC 306
DB 253 ACCGGCACTTCTGCTGGCGGCAAGGGCTGGGCCAACGGCGCGCGCGA---CCGTGACG 309

QY 307 TTGAGGGGTGTTTACCAGCCAAACGGCAACAGCTACTTGCGGTCTACGGTTGACCCGC 366
DB 310 TACTCGGCGAGCTTCAACCCCTCCGGCAACGCGTACTGCGCTTACGATGAGCTCG 369
QY 367 AACCCGCTGTCGAGTATTACATCGTCGAGAACTTTGGACCTATGATCTTCCCGGT 426
DB 370 AACCGCTCGTCGAGTACTACATCGTCGACAACTGGGGCACCTACCGGCCACGGCG- 427
QY 427 GCTACGATCTAGAACTGTGAGTGCAGCGGTAGCATCTATGACTCGGCAAGACCACT 486
DB 428 ----AGTACAAGGGCACCGCTCACAGGACGGCGGCACTTACATCTACAAGACGACC 483
QY 487 CGCGTCAACGCACTTAGCATCGACCGGCAACCACTTGCACCAATACTGTCGGTCCGC 546
DB 484 CGCGTCAACAAGCCCTCCGTGAGGGCAACCGGCACTTGCACCACTGAGAGCGTCCGG 543
QY 547 CAGACAAGCGGCAACCGGTACCGGTCCAGACGGGCTGCCACTTGCAGCGCTGGCTCGC 606
DB 544 CAGCGAAGCGGACCGGCGGCAACCATCACGACCGGCAACCACTTGCAGCGGTGGCCCGG 603
QY 607 GCTGTTGAATGTCAACGCTGACCACTACTACAGATCGTTGCAACGAGGCTACTTC 666
DB 604 GCGGGATGCCGCTCGGCACTTACGCTACTACATGATCATGCGCACGAGGGCTACAG 663
QY 667 AGCAGCGCTATGCTCGCATCACCGTGTGACGTGGGCTAAGAGCTAAGCTG 719
DB 664 AGCAGCGGCGAGCTCCAGCATCAAGCTGCGGGGAGCCGGCGCGGACACAGG 716

RESULT 14
AAT63044
ID AAT63044 standard; cDNA; 851 BP.
XX
AC AAT63044;
XX
DT 17-OCT-2003 (revised)
DT 22-JUL-1997 (first entry)
XX
DE Aspergillus niger xylanase cDNA.
KW Endoxylanase; xylanase; protein detection; enzyme detection;
KW library screening; ds.
XX
OS Aspergillus niger; strain N400 (CBS120.49).
XX
FH Key location/Qualifiers
FT CDS 30..707
FT /*tag= a
XX
PN WO9713853-A2.
XX
PD 17-APR-1997.
XX
PF 14-OCT-1996; 96WO-EP004510.
XX
PR 13-OCT-1995; 95EP-00202777.
XX
PA (KONN) GIST-BROCADES BV.
PI Van Den Broeck HC, De Graaff LH, Visser J, Van Ooyen AJJ;
XX
DR WPI; 1997-235889/21.
DR P-PSDB; AAW14597.
XX
PT Identifying DNA fragments encoding proteins, e.g. for new enzyme
PT discovery - by direct screening of a cDNA library in bacteria transformed
PT with DNA from eukaryotic organism producing the protein.
XX
PS Claim 6; Page 19-20; 30pp; English.
XX
CC A cDNA clone (AAT63044), deposited as CBS 590.95, codes for a xylanase
CC (AAW14597) of Aspergillus niger N400 (CBS120.49). It was isolated using a
CC method for identifying a DNA fragment encoding a protein of interest. The

CC method involves the direct screening of a cDNA library prepd. in bacteria
CC (e.g. *E. coli*) transformed with DNA from a eukaryotic organism (e.g. *A.*
CC *niger*) that produces the protein. Screening for xylanase-producing clones
CC can be performed on agar plates containing oat spelt xylan and RBB-xylan.
CC The method was utilised in the identification of cDNA clones (AAIT3042-
CC 46) coding for *A. niger* cellulase, xylanase and arabinoxylan degrading
CC enzymes (AAW14595-99). (Updated on 17-OCT-2003 to standardise OS field)

SQ Sequence 851 BP; 201 A; 244 C; 224 G; 182 T; 0 U; 0 Other;

Query Match	20.3%;	Score 199.6;	DB 2;	Length 851;
Best Local Similarity	61.3%;	Pred. No. 2.1e-43;		
Matches 357;	Conservative	0;	Mismatches 219;	Indels 6;
				Gaps 2

Oy	128	CAACCCCCAACTTCGGAGGGGCTGGCAGATGTTATTACTATTCTCGTGGTAGTGACGGTG	187
Db	142	CGACCCCGAGCTGCACC GGCGAGAACACGGGCTTCTACTACTCTCTTGAA CCGACGGCG	201
Oy	188	GAGCGAGGCCACGTACACCAACCTGAAGGGCGCACCTACGAGATCAGCTGGGAGATG	247
Db	202	GTGAGACGTGACCTACACCAACGAGATGCTGTGCTACACTGTGAGTGTCCAAG	261
Oy	248	GCGTAACCTCGTCGGTGGAAAGGGCTGNAACCCCGCCTGAACGCAAGCATCCACT	307
Db	262	TGGGCAACTTGTTCGGTGGAAAGGGCTGNAACCCCGG--AAGTCGGCAGGACATCACT	318
Oy	308	TTGAGGGTGTTTACCAAGCCCAAACGGCAACAGCTACCTTGGCGTCTACGGTTGAACCCGCA	367
Db	319	ACAGCGGCACCTTCAACCCCTAGCGGCAACGGCTACCTCTCCGTATAGGCTGGAACCACTG	378
Oy	368	ACCCGCTGTCGATTTACATTCATCGTCGAGACTTTGGCACCTATGATCTTCTCCGGTG	427
Db	379	ACCCCTGATCGAGTACTACATCGTCGAGTCTTACGGCGACTACAACCCCGCAGTGAAG	438
Oy	428	CTACCGATCTAGGACTGTCGAGTGCAGCGTAGCATCTATGCACTCGGCAAGACCACTC	487
Db	439	GCACGTACAAGGGCACCGCTCACCTCGGACGGATCCGTTTACGATATCTACACGGCTAACC	498
Oy	488	GCGTC AACGCACCTTAGCATCGACGGCA CCCC AAACCTTGACCAATACTGTCGGTCCGCC	547
Db	499	GTACCAATGCTGCTTCATTCAGGGAACCGCTACCTTCACTCAGTACTGGTCCGTTCCGC	558
Oy	548	AGGACAAGCGCACCAAGCGGTACCGTCCAGACGGGCTGCCACTTTCGACGCGCTGGGCTCGCG	607
Db	559	AGAACAAAGAGAGTTGGCGGAACCGTTACCACTTCCAACCACTTCAATGCTTGGGCTAAGC	618
Oy	608	CTGCTTTGAATGTCAACGGTGAACCACTACTACAGATCGTTGCAACGGAAGGGCTACTTCA	667
Db	619	TGGGAATGAAA---CTTGGGTACTACAACTACAGATCGTGGCTTACCGAGGTTACCAGA	675
Oy	668	GCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAG	709
Db	676	GCAGTGATCTTTCGTCATCACTGTTCCGTAACGGGTGAAG	717

RESULT 15
AAx90405
ID AAx90405 standard; DNA; 1375 BP.

XX
AC AAX90405;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-SEP-1999 (first entry)
XX
DE Actinomadura sp. DSM43186 35 kDa xylanase encoding DNA.
XX
KM Actinomadura sp. DSM43186; xylanase; Actinomadura flexuosa; lignin;
KM thermostable; biobleaching; wood pulp; bleaching; hemicellulase;
KM paper processing; hemicellulose; ss.
XX
OS Nonomuraea flexuosa.
XX

Key	Location/Qualifiers
FT CDS	303. .1337
FT	/*tag= a
FT	/product= "xylanase"

US5935836-A.

10-AUG-1999.

06-JUN-1995; 95US-00468812.

29-JUL-1994; 94US-00282001.

(ROHG) ROEHM ENZYME FINLAND OY.

Fagerstrom R, Lantto R, Paloheimo M, Suominen P, Vehmaangerae J;
Maentylae A;

WPI; 1996-141347/38.
P-PSDB; AAY24480.

Actinomadura xylan sequences and method of use.

Disclosure; Fig 13; 54pp; English.

The present invention describes a culture medium obtained from the culture of a recombinant host cell that is not *Actinomadura flexuosa* and has been transformed with a vector encoding a protein having xylanase activity, where the protein comprises an amino acid sequence from a xylanolytic fragment of the amino acid sequence in AA124480 or AA124481. Also described is an enzyme preparation derived from the culture medium. The enzyme composition can be used in a method for biobleaching, modifying plant biomass properties, especially for the reduction of lignin content in pulp and paper processing. The xylanases are hemicellulases which partially degrade the hemicellulose and enhance the extractability of lignins by conventional chemical bleaching of wood pulp. It can be used alone or as a supplement to other treatments that reduce lignin content of wood pulp, increase its drainability or decrease its water retention. The culture medium can be used directly without the need to purify the enzymes. *Actinomadura flexuosa* xylanases have a pH optimum and thermostability desirable for the biobleaching of wood pulp reducing the need to acidify the pulp prior to xylanase treatment. The xylanases partially degrade the hemicellulose in wood pulp which enhances the extractability of lignins by conventional bleaching chemicals and results in a lower consumption of bleaching chemicals reducing the formation of environmentally undesired organic compounds. The present sequence encodes *Actinomadura* sp. DSM43186 35 kDa xylanase. N.B. This sequence is indexed from US5935836 which is a treat as basic specification for FI9503639. (Updated on 25-MAR-2003 to correct DR field.) (updated on 16-OCT-2003 to standardise OS field)

SQ Sequence 1375 BP; 265 A; 517 C; 400 G; 193 T; 0 U; 0 Other;

Query Match	20.1%;	Score 197.2;	DB 2;	Length 1375;
Best Local Similarity	58.6%;	Pred. No. 1.1e-42;		
Matches 403; Conservative	0;	Mismatches 273;	Indels 12;	Gaps 3;

OY	35	TCGGCTTTACCCCGTGCCTTGCGGCTTAGCCGCGACTGGAGCCTTGCCCTTCCCGG	94
Db	349	TCGGCCTCCGGCGCATCGTCAACCAAGTGCCTTGCCCTGGCACTCGCCATCGCCGGTGC	408
OY	95	CAGGAATGCCACCGAGCTCGAAGAAGCAAGACAACCCCACTCGGAGGCTGGCAG	154
Db	409	TGCTGCCCGGCACGGCCCAACGCCGACACCAACCATCACCCAGAACCAGCCGGTACGACA	468
OY	155	ATGCTATTACTATTCTGTGTGAATGACCGGTGGAAGCGCACCGTACACCAACTGG	214
Db	469	ACGGCTACTTCTACTCGTTCTGGACCGACCGCCCCGGGACCGTCTCCATGACCCCTTCACT	528
OY	215	AAGCGGCACTACGAGATCAGCTGGGGAGATGGCGGTAACTCTGTCGGTGAAGAAGGCT	274
Db	529	CGGGCGGACGCTACAGCACCTCGTGGCGGAACACCGGGAATTCTGTCGCCGCGCAAGGCT	588

QY 275 GGAACCCCGGCTGAACGCAAGCAATCCATTGAGGGTGTATACCAAGCCAAACGGCA 334
 DB 589 GGTCCACCGG---GGGACGGCGGACCGGTACCTTACAACGCTCTTCAACCCGTCGGGTA 645
 QY 335 ACAGCTACCTTGGCGGTCTACGGTTGGACCCCGCAACCCGCTGGTTCAGTATTACATCGTCG 394
 DB 646 ACGGCTACCTCAGGCTCTACGGCTGGACAGAAACCGCTCGTGAAGTACTACATCGTCG 705
 QY 395 AGAAGTTGGCACTATGATCCTTCCTCGGCTCTACCGATCTAGGAACTGTGAGTGG 454
 DB 706 AGAGCTGGGGCACTACCGGCCACCC-----GGCAGCTTACAAGGGCACCGTCACCAACCG 759
 QY 455 ACGGTAGCATCTATCGACTCGGCAAGCACTCGGCTCAACGCACTTAGCATCGACGGCA 514
 DB 760 ACGGGGAACGTACGACATCTACGAGACTGGCGGTACAAAGCGCCGTCATCGAGGGCA 819
 QY 515 CCCAAACCTTGCACATATAGTGTGGTCCGCCAGGACAAAGCGCACAGCGGTACCGTCC 574
 DB 820 CCGGACCTTCCAGCAGTTCTGGAGCGTCCGGCAGCAGAAAGCGCACAGCGGCACCATCA 879
 QY 575 AGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGCTGTTGAATGTCAACGGTGACCACT 634
 DB 880 CCATCGGCAACCACTTCGACGCGCTGGGCGCGCGCATGAA--CCTGGGCAAGCCACG 936
 QY 635 ACTACCAAGATCGTTGCCAAGGAGGGCTACTCAGCAGCGGCTATGCTCGCATCACCGTTG 694
 DB 937 ACTACCAAGATCAAGCGACCGAGGGCTACAGAGCAGCGGTAGCTCCACCGTCTCATCA 996
 QY 695 CTGACGTGGGCTAAGACGTAACTGGTG 722
 DB 997 GCGAGGAGTGGCAACCCCGGCAACCCGGG 1024

Search completed: February 11, 2006, 18:30:52
 Job time : 619.413 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:13:54 ; Search time 4979.03 Seconds
(without alignments)
9237.078 Million cell updates/sec

Title: US-09-467-368-1
Perfect score: 983
Sequence: 1 TCGGCGCCGACGCTTGCAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_g881:*
10: gb_g882:*
11: gb_g883:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291.2	29.6	860	8 DR637934	DR637934 EST102855
2	291.2	29.6	883	8 DR643290	DR643290 EST103391
3	240.2	24.4	882	8 DR037502	DR037502 49478.2 L
4	233.4	23.7	675	8 DN588726	DN588726 49478.1 L
5	229	23.3	744	7 CF867983	CF867983 tric013xe
6	229	23.3	799	6 CB898036	CB898036 tric013xe
7	222.6	22.6	772	7 CN133022	CN133022 OX1_9 D10
8	220.4	22.4	639	8 DR624928	DR624928 EST101505
9	220.4	22.4	749	8 DR623097	DR623097 EST101322
10	220	22.4	768	7 CF881056	CF881056 tric083xj
11	220	22.4	822	6 CB907827	CB907827 tric083xj
12	219.4	22.3	686	8 DR624738	DR624738 EST101486
13	219.4	22.3	719	8 DR631520	DR631520 EST102164
14	219.4	22.3	733	8 DR630899	DR630899 EST102102
15	219.4	22.3	739	8 DR624376	DR624376 EST101450
16	219.4	22.3	741	8 DR625790	DR625790 EST101591
17	219.4	22.3	763	8 DR624330	DR624330 EST101445
18	219.4	22.3	784	8 DR628641	DR628641 EST101876
19	219.4	22.3	801	8 DR631291	DR631291 EST102141
20	219.4	22.3	807	8 DR621776	DR621776 EST101190
21	219.4	22.3	809	8 DR627394	DR627394 EST101752
22	219.4	22.3	842	8 DR630275	DR630275 EST102040

23	219.4	22.3	886	8 DR621753	DR621753 EST101188
24	219.4	22.3	891	8 DR632055	DR632055 EST102218
25	219.4	22.3	916	8 DR622008	DR622008 EST101213
26	219.2	22.3	729	8 DR629975	DR629975 EST102010
27	219.2	22.3	763	8 DR623625	DR623625 EST101375
28	219	22.3	734	8 DR622879	DR622879 EST101300
29	215.8	22.0	711	8 DR622988	DR622988 EST101311
30	215.8	22.0	770	8 DR622508	DR622508 EST101263
31	214.6	21.8	708	8 DR631672	DR631672 EST102180
32	211.4	21.5	921	6 CD458837	CD458837 Fg08_04b1
33	207.2	21.1	714	8 DR631518	DR631518 EST102164
34	202.8	20.6	671	8 DR632323	DR632323 EST102245
35	202	20.5	697	8 DR625721	DR625721 EST101584
36	201.8	20.5	673	8 DR625705	DR625705 EST101583
37	199.6	20.3	746	8 DR701170	DR701170 Asn_00615
38	199.4	20.3	655	8 DR625642	DR625642 EST101577
39	199.4	20.3	677	8 DR629147	DR629147 EST101927
40	199.4	20.3	738	6 CD464145	CD464145 ETH1_48_B
41	198.6	20.2	871	8 DR037503	DR037503 49478.3 L
42	196.4	20.0	746	6 CB901964	CB901964 tric028xi
43	196.4	20.0	746	7 CF871731	CF871731 tric028xi
44	196.2	20.0	680	8 DR707969	DR707969 Asn_08783
45	191.4	19.5	682	8 DR702584	DR702584 Asn_02201

ALIGNMENTS

RESULT 1
DR637934
LOCUS DR637934 860 bp mRNA linear EST 11-JUL-2005
DEFINITION EST1028559 FvM Gibberella moniliformis cDNA clone FVMB275, mRNA
sequence.
ACCESSION DR637934
VERSION DR637934.1 GI:70712768
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 860)
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,
Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
JOURNAL Contact: Brown, D.W.
COMMENT USDA/ARS/NCAUR
USDA
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVMB275TH
Seq primer: AAT TAA CCC TCA CTA AAG GG.
location/Qualifiers
1. 860
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVMB275"
/tissue_type="mycelia"
/clone_id="FvM"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FvM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was

QY		648	TGCAACGGAGGGCTACTTACAGCAGCGGCTATGCTGCATCACCCGTTCGTACGTTGG	703
Dn		636	CGCTACTGAGGGTACTTACAGCAGCGGATCTTCTCATCATGACCCTTCTGAGGGGG	691
RESULT 3				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				

DR037502 882 bp mRNA linear EST 31-MAY-2005
49478.2 late Blight-Challenged Tubers Solanum tuberosum cDNA clone
49478 5', mRNA sequence.
DR037502
DR037502.1 GI:66839397
EST.
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 882)
Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Laque,M., De
Koeyer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S.
Generation of ESTs from late blight-challenged potato tubers
Unpublished (2005)
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

FEATURES

source

Location/Qualifiers

1. .882

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Shepody"

/db_xref="taxon:4113"

/clone="49478"

/tissue_type="Tubers"

/lab_host="XLI0-Gold"

/clone_1lb="Late Blight-Challenged Tubers"

/note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI; Site_2: XhoI; supplier: Pathogen-challenge series. Tubers from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with 5 μ l of *Phytophthora infestans* (A2-mating type), through 2 puncture wounds 3 cm apart. The tubers were incubated 1 minute to allow inoculum absorption. The infection area was outlined for future collection reference. Surface slices were sampled from the tubers at 1 day, 5 days, 7 days, 11 days and 14 days post-infection. All samples were pooled and used for RNA isolation and library construction. A normalized library was constructed following a modified protocol of Bonaldo et al. (1996. Genome Research 6: 791-806)."

ORIGIN

Query Match	24.4%	Score 240.2;	DB 8;	Length 882;
Best Local Similarity	60.9%;	Pred. No. 1.1e-56;		
Matches 411; Conservative	0;	Mismatches 258;	Indels 6;	Gaps 1;

OY 31 ATGTCGGCTTTACCCCCGTGTGCCCTTGCCCGACTGGGGCCCTGCCTTC 90
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 ATGATTCCCTTACCCTACTCTTCATTTGTGCTGCGTCTGCCGTTGCTGCGAA 84

OY 91 CCGGCAGGGAATGCCACGAGCTCGAAAAGCAGACAGAACCCCACTCGAGGGCTGG 150
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 CCCGAGACCA GCCCTTAACCCCGCCACA-----AGAGCGCACGAACCA GACTGGCCAG 138

OY 151 CACGATGTTATTACTATTCTGTGTGAGTGACGCTGAGCGCAGGCCACTACCAAC 210
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 AACGGCGGGTACTACTACTCTCTCTGGA GTGATGACCAAGSCAAGCAACCTACCAAC 198

OY 211 CTGGAAGCGCGCACCTACGAGATCACTGGGGAGATGGCGGTAACCTCGTCGGTGAAG 270
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 AAGCGCGGTGAGAGTACTCTCTGACTGGA GCGGCAACGGCAACGTGCTGTGGAAG 258

QY 271 GGCTGGAAACCCCGGCTGAAACGCAAGACCATTCCACTTTGAGGGTGTTCACGACCAAC 330
 Db 259 GGATGGAAACCCAGGAAGTGGCCAGACAATCACCTACTCTGGGACCTTCAACCCCAATGTT 318
 QY 331 GGCAACAGTACTCCTTGCGGTCTACGGTTGGACCCCGCAACCCGCTGTGCGAGTATTACATC 390
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 Db 379 GTTGAAGCTTCGGTTCATATGACCCCTCTCCGCTGCGTGAAGCAAGGCGACGGTCAAC 438
 QY 451 TGGACGGTAGCATCTATGACTCGGCAAGACCACCTCGCGTCAACGCACTAGCATCGAC 510
 Db 439 GTTGATGGCAGCACCTCAACAATCTTCAGACTACCCGTTACCAACGACCTTCATCGAT 498
 QY 511 GGCACCCAAACCTTCGACCAATACTGTCGGTCCGCGCAGGACAAGCGCACACGCGTACC 570
 Db 499 GGCACCTCGACCTTTAGCAGTACTGCTGTTCGCGCAAGACCAACGACACGCGGATCC 558
 QY 571 GTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAC 630
 Db 559 GTTGATGTGCAAGCTCACTTTGCGGCGCTGGAAGTCCAAAGGAATGAACCTGGGCACTGAG 618
 QY 631 CACTACTACAGATCGTTGCAACGAGGGCTACTTACGACAGCGGCTATGCTCGCATCAC 690
 Db 619 CACAACCTACAGATTGTTGCTTCGAGGGTTACCAACAGCAGCGGTTCCGCCGATATCACT 678
 QY 691 GTTGCTGACGTGGGC 705
 Db 679 GTTGATCCGGTGGC 693

RESULT	4
LOCUS	DN588726
DEFINITION	DN588726 675 bp mRNA linear EST 15-MAR-2005 49478.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
ACCESSION	49478 5' , mRNA sequence.
VERSION	DN588726
KEYWORDS	DN588726.1 GI:61239134
SOURCE	EST.
ORGANISM	Solanum tuberosum (potato)
AUTHORS	Solanum tuberosum
TITLE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Solanum. 1 (bases 1 to 675) Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Laque,M., De Koeyer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S. Generation of ESTs from late blight-challenged potato tubers Unpublished (2005)
JOURNAL	Contact: Barry Flinn
COMMENT	

FEATURES

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source
1. .675
/organism="Solanum tuberosum"
/mol_type="mRNA"
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/db_xref="taxon:4113"
/clone="49478"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
/clone_lib="Late Blight-Challenged Tubers"
/note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future

```


Db 693 ATTACCAGATTGTTGCCGTGGAGGGTTACTTtagctctgctctc 741

RESULT 6
CB898036 799 bp mRNA linear EST 02-JUL-2003
LOCUS tricol3xe09 T.reesei mycelial culture, Version 3 april Hypocrea
DEFINITION jecorina cDNA clone tricol3xe09, mRNA sequence.
ACCESSION CB898036
VERSION CB898036
KEYWORDS GI:30112694
SOURCE EST.
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1 (bases 1 to 799)
Foreman,P.K., Brown,D.E., Dankmeyer,L., Dean,R., Diener,S.,
Dunn-Coleman,N.S., Goedegebuer,F., Houfek,T.D., England,G.J.,
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
JOURNAL 12788920
PUBMED
AUTHORS
COMMENT Contact: Pamela K. Foreman
Genencor Inc.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
1..799
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/db_xref="taxon:51453"
/clone="tricol3xe09"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN

Query Match 23.3%; Score 229; DB 6; Length 799;
Best Local Similarity 61.6%; Pred. No. 1.6e-53;
Matches 400; Conservative 0; Mismatches 245; Indels 4; Gaps 2;

QY 35 TCGGCTTTACCCCGTTGCCCTTGCGGCTTAGCCGCGACTGGGGCCCTTGCCCTCCCG 94
DB 151 TCACCTCCCTCCTCGCGCGCTGCGCCATCTCGGCGTCTTGCGCGCTCCCGCGCG 210
QY 95 CAGGAATGCCAGGAGCTCGAAAAGCAGACAAACCCCACTCGAGGGCTGCGACG 154
DB 211 AGTTCGAATCCGTGGCTGTGAGAAAGCGCCAGAGATTGAGGCCGCGACGCGCTACAACA 270
QY 155 ATGTTATTACTATTCTCGTGTGAGTGAAGGTGAGCGGCAAGCTACACCAACTGG 214
DB 271 ACGGCTACTTCTACTCGTACTGGAAGATGGCCACGCGCGGTGACGTACACCAATGTC 330
QY 215 AAGCGGCACTACGAGATCAGCTGGGAGATGGCGGTAACTCTCGGTGMAAGGCT 274
DB 331 CCGGCGGGAGTTCTCCGTCAACTGTGCCAACTCGGGCAACTTTGTGCGCGGCAAGGAT 390
QY 275 GGAACCCCGGCTGAACGCAAGACCATCTTGAAGGTTTACCAGCCAAAGGCA 334
DB 391 GGCAAGCCCGGCAACGAACAAGTCACTTCTCGGCAAGCTACAAACCCCAAGGCA 450
QY 335 ACAGCTACTTGGCGGTCTACAGGTTGAGCCCGCAACCCGCTGCTGAGTATTACATCGTCG 394
DB 451 ACAGCTACTTCTCGGTACGCGGTGTCGCCCAACCCCTGATCGAGTACTACATCGTCG 510

QY 395 AGACTTTGGACCTATGATCCTTCCCGTGCTACCGATCTAGAACTGTGAGTCG 454
DB 511 AGAAGCTTTGGACCTATCAACCCCGTCCACGGGCGCCACCAAGCTGGCGAGGTACCTCCG 570
QY 455 ACGTAGCATCTATCGACTCGGCAAGACCACTCGCGCTCAACGCCACTAGCATCGACGCA 514
DB 571 ACGGAGCGCTTACGACATTTTACCGCAGCGCGCTCAACGACCGTCCATCATCGGCA 630
QY 515 CCCAACTTTCGACCAATACCTGTCGTCGCCCGCAGACAGCGCACCGGCTACCGTCC 574
DB 631 CCGCACTTTTACAGTACTGTCGTCGCCCGCAACCAACCGCTCGAGCGGCTCGTCA 690
QY 575 AGACGGGCTGCCACTTCGACGCGCTGGCTCGCGCTGTTGAATGTCAACGCTGACCACT 634
DB 691 ACACGGCGAACCACTTCAACGCGTGGGCTCAGCAAGGCTGACGCT---CGGACGATGG 747
QY 635 ACTACCATTCGTTG-CAACGAGGGCTACTTCAGCAGCGGCTATGCTC 682
DB 748 ATTACCAGATTGTTGCCGTGGAGGGTTACTTtagctctgctctc 796

RESULT 7
CN133022 772 bp mRNA linear EST 01-APR-2004
LOCUS OX1_9_D10_g1_A002 Oxidatively-stressed leaves and roots Sorghum
DEFINITION bicolor cDNA clone OX1_9_D10_A002 5', mRNA sequence.
ACCESSION CN133022
VERSION CN133022.1 GI:45963542
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 772)
Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C.,
Sun,F., Sullivan,R., Lim,S., Eastman,A. and Pratt,L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots
Unpublished (2003)
Other ESTs: OX1_9_D10_b1_A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTGTGCTTAAAGCTGCG).
Location/Qualifiers
1..772
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="OX1_9_D10_A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/note="Organ: Leaf and Root; Vector: pME18S-FL3; Site_1:
XhoI; Site_2: XhoI; The library was prepared from polyA+
RNA from oxidatively stressed, hydroponically grown
sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.003% and leaves
were misted with 10 uM methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all

Db 558 TTCTAGCTACCGAGGATACCAAGACAGTGGATCTTCTTCCATCTATGTT 607

RESULT 9
DR623097 749 bp mRNA linear EST 11-JUL-2005
LOCUS EST1013225 Fvi Gibberella moniliformis cDNA clone FVIAM22, mRNA
DEFINITION sequence.
ACCESSION DR623097
VERSION DR623097
KEYWORDS DR623097.1 GI:70697745
SOURCE EST.
ORGANISM Gibberella moniliformis
Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 749)
AUTHORS Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
Utterback,T., Smith,S., Feldblyum,T., Glenn,A.B., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
JOURNAL Unpublished (2005)
COMMENT Contact: Brown, D.W.
USDA/ARS/NCAUR
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVIAM22TH
Seq primer: AAT TAA CCC TCA AAG GG.
Location/Qualifiers
1..749
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVIAM22"
/class_type="mycelia"
/clone_lib="Fvi"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fvi was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIZOL Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIZOL. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA synthesis kit; Stratagene)."

ORIGIN

Query Match 22.4%; Score 220.4; DB 8; Length 749;
Best Local Similarity 63.2%; Pred. No. 4.5e-51;
Matches 373; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

Qy 104 CCACGGAGCTGAAAAAGCGACAGACACCCCACTCGAGGGCTGGCAGATGTTATT 163
Db 114 CCTGTCTCTTGAGGCCCGCCAGGTCAACCGTAACCTTGAGGGTTACCAACGCGATACT 173
Qy 164 ACTATTCTGTGAGTGAAGTGAAGCGCAGGCCAGCTACACCAACCTGGAAGCGGCA 223
Db 174 TCTACTCTGTGCTGCTGATGCTGCTATGCCAACTACCGTATGGTGAAGGAAGTC 233
Qy 224 CCTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCGTGGAAAAAGGCTGAACCCCG 283
Db 234 ACTACCAAGTTGATTGGCGCAACACTGTAACCTTGTGTGGAAAAAGGTTGAACCCCTG 293

Qy 284 GCCTGAACGCAAGACCCATCCACTTTGAGGGTGTTTACCAAGCCAAACGGCAACAGTACC 343
Db 294 G---TACTGGCCGAACATATCAACTATGACGGTTCCTTTCAGCCCTCAGGGTAACGGTATC 350
Qy 344 TTGCGGTCTACGGTTGGACCCGCAACCCGCTGTGAGTATTACATCGTGAAGACTTTG 403
Db 351 TCTGCGTCTACGGCTGGACCCGCAACCCCTCTGTCGAGTACTACGTCATCGAAGTACG 410
Qy 404 GCACCTATGATTCCTTCTCCGGTGTACCGATCTAGGAAGTGTGAGTGCGACGGTAGCA 463
Db 411 GCACTTACATCCCGGCTCTGCTGGCCAGCACAAGGGCACCGTCTACAACGACGGCACA 470
Qy 464 TCTATCGACTCGGCAAGACCACTCGCGTCAACGCACTTACATCGACGGCAACCAACT 523
Db 471 CCTATGATCTGTACCAAGACCAACCCGCTTATCGACGGCCAAACAGACT 530
Qy 524 TCGACCAATACTGCTGCTCGGTCGCGCAGGACAAGCGCACCGGTAACGTCAGACGGCT 583
Db 531 TCAACCACTACTGGCGCATCCGCGCAACAAGCGCAGACGGCGCTGTCAACATGACAGA 590
Qy 584 GCCACTTCGACGCGCTGGGCTCGCGCTGCTTGAATGTCAACGGTGACCACTACTACAGA 643
Db 591 CTATCTCAATGCTTGGGCTAATGTGCGCATGAGACT---TGAACAACACTACTATCAGA 647
Qy 644 TCGTTCACACGAGGGCTACTCTTACGACGCGGTATGCTGCATCACCGTT 693
Db 648 TTCTAGCTACCGAGGATACCAAGACAGTGATCTTCTTCATCTATGTT 697

RESULT 10
CF881056 768 bp mRNA linear EST 31-OCT-2003
LOCUS tric083xj11.b1 T.reesei mycelial culture, Version 6 October 2003
DEFINITION Hypocrea jecorina cDNA clone tric083xj11, mRNA sequence.
ACCESSION CF881056
VERSION CF881056.1 GI:38135738
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1 (bases 1 to 768)
AUTHORS Diener,S.R., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
TITLE Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
reesei.
JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
PUBMED 14757250
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: 1T-F1 primer.
Location/Qualifiers
1..768
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric083xj11"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
2003"
/note="Vector: PREP3Y; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN

RESULT 12
DR624738
LOCUS
DEFINITION DR624738 686 bp mRNA linear EST 11-JUL-2005
sequence.
EST1014866 Fvi Gibberella moniliformis cDNA clone FVIB801, mRNA
ACCESSION
VERSION DR624738
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVIB801TH
Seq primer: AAT TAA CCC TCA AAG GG.
location/Qualifiers
1. 686
/organism="Gibberella moniliformis"
/mol_type="mRNA"
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/db_xref="taxon:117187"
/clone="FVIB801"
/tissue_type="mycelia"
/clone_lib="Fvi"
/note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioides. Library
Fvi was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit, Stratagene)."

ORIGIN
Query Match 22.3%; Score 219.4; DB 8; length 686;
Best local similarity 63.2%; Pred. No. 8.5e-51;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

OY 104 CCACGAGCTCGAAAAAGCGACAGCAACCCCACTCGAGGGCTGGCAGATGTTATT 163
DB 70 CCTGTGCTTGAGGCCCGCCAGGTACCGGTACTGTAGGGTTACCAACGAGTACT 129
OY 164 ACTATTCCTGTGAGTGCAGGTGAGCGCAGCCACGTACCAACCTGGAAGCGGCA 223
DB 130 TCTACTCTTGTGTGTCTGATGTGTGCTATGCCAATACCGTATGGTGAAGGATC 189
OY 224 CCTACGAGATCAGCTGGGAGATGGCGTTAAGCTGTGGTGAAGGGCTGAACCCCG 283
DB 190 ACTACCAAGTTGATTGGCGCAACACTGTACTTGTGTGGAAGGGTTGAACCCCTG 249
OY 284 GCCTGAACGAAGCCATCTTGAAGGGTGTTCACCAAGCGCAACGCACTACC 343

DB 250 G--TACTGGCCGGAAGCTATCACTATGCGGTTCTTTCAGCCCTCAGGGTAAAGGCTATC 306
OY 344 TTGCGGTCTACGGTTGAGCCCGCAACCCGCTGTGAGTATTACATCGTCGAACTTTG 403
DB 307 TGTGCGTCTACGGCTTGAGCCCGCAACCCCTCTCGTGAAGTACTACGTATCGAAGTACG 366
OY 404 GCACCTATGATCCTTCTCCGGTGTCTACCGATCTAGAACTGTGAGTGCAGCGTAGCA 463
DB 367 GCACTTACATCCCGGCTGTGCTGGCCAGCACAAGGGCACCCTTACACAGCAGCGGACA 426
OY 464 TCTATCACTCGGCAAGACCACTCGCGTCAACGCCACTAGCATCGACGGCAACCAACT 523
DB 427 CCTATGATCTGTACCAAGACCAACCCGCTTACCAACGACCCCTTATCGACGGCCACAGACT 486
OY 524 TCGACCAATACTGTGTCGGTCCGCCAGGACCAAGCGCACCGGTACCGTCCAGCGGCT 583
DB 487 TCAACCACTACTGGGCGCATCGCCGCAACAGCGCAGCGCGGTGTCAACATGCAGA 546
OY 584 GCCACTTCAGCGCCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACTATCCAGA 643
DB 547 CTATCTTCAATGCTTGGGTATGCTGGCATGAGACT--TGAAACCACTACTATCAGA 603
OY 644 TCGTTGAACGAGGAGCTACTTCAGACGCGGTATGCTGCATCACCGT 692
DB 604 TTCTAGTACCGAGGAGTACCAAGACAGAGTGTGATCTTCCATCTATGT 652

RESULT 13
DR631520
LOCUS
DEFINITION DR631520 719 bp mRNA linear EST 11-JUL-2005
sequence.
EST1021648 Fvi Gibberella moniliformis cDNA clone FVIEA21, mRNA
ACCESSION
VERSION DR631520
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVIEA21TH
Seq primer: AAT TAA CCC TCA AAG GG.
location/Qualifiers
1. 719
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVIEA21"
/tissue_type="mycelia"
/clone_lib="Fvi"
/note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioides. Library
Fvi was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,

frozen in liquid nitrogen, ground to a powder, and then added to TRIZOL Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIZOL. The cDNA was directionally ligated into the pBluescript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 22.3%; Score 219.4; DB 8; Length 719;
Best Local Similarity 63.2%; Pred. No. 8.6e-51;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

QY 104 CCACGGAGCTCGAAAAAGCCAGACACACACCCCACTCGGAGGGCTGGCACGATGTTATT 163
DB 108 CCTCTGTCTTGAGGCCCCCGCCAGGTACCGGTAACTTGAGGGTTACCACACGATACT 167
QY 164 ACTATTCTGTGGTGGAGTGACGGTGGAGCGGACGTAACCAACCTGGAAGCGGCA 223
DB 168 TCTACTCTTGGTGTGATGGTGGTGGCTATGCAACTACCGTATGGGTGAGGAAATC 227
QY 224 CCTACGAGATCAGTGGGAGATGGCGGTAACTCTGCGGTGAAAGGGCTGGAACCCCG 283
DB 228 ACTACGAGGTGATTGGCGCAACTGTAACTTTGTGGTGAAAGGGTTGGAACCTTG 287
QY 284 GCCTGAACGCAAGAGCCATCCACTTTGAGGGTGTATACAGCCAAACGCAACACTACC 343
DB 288 G---TACTGGCCGAACATCACTATGGCGGTCTTTCAAGCCCTCAGGGTAACGGCTATC 344
QY 344 TTGCGGTCTACGGTTGGACCCCGCAACCCGCTGTGAGTATTACATCGTGAGAACTTTG 403
DB 345 TCTGCGTCTACGGCTGGACCCCGCAAGCCCTCTGTCGAGTACTACGTCATCGAGAACTACG 404
QY 404 GCACCTATGATCTCTCTCCGGTGTACTACCGATCTAGAACTGTGAGTGGCAGGCTAGCA 463
DB 405 GCACCTTAAATCCCGGCTGTGTCGCGCAGCACAAGGGCAACGCTCTACACGACGCGACA 464
QY 464 TCTATCGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATGACGCGCACCAACCT 523
DB 465 CCTATGATCTGTACAGACCAACCCGCTAACACCAAGCCCTCTATGACGCGCAAGACCT 524
QY 524 TCGACCAATACTGTCGTCCGCGCAGACGAAGCGCAACGCGTACCGTCCAGACGGGCT 583
DB 525 TCAACCAAGTACTGGGCCATCCGCGCAACAAGCGCAGCGGCTGTCAACATGACAGA 584
QY 584 GCCACTTCGACGCGCTGGGCTCGCGTGTGATGTCAACGGTGAACCACTACTATACAGA 643
DB 585 CTATCTTCAATGCTTGGGCTAATGCTGSCATGAGACT---TGGAAACCACTACTATCAGA 641
QY 644 TCGTTGCAACGAGGGCTACTTACAGACGGCTATGCTCCGATCAACCGT 692
DB 642 TTCTAGTACCGAGGATACAGACAGTGATCTTCTTCATCTATGT 690

RESULT 14
DR630899 733 bp mRNA linear EST 11-JUL-2005
LOCUS EST1021027 FvI Gibberella moniliformis cDNA clone FVIDX40, mRNA
DEFINITION
ACCESSION DR630899
VERSION DR630899.1 GI:70705629
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
REFERENCE 1 (bases 1 to 733)
AUTHORS Brown,D.W., Cheung,F., Proctor,R.H., Butenko,A.E., Zheng,L., Lee,Y.,
Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and WhiteIaw,C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
JOURNAL spliced introns in multiple genes of the funomistn gene cluster
COMMENT Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR

USDA
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVIDX40TH
Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES

source

1. .733
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVIDX40"
/tissue_type="mycelia"
/clone_1ib="FvI"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioides. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10e6 conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIZOL Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIZOL. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 22.3%; Score 219.4; DB 8; Length 733;
Best Local Similarity 63.2%; Pred. No. 8.6e-51;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

QY 104 CCACGGAGCTCGAAAAAGCCAGACACACCCCACTCGGAGGGCTGGCACGATGTTATT 163
DB 147 CCTCTGTCTTGAGGCCCCCGCCAGGTACCGGTAACTTGAGGGTTACCACACGATACT 206
QY 164 ACTATTCTGTGTGAGTGACGGTGGAGCGGCAACGTAACCAACCTGGAAGCGGCA 223
DB 207 TCTACTCTTGGTGTGATGGTGGTGGCTATGCCAACTACCGTATGGGTGAGGAAATC 266
QY 224 CCTACGAGATCAGCTGGGAGATGGCGGTAACTCTGTCGCTGGAAGGGCTGGAACCCCG 283
DB 267 ACTACGAGTGTATTGGCGCAACTGTAACTTTGTGGTGAAAGGGTTGGAACCCCTG 326
QY 284 GCCTGAACGCAAGAGCCATCACTTGAGGGTGTTAACGACCAACGCGCAACACTACC 343
DB 327 G---TACTGGCCGAACATCACTATGGCGGTCTTTCAGCCCTCAGGGTAACGGCTATC 383
QY 344 TTGCGGTCTACGGTTGGAACCCCGCAACCCGCTGTGAGTATTACATCGTCGAGAACTTTG 403
DB 384 TCTGCGTCTACGGCTGAGCCCGCAGCCCTCTCGTCACTACTACGTCATCGAGAACTACG 443
QY 404 GCACCTATGATCTCTCTCCGCTGTCTACCGATCTAGGAATGTGAGTGGACGGTAGCA 463
DB 444 GCACCTTAAATCCCGGCTGTGTCGCGCAGCACAAGGGCAACCGTCTACAAACGACGGCACA 503
QY 464 TCTATGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATGACGCGCACCAACCT 523
DB 504 CCTATGATCTGTACAGACCAACCGCTTCAACCAAGCCCTCTATGACGCGCAACAGACT 563
QY 524 TCGACCAATACTGTCGTCCGCGCAGGACGAAGCGCAGCGGTACCGTCCAGACGGGCT 583
DB 564 TCAACCAAGTACTGGGCCATCCGCGCAACAAGCGCAGCGGCTGTCAACATGACAGA 623
QY 584 GCCACTTCGACGCGCTGGGCTGGGCTGTGATGTCAACGGTGAACCACTACTATCAGA 643
DB 624 CTATCTTCAATGCTTGGGCTAATGCTGCGATGAGACT---TGGGAACCACTACTATCAGA 680
QY 644 TCGTTGCAACGAGGGCTACTTACAGACGCGCTATGCTCCGATCAACCGT 692

Db 681 TTCTAGCTACGAGGATACCAAGAGCTGATCTTCTTCATCTATGT 729

RESULT 15
DR624376 739 bp mRNA linear EST 11-JUL-2005
LOCUS EST1014504 FvI Gibberella moniliformis cDNA clone FVIB280, mRNA
DEFINITION
ACCESSION DR624376
VERSION DR624376
KEYWORDS DR624376.1 GI:70699058
SOURCE EST.
ORGANISM Gibberella moniliformis
Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 739)
AUTHORS Brown, D.W., Cheung, F., Proctor, R.H., Butcho, A.E., Zheng, L., Lee, Y.,
Uterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Platner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
applied introns in multiple genes of the fumonisin gene cluster
JOURNAL unpublished (2005)
COMMENT Contact: Brown, D.W.
USDA/ARS/NCAUR
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVIB280TH
Seq primer: AAT TAA CCC TCA AAG GG.
Location/Qualifiers

FEATURES
source 1..739
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVIB280"
/tissue_type="mycelia"
/clone_lib="FvI"
/note="Vector: pBluescript II SK(+); Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 22.3%; Score 219.4; DB 8; Length 739;
Best Local Similarity 63.2%; Pred. No. 8.6e-51;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

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QY 224 CTTACGAGTCACTGGGAGATGGCGGTAACTCTGCTGGTGAAGGCTGAACCCG 283
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QY 284 GCCTGAACGCAAGAGCCATCCATTGAGGGTGTTTACAGCCCAACGGCAAGCTACC 343
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QY 404 GCACCTATGATCCTCTCCGGTGTCTACCGATCTAGGAATGTGAGTGGAGCGGTAGCA 463
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QY 524 TCGACCAATACTGTGTCGGTCCGCCAGGACCAAGCGCACCGGTACCGTCCAGACGGGCT 583
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QY 644 TCGTGAACGGAAGGCTACTTCAAGCAGCGGCTATGCTGCATCACCGT 692
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Search completed: February 11, 2006, 20:39:40
Job time : 4981.03 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:19:44 ; Search time 215.809 Seconds
(without alignments)
8096.696 Million cell updates/sec

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Perfect score: 983
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	983	100.0	983	3	US-09-115-660-1 Sequence 1, Appli
3	239	24.3	1123	2	US-08-458-023B-3 Sequence 3, Appli
4	197.2	20.1	1375	2	US-08-468-812-1 Sequence 1, Appli
5	197.2	20.1	1375	3	US-08-590-563-1 Sequence 1, Appli
6	197.2	20.1	1375	3	US-09-770-621-1 Sequence 1, Appli
7	197.2	20.1	1375	3	US-09-235-832-1 Sequence 1, Appli
8	194.2	19.8	822	3	US-09-254-733-8 Sequence 8, Appli
9	190	19.3	1015	2	US-08-121-436A-1 Sequence 1, Appli
10	181.8	18.5	1281	3	US-08-768-373-1 Sequence 1, Appli
11	181.8	18.5	1281	3	US-09-849-242A-1 Sequence 1, Appli
12	168.4	17.1	675	2	US-07-744-570B-1 Sequence 1, Appli
13	165.2	16.8	927	2	US-08-507-431-5 Sequence 5, Appli
14	165.2	16.8	927	2	US-08-902-655A-5 Sequence 5, Appli
15	165.2	16.8	927	3	US-09-116-622-5 Sequence 5, Appli
16	165.2	16.8	927	3	US-09-219-277-5 Sequence 5, Appli
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18	162.4	16.5	489	2	US-08-119-169A-7 Sequence 7, Appli
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28	119	12.1	744	3	US-09-189-060B-11	Sequence 11, Appli
29	108.8	11.1	1207	2	US-08-575-964-2	Sequence 2, Appli
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33	101.4	10.3	2967	3	US-09-367-891A-4	Sequence 4, Appli
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36	97.6	9.9	954	2	US-08-315-695-15	Sequence 15, Appli
37	97.6	9.9	1945	3	US-09-595-344-1	Sequence 1, Appli
38	96.2	9.8	234	3	US-09-189-060B-46	Sequence 46, Appli
39	95.8	9.7	847	3	US-09-260-283-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-08-886-765-1
; Sequence 1, Application US/08886765
; Patent No. 5817500
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; APPLICANT: Wagner, Peter
; APPLICANT: Mullertz, Anette
; APPLICANT: Knapp, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 58175000 No. 5817500disk of No. 5817500th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Thermomyces lanuginosus
; STRAIN: DSM 4109
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..705

US-08-886-765-1

Query Match	100.0%;	Score 983;	DB 2;	Length 983;
Best Local Similarity	100.0%;	Pred. No. 3.6e-269;		
Matches 983; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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RESULT 2
US-09-11

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: Sequence 1, Application US/09115660
: Patent No. 6245546
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: GENERAL INFORMATION:
:
: APPLICANT: Hansen, Peter Kamp
: APPLICANT: Wagner, Peter
: APPLICANT: Mullertz, Anette
: APPLICANT: Knap, Inge Helmer
: TITLE OF INVENTION: Animal Feed Additives
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 62455460 No. 6245546disk of No. 6245546th America, Inc.
: STREET: 405 Lexington Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10174
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/115,660
: FILING DATE:
:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/886,765
: FILING DATE:
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias J
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4324.204-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 983 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: ORIGINAL SOURCE:
: ORGANISM: Thermomyces lanuginosus
: STRAIN: DSM 4109
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: FEATURE:
: NAME/KEY: CDS
: LOCATION: 31..705
:
US-09-115-660-1

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Query Match	100.0%;	Score 983;	DB 3;	Length 983;
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DB 961 AAAAAAAAAAAAAAAAAA 983

RESULT 3
US-08-458-023B-3
Sequence 3, Application US/08458023B
Patent No. 5667990

GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boomlathan, Karuppan C.
TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56679900 No. 5667990disk of No. 5667990th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458, 023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowmey Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Humicola insolens
INDIVIDUAL ISOLATE: DSM 6995
FEATURE:
NAME/KEY: CDS
LOCATION: 126..806
US-08-458-023B-3

Query Match 24.3%; Score 239; DB 2; Length 1123;
Best Local Similarity 64.4%; Pred. No. 1.1e-57;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;
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QY 147 CTGACGATGTTATTACTTCTGTGTGAGTGAAGTGAAGCGGACGACGTAAC 206
DB 257 CTGACGATGTTATTACTTCTGTGTGAGTGAAGTGAAGCGGACGACGTAAC 206
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QY 447 CGAGTGGACGCTAGCATCTATCGACTCGGCAAGACCACTGCGTCAACGCACTAGCAT 506
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-08-590-563-1

Query Match 20.1%; Score 197.2; DB 3; Length 1375;
Best Local Similarity 58.6%; Pred. No. 9.1e-46;
Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;

QY 35 TCGGCTTACCCCGTTGCCCTTGACCGGAGTGGGGCCCTGCGCTCCCGG 94
DB 349 TCGGCTCCGGCGCATCGTCAACAGTGCCTTCCCTGCACTCGCCATCGCCGGTGGC 408
QY 95 CAGGAATGCCACGAGCTCGAAAAGCAGACAAACCCCACTCGGAGGCTGGCAG 154
DB 409 TGCTGCCCGGACGCGCCACGCGGACCAACCATCAACCCAGAACAGACCGGGTACACA 468
QY 155 ATGTTATTACTATTCTCTGTGTGAGTGAAGGTGAGCGGACGCGTACACCAACTGG 214
DB 469 ACGGCTACTTCTACTCGTTCTGACCGACGCGCCGCGGACCGTCTCATGACCTTCACT 528
QY 215 AAGCGGACACTACGAGATCAGTGGGAGATGGCGTAACCTCGTGGTGAAGGGCT 274
DB 529 CGGCGGACAGTACAGACCTCGTGGGGAACACCGGAATTCTGCGCGCAAGGGCT 588
QY 275 GGAACCCCGGCTGAACGAGACCATCACTTGAGGGTTTACCAGCCAAAGGCA 334
DB 589 GGTCCACCGG---GGGACGGCGGACCGTGAACCTACACGCTCTTCAACCCGTCGGTA 645
QY 335 ACAGCTACTTGGCGTCTACGCGTTGACCCCGCAACCCCGTGGTGAATATTACATCTCG 394
DB 646 ACGGCTACTCAAGCTCTACGCGTGAACGAAACCCGCTGTGAGTACTACATCTGTG 705
QY 395 AGAATTGGCACTATGATCCTTCTCCGCTGCTACCGGATCTAGGAAGTGTGAGTGG 454
DB 706 AGAGCTGGGGCACTTACCGGCCACCC-----GGCACTTCAAGGGGCAACCGTACCA 759
QY 455 ACGGTAGCATCTATGACTCGGCAAGACCACTGCGGTCAAGGCACTAGCATGACGGCA 514
DB 760 ACGGGGAACGTACGACATCTACGAGACTGCGGTACAAAGCGCCGTCCATCGAGGGCA 819
QY 515 CCAAACTTGACCAATACTGTGTGCTCCGCGCAGAGACAGCGCACAGCGGTACCGTCC 574

DB 820 CCGGACCTTCCAGACAGTCTTGACCGCTCCGGCAGCAGAACGAGACCGGACCATCA 879
QY 575 AGACGGGCTGCCACTTTCGACGCGCTGGGCTCGCGCTGTTGAATGTAACGGTACCACT 634
DB 880 CCATCGGCAACCACTTTCGACGCGCTGGGCTCCGCGCGGATGAA---CCTGGGACGCA 936
QY 635 ACTACCAATCTGTTGCAACCGGAGGCTACTTACGACGCGGCTATGCTCGCATCACCGTTG 694
DB 937 ACTACCAATCTATGCGGACCGGAGGCTTACAGAGCAGCGGTAGCTTCCACCGTCTCATCA 996
QY 695 CTGACGTGGGCTAAGACGTAACTGTG 722
DB 997 GCGAGGTGGCAACCCCGGCAACCCGGG 1024

RESULT 6
US-09-770-621-1
Sequence 1, Application US/09770621
Patent No. 6506593
GENERAL INFORMATION:
APPLICANT: M ntyl, Arja
APPLICANT: Vehmaanger, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. 6506593 Relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

Db 706 AGAGCTGGGGACCTACCGGGCCACC-----GGACCTACAAGGGACCGTCAACCAACC 759
QY 455 ACGGTAGCATCTATGCACTCGGCAAGACCACTCGCGTCAACCGCACTAGCATGACGGCA 514
Db 760 ACGGGGAAACGTACGACATCTACGAGACCTGGCGGTACAAAGCGCGTCCATCGAGGGCA 819
QY 515 CCCAACCCTTCGACCAATACTGTGCTCGGCCAGACAGCAAGCGCAACCGGTACCGTCC 574
Db 820 CCGGACCTTCAGCAGTCTGTGAGCGTCCGCGACAGCAAGCGGACCAACCGGACCATCA 879
QY 575 AGACGGGCTGCCATCTGACGCGCTGGCTCGCGCTGTTGAATGTCAACGGTGACCACT 634
Db 880 CCATCGCAACCACTTCGACGCGCTGGCGCGCGCGCATGAA---CCTGGCAGCGCA 936
QY 635 ACTACCAAGATCGTGCACAGGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCAACGTTG 694
Db 937 ACTACCAAGATCATGGCGGACCGAGGGCTACGAGCAGCGGTAGCTCCACCGTCTCATCA 996
QY 695 CTGACGTGGGCTAAGACGTAACCTGGTG 722
Db 997 GCGAGGGTGGCAACCCCGGCAACCCGGG 1024

RESULT 8

US-09-254-733-8
; Sequence 8, Application US/09254733
; Patent No. 6277596
; GENERAL INFORMATION:
; APPLICANT: WATANABE, MANABU
; APPLICANT: MORIYA, TATSUKI
; APPLICANT: AOYAGI, KAORU
; APPLICANT: SUMIDA, NAOMI
; APPLICANT: MURAKAMI, TAKESHI
; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING
; TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
; TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
; FILE REFERENCE: 99-0266/LC(WMC)/00144
; CURRENT APPLICATION NUMBER: US/09/254,733
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 822
; TYPE: DNA
; ORGANISM: TRICHODERMA VIRIDE MC300-1
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (14)..(112)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)..(112)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (113)..(809)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)..(285)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (286)..(412)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (413)..(809)
US-09-254-733-8

Query Match 19.8%; Score 194.2; DB 3; Length 822;
Best Local Similarity 69.0%; Pred. No. 5.1e-45;
Matches 281; Conservative 0; Mismatches 123; Indels 3; Gaps 1;
QY 286 CTGAACGCAAGAGCCATCCACTTTGAGGGTGTTCACAGCCAAACGGCAACAGTACCTT 345
Db 402 CTGAAACCAAGGGTCACTCACTTCTCGGGCACTACAAACCCCAACGGCAACAGTACCTC 461

QY 346 GCGGTACCGTTGACCCCGCAACCCCGCTGCTCGAGTATTACATCGTCGAGACTTTGGC 405
Db 462 TCCGTGATCGGCTGTGTCGCGCAACCCCTGATCGAGTACTACATCGTCGAGACTTTGGC 521
QY 406 ACCTATGATCTTCTCTCGGTGCTAACGATCTAGGAACGTGCGAGTCGACGGTAGCATC 465
Db 522 ACCTACAACCCGTTCACCGCGCGCAACCAAGCTGGCGAGGTGACGTGCGACGGCAGCTC 581
QY 466 TATGACTCGGCAAGACCACTCGCGTCAACGCAACCTAGCATCGACGCAACCAACTTC 525
Db 582 TAGCATCTAACCGACGACGCGGTCAACAGCCGTTCATCGAGGGCACTCCACTTT 641
QY 526 GACCAATAGTGTGCTCGTCCGCGCAAGCAAGCGCAACCGGTACCGTCCAGACGGGCTGC 585
Db 642 TACCACTACTGGTCCGTCCCGCGCAACCAACCGCTCCAGCGGCTCCGTAACACGGCGAAC 701
QY 586 CACTTCGACCGCTGGGCTCGCGCTGTGATGTCAACGGGTGACCACTACTACAGATC 645
Db 702 CACTTCAACCGGTGGGCTCGCGCAACCGCTGACGCT---GGGCAACCATGATTACAGATT 758
QY 646 GTTGAACGAGGGCTACTTTCAGCAGCGGCTATGCTCGCATCAACCGT 692
Db 759 GTTCCGTGAGGGCTACTTATGCTGTGCTGTGCTTCCATCAACCGT 805

RESULT 9

US-08-121-436A-1
; Sequence 1, Application US/08121436A
; Patent No. 5837515
; GENERAL INFORMATION:
; APPLICANT: Suominen, Pirkko
; APPLICANT: Nevalainen, Helena
; APPLICANT: Saarelainen, Ritva
; APPLICANT: Paloheimo, Marja
; APPLICANT: Lahtinen, Tarja
; APPLICANT: Paegerstr m, Richard
; TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
; TITLE OF INVENTION: for Their Production
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,436A
; FILING DATE: 16-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,478
; FILING DATE: 18-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI93/00221
; FILING DATE: 24-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,893
; FILING DATE: 29-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/524,308
; FILING DATE: 16-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbal, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.008000C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(176..448, 557..952)
US-08-121-436A-1

Query Match 19.3%; Score 190; DB 2; Length 1015;
Best Local Similarity 68.5%; Pred. No. 8.8e-44;
Matches 278; Conservative 0; Mismatches 125; Indels 3; Gaps 1;

QY 287 TGAACGCAAGACCATCCACTTTGAGGGTGTACCAAGCCAAACGGCAACAGCTACCTTG 346
DB 546 TAAAAAAGGGTCATCACTTCTCGGGAAGCTACAACCCCAACGGCAACAGCTACCTCT 605
QY 347 CGGTCTACGGTTGGACCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTTGGCA 406
DB 606 CCGGTACGGGTGGTCCCGCAACCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCA 665
QY 407 CCTATGATCTTCTCCTCCGGTCTACCGATCTAGAACTGTGAGTGCAGCGGTAGCATCT 466
DB 666 CCTACAACCGCTCCACGGCGCCACCAAGCTGGCGAGGTCACTCCGACGGCAGCTCT 725
QY 467 ATCGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATGACGGACCCAAACCTTCG 526
DB 726 ACGACATTTACCGCAACGCAAGCGGTCAACAGCCGTCCATCATTCGGCACCGCACTTTT 785
QY 527 ACCAATACCTGTCGGTCCGCCAGACCAAGCCACACGGGTACCGTCCAGACGGGCTGCC 586
DB 786 ACCAGTACTGTTCCGTCCGCCAGCAACCGCTCGAGCGGCTCCGTCAACACGGCGCAAC 845
QY 587 ACTTCGACCGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACTACTACCATCG 646
DB 846 ACTTCAACGCGTGGGCTCAGCAAGGCTGACGCT--CGGACGATGATTACAGATTG 902
QY 647 TTGCAACGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 692
DB 903 TTGCCGTGAGGGTTACTTTAGCTCTGCTCTGCTTCATCACCGT 948

RESULT 10
US-08-768-373-1
; Sequence 1, Application US/08768373
; Patent No. 6228629

GENERAL INFORMATION:

APPLICANT: PALOHEIMO, MARJA
APPLICANT: HAKOLA, SATU
APPLICANT: M NTYL, ARJA
APPLICANT: VEHEMAANPER, JARI
APPLICANT: LANTTO, RAJJA
APPLICANT: LAHTINEN, TARJA
APPLICANT: PAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95

FEATURE:

NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION: /product= "XLNA"
FEATURE:
NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION: /product= "XLNA"
US-08-768-373-1

Query Match 18.5%; Score 181.8; DB 3; Length 1281;
Best Local Similarity 65.4%; Pred. No. 2.1e-41;
Matches 283; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

QY 267 AAAGGGTGAACCCCGGCTGAACGCAAGACCATCCATTGAGGGTGTTCACAGCC 326
DB 478 AACAGGCTGAACCCCGGTACGATAACCGTGTATCACTACACAGCCGATCAGACC 537
QY 327 AAACGGCAACGCTACCTTGCGGTCTACGGTTGACCCGCAACCCGCTGTCAGTATTA 386
DB 538 CAACGGCACTCTACCTCGCCGCTTACGGCTGACCCGCAACCCGCTGATCGAGTACTA 597
QY 387 CATCGTCGAACTTTGGCACTTATGATCTTCTCCGCTGCTACCGATCTAGGAATGT 446
DB 598 CGTGTGAGAGCTTCGGCACTTACGACCCGTCGACGGGGCCACCCGATGGGCAAGCT 657
QY 447 CGAGTGCAGCGGTAGCATCTATGACTCGGCAAGACCACTGCGTCAACGCACTTAGCAT 506
DB 658 GACCACCGAGCGGCGCACCTTACATATCTACCGCACGAGCGGTCAACGCGCCTCCAT 717
QY 507 CGACGGCAACCAACCTTGCACATATGTCGGTCCGCGCAGGACGAGCGCACCGAGCGG 566
DB 718 CGAGGGCAACAAGACTTCTACCAATACTGCTGTGCGCACTCCAAAGCGCACCGCGG 777
QY 567 TACCGTCAGACGGGCTGCCACTTGAACGCGCTGGGCTCGCGCTGTTGAATGTCAACGG 626
DB 778 TACTGTTCATATGCGCAACCACTTCAATGCTTGAAGGAGGCTGTGCAAGCT---GGG 834
QY 627 TGACCACTTACTACAGATCGTTGCAACGGAAGGCTACTTCAAGACGCGGTATGCTGCAT 686
DB 835 TTCCCATGATTATCAGATTGTGGCTACTGAGGGTACTACTGCTGCGCGGCACTGT 894
QY 687 CACCGTTGCTGAC 699
DB 895 CAATGTTGGCGGC 907

RESULT 11
US-09-849-242A-1
; Sequence 1, Application US/09849242A
; Patent No. 6635464
; GENERAL INFORMATION:
; APPLICANT: PALOHEIMO, MARJA
; HAKOLA, SATU
; MONTYLO, ARJA
; VEHMAANPERO, JARI
; LANTTO, RAIIJA
; LAHTINEN, TARJA
; FAGERSTRM, RICHARD
; SUOMINEN, PIRKKO
; TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
; AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/849,242A
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/768,373
; FILING DATE: 17-DEC-1996
; APPLICATION NUMBER: US 60/008,746
; FILING DATE: 18-DEC-1995
; APPLICATION NUMBER: US 60/020,839
; FILING DATE: 28-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CIMBALA, MICHELE A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1716.0540004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Chaetomium thermophilum
; STRAIN: CBS730.95
; FEATURE:
; NAME/KEY: exon
; LOCATION: 195..423
; OTHER INFORMATION: /product= "XLNA"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 483..1039
; OTHER INFORMATION: /product= "XLNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-849-242A-1
Query Match 18.5%; Score 181.8; DB 3; length 1281;
Best Local Similarity 65.4%; Pred. No. 2.1e-41;
Matches 283; Conservative 0; Mismatches 147; Indels 3; Gaps 1;
QY 267 AAAGGCTGAACCCCGCCTGAAGCAAGACCATCTTGAGGGTGTTCACGACC 326

Db 478 AACAGGCTGAACCCCGGTACCGATAACCGTGTATCACTACACAGCCGACTACAGACC 537
QY 327 AAACGGCAACAGCTACCTTGGCGTCTAACGGTTGGACCCGCAACCCGCTGGTCCAGTATTA 386
Db 538 CAACGGCACTCCTACCTCGCGCTTACCGCTGACCCGCAACCCGCTGATCGAGTACTA 597
QY 387 CATCGTCAGAACTTTGGCACCTATGATCCTTCTCCGCTGCTACCGATCTAGAACTGT 446
Db 598 CGTGTGAGAGCTTCGGCACTTACGACCCGTCGACGGCGCCACCCGATGGGCAAGCT 657
QY 447 CGAGTCGACGCTAGCATCTATGACTCGGCAAGACCACTCGCGTCAACGCACTAGCAT 506
Db 658 GACCACCGACGGCGCACCTACATCTACCGCAGCAGCGCTCAACGCGCCCTCCAT 717
QY 507 CGACGGCAACCAACCTTGCACCAATACTGTCGGTCCGCAAGACAAGCGCAGCGG 566
Db 718 CGAGGGCAACCAAGACCTTCTACCAATACTGTCGTGCGCACTCCAGCGCAGCGG 777
QY 567 TACCGTCAGACGGGCTGCCACTTGCACCGCCTGGGCTCGGCTGTTGAATGTCAACGG 626
Db 778 TACTGTACCATGGCCAACCACTTCAATGCTTGAGGCAAGGCTGTCTGCACT---GGG 834
QY 627 TGACCACTACTACCATGCTGTGCAACGAGGCTACTTCAAGCAGCGCTATGCTGCAT 686
Db 835 TTCCATGATTTATCAGATTGGCTACTGAGGGTTACTACTGCTGCTCGGCGGACTGT 894
QY 687 CACCGTGTCTGAC 699
Db 895 CAATGTGGCGGC 907

RESULT 12
US-07-744-570B-1
; Sequence 1, Application US/07744570B
; Patent No. 5202249
; GENERAL INFORMATION:
; APPLICANT: Kluepfel, D.
; APPLICANT: Morosoli, R.
; APPLICANT: Shareck, F.
; TITLE OF INVENTION: Xylanase for Bioleaching
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael J. Bradley
; STREET: 1200 South 47th Street
; STREET: Box Number 4023
; CITY: Richmond
; STATE: California
; COUNTRY: United States
; ZIP: 94804-0023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb storage
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/744,570B
; FILING DATE: 19910813
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 675 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Single strand
; TOPOLOGY: Circular
US-07-744-570B-1

Query Match 17.1%; Score 168.4; DB 2; length 675;
Best Local Similarity 60.0%; Pred. No. 1e-37;
Matches 343; Conservative 0; Mismatches 211; Indels 18; Gaps 3;
QY 127 ACAACCCCACTCGAGGGCTGGCAAGATGTTATTAATTCTCTGTGAGTGAAGGT 186

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Db 34 ACCATCAACCAACCAAGACCGGCAACCGGCATGTACTCTGTTTGACCGACGGC 93
Qy 187 GGAGCGGAGGCCACGTACCAACCTGGAAGCGGCACTACGAGATCAGTGGGAGAT 246
Db 94 GCGGCTCCGTCTCCATGACGCTCAACGGTGGCGGCACTATAGCACCCAGTGAACCAAC 153
Qy 247 GCGGTAACCTCGTGGTGAAGGGCTGGAACCCCGGCTGAACGCAAGAGCCATCCAC 306
Db 154 TGCGGCACTTCGTGCGCGGCAAGGGCTGAGCACCGG-----CGACGGCAACGTCCGC 207
Qy 307 TTTGAGGGTGTTTACCAAGCAACGGCAACAGACTATGCGGTCTACGGTGAACCCGC 366
Db 208 TACAACGGCTACTTCAACCCCGTGGCAACGGCTACGGCTGCTCTACGGCTGACCTCG 267
Qy 367 AACCCGCTGTCGAGTATTACATCGTCGAGAATTGGCACTTATGATCCTCCCGT 426
Db 268 AACCCGCTGTCGAGTACTACATCGTCGACAACTGGGGCACTTAACCGCCACC----- 321
Qy 427 GCTACCGATCTAGGAAGTGTGCGAGTGGCAACGGTACATCTATCGACTCGGCAACCACT 486
Db 322 GGTACGTACAAAGGGCAACCGTCTCCAGCGACGGAGCACCTTACGACATCTTACGACGACC 381
Qy 487 CGGCTCAACGACCTAGCATGACGGCAACCAACCTTGAACCAATACTGGTGGTCCGC 546
Db 382 CGGTACAAAGCCCCCTCCGTGAAGGCAACAAAGACCTTCAAGCACTGAGTGTCCGG 441
Qy 547 CAGACAAAGCGCACAG-----CGGTACCGTCCAGACGGGCTGCCACTTCAAGCCTGG 600
Db 442 CAGTGAAGGTGACAGTGTGCTCCGGCAACATCACACCGGCAACCACTTCAAGCCTGG 501
Qy 601 GCTCGCGTGTGTTGAATGTCAACGGTGAACCACTACTACAGATCGTTGCAAGGAGGC 660
Db 502 GCGCGCGCGGCATGAACATGGGCGCATTCAGGTACTACATGATCATGGCCACGAGGGC 561
Qy 661 TACTTCAGCAGCGGCTATGCTCGCATCACCGT 692
Db 562 TATCAGAGCAGTGGAAGCTCGAACATCACGGT 593
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RESULT 13

US-08-507-431-5

Sequence 5, Application US/08507431

Patent No. 5693518

GENERAL INFORMATION:

APPLICANT: Kofod, Lene V.

APPLICANT: Kaupinen, Markus S.

APPLICANT: Christgau, Stephan

APPLICANT: Heldt-Hansen, Hans P.

APPLICANT: Dalboge, Henrik

APPLICANT: Andersen, Lene N.

APPLICANT: St, Joan O.

APPLICANT: Jacobson, Tina

APPLICANT: Munk, Niels

APPLICANT: Mullertz, Anette

TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM

TITLE OF INVENTION: ASPERGILLUS ACULEATUS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESSES:

ADDRESSEE: No. 56935180 No. 5693518disk of No. 5693518th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/507,431

FILING DATE: 15-FEB-1996

CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,800
; FILING DATE: 25-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3954.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(31..723, 727..849, 853..900, 904..927)
; US-08-507-431-5
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Query Match 16.8%; Score 165.2; DB 2; Length 927;
Best Local Similarity 57.9%; Pred. No. 9.4e-37;
Matches 352; Conservative 0; Mismatches 248; Indels 8; Gaps 3;

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Db 134 CTGCCCTTGCTGGCGCTCGACTGCGAGCTCCACTGCTACTCGAACGGCTATTACTATA 193
Qy 167 ATTCTGTGTGAGTGAACGGTGAAGCGGACGACAGTACCAACCTTGAAGCGGACCT 226
Db 194 GCTTGTGAACCGATGGCGCAAGCGCGATGTTGAATACAGCAACGCGCGGGGGTCTCT 253
Qy 227 ACGAATCAAGTGGGAGATGGCGGTAACTCGTGGTGAAGAGGCTGGAACCCCGGCC 286
Db 254 ACAGCGTGAAGCTGTGATCGGCTCGAAGCTTCTGCGGTGAAGAGGCTGGAACCTGG-A 312
Qy 287 TGAACGCAAGAGCCATCCACTTTGAGGGTGTTTACCAAGCC---AAACGGCAACAGCTAC 342
Db 313 AGTGTCTATGACATTATTAAGTATCCGGCTCCTGACCAAGCAAGAAATAGCAACAGCTAC 372
Qy 343 CTTCGGGTCTACGTTGGAACCGGCAACCGGCTGGTGAATATTACATCGTCCAGAACTTT 402
Db 373 CTTCGGTCTACGCTGGAACCGGCTCCTCTGCTGAGTACTATATCTTGAAGAACTAC 432
Qy 403 GGACCTATGATCCTTCCTCCGGTGTCTACCGATTAAGAACTGTGAGTGGACGGTAGC 462
Db 433 GGGAGTAAACACCCCGCTCAGCTGGCACTTAAAGAGCTCGGTACTCCGACGATCG 492
Qy 463 ATCTATGACTCGGCAAGCACTCGCGTCAACGCACTTAGCATGACGCGCAACCAACC 522
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Qy 523 TTGACCAATATCTGTCGGTCCGCCAAGACAGGCGCAACGCGGTACCGTCCAGCGGGC 582
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Qy 583 TGCCACTTGAAGCGCTGGGCTGGCGCTGTTGATGATCAACGCTGACCACTACTACAG 642
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Db 730 CGTGAGA 737
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RESULT 14

US-08-902-655A-5

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: Sequence 5, Application US/08902655A
: Patent No. 5885819
: GENERAL INFORMATION:
: APPLICANT: Kofod, Lene V.
: APPLICANT: Kauppinen, Markku S.
: APPLICANT: Christgau, Stephan
: APPLICANT: Heldt-Hansen, Hans P.
: APPLICANT: Dalboge, Henrik
: APPLICANT: Andersen, Lene N.
: APPLICANT: St, Joan Q.
: APPLICANT: Jacobson, Tina
: APPLICANT: Munk, Niels
: APPLICANT: Mullertz, Anette
: TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
: TITLE OF INVENTION: ASPERGILLUS ACULEATUS
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: No. 58858190 No. 5885819disk of No. 5885819th America, Inc.
: STREET: 405 Lexington Avenue, 64th floor
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/902,655A
: FILING DATE: 30-July-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Agtis, Cheryl T.
: REGISTRATION NUMBER: 34,086
: REFERENCE/DOCKET NUMBER: 3954.214-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 927 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-08-902-655A-5

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	Query Match	16.8%;	Score 165.2;	DB 2;	Length 927;	
	Best Local Similarity	57.9%;	Pred. No. 9.4e-37;			
	Matches 352;	Conservative	0;	Mismatches 248;	Indels 8;	Gaps 3;
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Oy	167 ATTCTTGSTGGAGTGACCGGTGAGCGCAGGCCACGTACCAACCTTGAAAGCGGGCACCT					226
Db	194 GCTTTCGACCgATGCGCAAGCGCGATGTTGAATACAGCAACGGCGCGGGGGGTCTCT					253
Oy	227 ACAGATTCAGCTGGGGAGATGCGGTAACCTCGTCGCTGGAAGAAGGCTGAAACCCGGCC					286
Db	254 ACAGCGTCAGCTGTGCATCGGCTCGAAGCTTCGTGGGGAAGGGCTGAAACCTGG-A					312
Oy	287 TGAACGCAAGACCATCCACTTTAGGGGTTTACCAAGC---AAACGGCAACAGCTAC					342
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Db	433	GGGAGTACAACCCCGGCTCAGCTGGCACTTACAAGGCTCGGTCTACTCCGACGATCG	4922
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RESULT 15
; US-09-116-622-5
; Sequence 5, Application US/09116622
; Patent No. 6080567
; GENERAL INFORMATION:
; APPLICANT: Kofoed, Lene V.
; APPLICANT: Kauppinen, Markus S.
; APPLICANT: Christgau, Stephan
; APPLICANT: Heidt-Hansen, Hans P.
; APPLICANT: Dalboge, Henrik
; APPLICANT: Andersen, Lene N.
; APPLICANT: Si, Joan O.
; APPLICANT: Jacobson, Tina
; APPLICANT: Munk, Niels
; APPLICANT: Mullertz, Anette
; TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
; TITLE OF INVENTION: ASPERGILLUS ACULEATUS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6080567o No. 6080567disk of No. 6080567ch America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/116,622
; FILING DATE: 16-July-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Agtis, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3954.224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
;

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-09-116-622-5

Query Match 16.8%; Score 165.2; DB 3; Length 927;
Best Local Similarity 57.9%; Pred. No. 9.4e-37;
Matches 352; Conservative 0; Mismatches 248; Indels 8; Gaps 3;

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QY 107 CGAGCTCGAAAAAGCGACAGACAACCCCAACTCGAGGGCTGGCACGATGTTATTACT 166
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DB 670 ATCGTCGCTACTGAAGGCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 729
QY 703 GGCTAAGA 710
DB 730 CGTGACAGA 737
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Perfect score: 983
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Scoring table: IDENTITY NUC
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Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications NA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	585	59.5	588	6 US-10-237-386-9	Sequence 9, Appli
3	374	38.0	678	3 US-09-803-454-3	Sequence 3, Appli
4	257.2	26.2	850	8 US-10-425-115-177283	Sequence 177283,
5	246.6	25.1	749	8 US-10-425-115-82922	Sequence 82922, A
6	240.4	24.5	818	8 US-10-425-115-37173	Sequence 37173, A
7	224.6	22.8	666	5 US-10-213-990-65	Sequence 65, Appli
8	223	22.7	705	5 US-10-213-990-68	Sequence 68, Appli
9	197.2	20.1	1375	3 US-09-770-621-1	Sequence 1, Appli
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16	146.4	14.9	596	6 US-10-307-441-39	Sequence 39, Appli
17	136.8	13.9	2225	3 US-09-790-070A-8	Sequence 8, Appli
18	124	12.6	2898	5 US-10-299-393-1	Sequence 1, Appli
19	124	12.6	2898	10 US-11-154-793-1	Sequence 1, Appli
20	119.2	12.1	557	3 US-09-970-616-1	Sequence 1, Appli
21	119.2	12.1	557	9 US-10-765-716-1	Sequence 1, Appli
22	119.2	12.1	642	3 US-09-149-310-31	Sequence 31, Appli
23	118	12.0	594	10 US-11-018-645-17	Sequence 17, Appli

24	103.6	10.5	2054	6 US-10-419-969-5	Sequence 5, Appli
25	101.8	10.4	643	6 US-10-340-860A-39	Sequence 39, Appli
26	94.2	9.6	561	10 US-11-018-645-13	Sequence 13, Appli
27	90.2	9.2	561	10 US-11-018-645-15	Sequence 15, Appli
28	89.4	9.1	972	10 US-11-018-645-19	Sequence 19, Appli
29	83.6	8.5	394	8 US-10-425-115-48309	Sequence 48309, A
30	82.6	8.4	642	8 US-10-626-583-4	Sequence 4, Appli
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32	80.8	8.2	539	7 US-10-437-963-15625	Sequence 15625, A
33	78.4	8.0	591	10 US-11-018-645-3	Sequence 3, Appli
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35	72.4	7.4	663	3 US-09-909-207-1	Sequence 1, Appli
36	72.4	7.4	663	3 US-09-909-207-2	Sequence 2, Appli
37	72.4	7.4	744	3 US-09-909-207-4	Sequence 4, Appli
38	72.4	7.4	744	3 US-09-909-207-5	Sequence 5, Appli
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40	72.4	7.4	1513	3 US-09-909-207-11	Sequence 11, Appli
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45	71.8	7.3	645	6 US-10-237-386-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-467-368-1
; Sequence 1, Application US/09467368
; Patent No. US20020160080A1
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; Wagner, Peter
; Mullertz, Anette
; Knap, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20020160080A1o No. US20020160080A1disk of No. US200201600
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,368
; FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Thermomyces lanuginosus

STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-467-368-1

Query Match 100.0%; Score 983; DB 3; Length 983;
Best Local Similarity 100.0%; Pred. No. 7.8e-305;
Matches 983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 901 TTGTTATTGCTTGTGTTGTTAGTGTACATAGCCGACAAATTGAGGCTCAGCCTTGGGA 960
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Db 961 AAAAAAAAAAAAAAAAAAAAAA 983
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RESULT 2
US-10-237-386-9
Sequence 9, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 588
TYPE: DNA
ORGANISM: Thermomyces lanuginosus
US-10-237-386-9

Query Match 59.5%; Score 585; DB 6; Length 588;
Best Local Similarity 100.0%; Pred. No. 5.7e-177;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 244 GATGGCGGTAACTCTGTCGGTGAAAAGGGCTGGAACCCCGGCTGAACGCAAGCCATC 303
Db 124 GATGGCGGTAACTCTGTCGGTGAAAAGGGCTGGAACCCCGGCTGAACGCAAGCCATC 183
OY 304 CACTTTGAGGGGTGTTTACAGGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGACC 363
Db 184 CACTTTGAGGGGTGTTTACAGGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGACC 243
OY 364 CGAACCCGCTGTGAGTATTACATGTCGAGAACTTTGGCACTATGATCCTTCCTCC 423
Db 244 CGAACCCGCTGTGAGTATTACATGTCGAGAACTTTGGCACTATGATCCTTCCTCC 303
OY 424 GGTGCTACCGATCTAGGAATGTGAGTGCAGCGGTAGCACTTATCGACTCGGCAAGACC 483
Db 304 GGTGCTACCGATCTAGGAATGTGAGTGCAGCGGTAGCACTTATCGACTCGGCAAGACC 363
OY 484 ACTGCGGTCAACGCACCTAGCATGACGGCACCCAAACCTTGCACCAATACCTGTCGTC 543
Db 364 ACTGCGGTCAACGCACCTAGCATGACGGCACCCAAACCTTGCACCAATACCTGTCGTC 423
OY 544 CGCCAGGACAAAGCGCACAGCGGTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCT 603
Db 424 CGCCAGGACAAAGCGCACAGCGGTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCT 483
OY 604 CGCGTGTGTTGAATGTCAACGGTGAACCACTACTACAGATCGTTCGAACGAGGGCTAC 663
Db 484 CGCGTGTGTTGAATGTCAACGGTGAACCACTACTACAGATCGTTCGAACGAGGGCTAC 543
```

Oy	664	TTCAGCAGCGGCTATGCTGCATCACCGTTGCTGACGTGGGCTAA	708
Db	544	TTCAGCAGCGGCTATGCTGCATCACCGTGTGCTGACGTGGGCTAA	588

RESULT 3

```

US-09-803-454-3
/ Sequence 3, Application US/09803454
/ Publication NO. US20030022280A1
/ GENERAL INFORMATION:
/ APPLICANT: NO. US20030022280A1ozymes A/S
/ APPLICANT: Takagi, Shinobu
/ APPLICANT: Terui, Yuri
/ TITLE OF INVENTION: High Expression of Industrial Enzymes
/ FILE REFERENCE: 6125.200-US
/ CURRENT APPLICATION NUMBER: US/09/803,454
/ CURRENT FILING DATE: 2001-03-09
/ NUMBER OF SEQ ID NOS: 52
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 678
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-09-803-454-3

```

Query Match	38.0%	Score 374;	DB 3;	Length 678;
Best Local Similarity	72.0%	Pred. No. 4.2e-109;		
Matches 488; Conservative	0;	Mismatches 190;	Indels 0;	Gaps 0;

Qy	31	ATGTCGGCTTACCCCCGTTGCCCTTCGGCCCTTAGCCCGCACTGGGGCCCTGGCCTTC	90
Db	1	ATGTTGGTTTACTCCAGTTGCTTACGCTCTTAGCTGCTACTGGTCTTACGCTTTC	60
Qy	91	CCGGCAGGGAATGCCACGGAGCTCGAAAAGCAGACAACTCCCACTCGAGGGCTGG	150
Db	61	CCAGCAGGTAAATGCTACTGAATTAGAAAAAAGACAAACAATCCAAATTCGAAGTTGG	120
Qy	151	CACGATGTTATTACTATTCTCGTGAGTGACGGTGAGCGCAGGCCACGTACCAAC	210
Db	121	CATGATGGTTATTATTATTCTGTGGTCTGATGCTGTGCTCAAGCTACTATATACTAAT	180
Qy	211	CTGAAGCGCGCACTACGAGATCAGCTGGGAGATGGCGTTAACTCGTCGGTGAAG	270
Db	181	TTAGAAGGTGTATCTATGAAATTTCTTGGGGTGATGTGTGTAAATTAGTTGGTGTAAA	240
Qy	271	GGCTGGAACCCCGGCCCTGAACGCAAGCCATCCACTTTGAGGGTGTTTACCAAGCCAAAC	330
Db	241	GGTTGGAATCCAGGTTTAAATGCAAGAGCTATTCAATTTTGAAGTGTATTATCAACCAAT	300
Qy	331	GGCAACAGCTACTTGCCTCTACCGTTCAGCCGCAACCCGCTGTCAGTATTACATC	390
Db	301	GGTAATCTTATTAGCTGTTATGTTGAGCTAGAAATCCATTAGTGAATATTATTAT	360
Qy	391	GTCGAACTTTGGCACCTATGATCTTCTCCGGTCTACCGATCTAGAACTGTGAG	450
Db	361	GTTGAAAATTTGGTACTTATGATCCATCTCTGTGCTACTGATTTAGTACTGTGAA	420
Qy	451	TGCGACGTAGCATCTATGCACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATCGAC	510
Db	421	TGTGATGGTTCTATTATTAGATTAGTAAAACTACTAGAGTTAATGCACCATCTATTGAT	480
Qy	511	GGCACCBAACCTTCGACCAATACGTGTCCGTCGCCAGAGACAAGCGCACCAAGCGGTACC	570
Db	481	GGTACTCAAACTTTCGATCAATATTGGTCTGTTAGACAAGATBAAGAACTTCTGGTACT	540
Qy	571	GTCAGACGGGCTGCCACTTCGACGCTGGGCTCGCGCTGTGTTGAATGTCAACGGTGAAC	630
Db	541	GTTCAAACTGTGTCTATTTCGATGCTTGGGCTAGAGCTGTGTTGAATGTTAATGTGAT	600
Qy	631	CACACTACCAAGATCGTTGCAACGGAAGGCTACTTCAGCAGCGGCTATGCTCGCATCAC	690

Db	601	CATTATTATCAAAATGTTGCAACTGAAGGTATTTCCTTCCTGTTATGCTAGCAATTACT	660
Qy	691	GTTGCTGACGTGGCTAA	708
Db	661	GTTGCTGATGTTGTTAA	678

RESULT 4

```

US-10-425-115-177283
; Sequence 177283, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 177283
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_93271C.1
US-10-425-115-177283

```

Query Match	26.2%;	Score 257.2;	DB 8;	Length 850;
Best Local Similarity	64.2%;	Pred. No. 1.6e-71;		
Matches 420; Conservative	0;	Mismatches 228;	Indels 6;	Gaps 2;

QY	44	CCCCCGTGGCCCTTGGCGGCTTAGCCCGCACTGGGGCCCTGGCCCTTCCCGGCAAGGAATG	103
Db	139	CCACCGGTGCTTGCGCCGCCCGGTTGCTGACGCCAGCACCGACTTGTGTAGCGCTCCC	198
QY	104	CCACCGAGCTCGAAAAAGCGACAGACAACCCCCCACTCGAGAGGGCTGGCAGCATGCTTATT	163
Db	199	TCAGTGTATTGACTGCACGTCGCGGTATCCCCAGCTCCAGGGCACCCACAACGGCTGCT	258
QY	164	ACTATTCTGTGTGAGTGA CGGTGAGCGCAGGCGCACTACCAACCTGGAAGCGGCA	223
Db	259	TCTACTCTGTGTGAGACCGACGGTGGCGCCAGGCTACTACACCAACGAGGCGCGGCA	318
QY	224	CCTACGAGATCAGCTGGGGAGATGGCGGTAACTTCGTGGTGGAAAGGGCTGGAACCCCG	283
Db	319	AGTACAGGCTCAACTGGAAGACCGGTGTATACATGTTGGTGAAGGGCTGGAACCTCTG	378
QY	284	GCCGTGAAGCAAGAGCCATCCACTTGAAGGTGTTTACCAGCCAAACGGCAACAGTACC	343
Db	379	GTGCG---GCCCGCACCATCACTACTCCGGTACTTACAGCCCCAGGGTAACTCCTACC	435
QY	344	TTGCGGTCTACGGTTGGAACCGCAACCCGCTGGTCAGTATTACATCGTCGAACTTTG	403
Db	436	TTGCCATCTACGGCTGGAACCGCAACCCCTTGTGAGTACTACGTTGTTGAAACTTTG	495
QY	404	GCACTATGATCTCTTCTCCCGGTCTACCGATCTAGGAATGTGAGTGCACGGTAGCA	463
Db	496	GTACCTTAGCACCCGTCTCTGCGGCCAGCGTCAAGGGCTCCGTCAACCGCAGACGGCTCGT	555
QY	464	TCTATGCACTCGGCAAGACCACTGCGTCAACGCACTAGCATGACGGCAACCAACT	523
Db	556	CCTACAGATTGCGCAGACTCAGCGTGTCAACCAAGCCCTTCATGACGGCAACCAAGACT	615
QY	524	TCGACCAATACTGTGTGTCGTCGCGCAGAGCAAGCGCAACGCGTACCCTCAGACGGGCT	583
Db	616	TCAACGAGTACTGTGTCGTCGCGCAGAACGCAAGCGCAAGCTCCGCTCAACATGAAGA	675
QY	584	GCCACTTTCGACGCGCTGGGCTCGCGCTGGTTGATGTCAACGGTGACCACTTACTACCA	643
Db	732	CCCACTTCGACGCGCTGGGCTTCGACAGGGCATGTGAGCT---CGTCAAGCAACTACCA	732

Qy 644 TCGTTGCAACGGAGGCTACTTTCAGACGGGCTATGCTGCATCACCGTTGCTG 697
Db 733 TCGTCCGCCACCGAGGGTTACTTCTCCGGCAGCTCGTCGATCACCGTTACTG 786

RESULT 5

US-10-425-115-82922
; Sequence 82922, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 82922
; LENGTH: 749
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(749)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_175642C.1
US-10-425-115-82922

Query Match 25.1%; Score 246.6; DB 8; Length 749;
Best Local Similarity 63.9%; Pred. No. 4e-68;
Matches 423; Conservative 0; Mismatches 230; Indels 9; Gaps 3;

Qy 31 ATGTCGGCTTACCCCCGTTGCCCTGCGGCTTACCGCGACTGGGCCCTGCTTC 90
Db 80 ATGTTTCTTTCACCTCCATCATCACCGTGTGTCGGCTACCGGCTCTTGCGCC 139
Qy 91 CCGGCAAGGATGCCACGGAGCTCGAAAGCGACAGACACCCCACTCGAGGGCTGG 150
Db 140 CCGGC--CACTGATGTGTCTCTCGTTGCCCGTCAGAACACCCCAACGGCGGTAAC 196
Qy 151 CACGATGTTATTAATTAATTCCTGCTGAGTGAAGTGAAGCGGAGCGGCAAGTACCAAC 210
Db 197 CACAACGGCTGCTTGTGCTTGTGCTGATGAGCGGTGCGCGCTACCTACCAAC 256
Qy 211 CTGAAGCGGCACTACAGATCAGTGGGAGATGGCGTAACCTGTCGTGAAG 270
Db 257 GGTGCCGTGTAAGTACAGCGTAAGTGGGGAAGCGTGCAACCTCGTGGTAAG 316
Qy 271 GGCTGAACCCCGCTGAACGCAAGACCATCTTGAAGGTGTTACAGCAAC 330
Db 317 GGATGAACCCAGG--AACTGCCGTACATCACTACTCTGTAATTACACTAGAAC 373
Qy 331 GGCAACAGCTACTTGGCTGCTACCGGTGAACCGGCAACCCGCTGAGTATTATC 390
Db 374 GGCAACTCTTACTTGGCTGCTACCGGTGAACCGGCAACCCCTTGTGAGTACTAGCTC 433
Qy 391 GTCGAGAACTTTGGCACTATGATCTTCTCCGGTCTACCGATCTAGGAAGTGTGAG 450
Db 434 GTTGAACCTTCGGCACTACGACCCCTCTTCCAGTCCAGAACAGGGTACCGTAC 493
Qy 451 TGCAGCGTAGCATCTATGACTCGGCAAGCACTCGCTCAAGCAAGCACTAGCATGAC 510
Db 494 TCTGATGATCTTCTCAAGATCGTCAAGTGAACCGGTACCAACAGCCCTCATGAT 553
Qy 511 GGCACCAACCTTGCACCAATATCTGTCGTCGGCCAGGACAGGCAACAGCGGTAC 570
Db 554 GGCACCAAGACCTTTCAGCAGTATGTCGTCTGTCAGAACAGCGCTCTTCCGCTCC 613

Qy 571 GTCCAGACGGGCTGCCACTTTCGACGCCCTGGGCTCGCGCTGTTGAATGTCAACGGTGAC 630
Db 614 GTCAATATGAAGACTCACTTTGACGCCCTGGGCCAGCAAGGGCATGAA--CCTGGCCAG 670
Qy 631 CACTACTACCAAGATCGTTGCAACGGAGGCTACTTTCAGCAGCGGCTATGCTGCATCAC 690
Db 671 CACTACTACCAAGATGTCGCAACCGANGTTACTTCTCACTGTGAACGGCCAGATCAC 730

Qy 691 GT 692
Db 731 GT 732

RESULT 6

US-10-425-115-37173
; Sequence 37173, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 37173
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133906C.1
US-10-425-115-37173

Query Match 24.5%; Score 240.4; DB 8; Length 818;
Best Local Similarity 62.5%; Pred. No. 4.1e-66;
Matches 411; Conservative 0; Mismatches 241; Indels 6; Gaps 2;

Qy 35 TCGGCTTACCCCCGTTGCCCTTGGCGCTTACCGCGACTGGGCCCTGCTTCCCG 94
Db 96 TCATCACTGCTGCTGTTGCTGCGACTGTGCTTTCGCTGCTCCCGCACTGATGATGCTG 155
Qy 95 CAGGAATGCCACGGAGCTCGAAAGCGACAGACACCCCACTCGAGGGCTGGCAAG 154
Db 156 CTGTTCTCCGCGAGCTGTCGCTCGCCAGAGCACCCCAACCGCAAGGAACACACA 215
Qy 155 ATGTTATTAATTAATTCCTGCTGAGTGAAGTGAAGCGGAGCGGCAAGTACCAACCTGG 214
Db 216 ACGGCTGCTTCTACTCTTGTGTAAGTGAAGTGTGCTCAAGGTTACTTACACCAAGGCTG 275
Qy 215 AAGCGGCACTACAGATCAGTGGGAGATGGCGGTAACCTCGTGGTGAAGGGCT 274
Db 276 CAGGTGGCAGTACAGCGTCACTGGGGAAGCGCGCACTTGTGTGTAAGGCT 335
Qy 275 GGAACCCCGGCTGAACGCAAGACCATCTTGAAGGTGTTTACCAAGCAAGCGCA 334
Db 336 GGAACCTGATG--GCCCGCACCGTTACCTACTCGGGCTCTTCAACCCCAACGGCA 392
Qy 335 ACAGCTACTTGGCTGCTACAGGTTGACCCGCAACCCGCTGCTGAGTATTACATGCTG 394
Db 393 ACTCTACTTGCATCTATGAGTGAACAGTAAACCTCTGCTGAATACTATGTCGTTG 452
Qy 395 AGAATTTGGACCTATGATCTTCTCCGGTGTACCGATCTAGAACTGTGAGTGG 454
Db 453 AGAATTCGGAACCTATGACCCGAGTCCAGGCTAGCAACAGGGTACCGTACGCGG 512
Qy 455 ACGTAGCATCTATGACTCGGCAAGACCACTCGGCTCAAGCAAGCACTAGCATGACGCA 514
Db 513 ACGGCTCTTCTTCAAGATCGCTCAGTGAACCCGTACTAACCAAGCATTCATGATGAA 572
Qy 515 CCCAAACCTTGACCAATATCTGTCGGTCCGCCAGGACAAAGCGCAACAGCGTACCGTCC 574


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Db      573 CAAGGACCTTTCAGCAGTACTGCTGTCTTCCGCAAGAACAGCGCTCCAGCGGATCCGTGA 632
Qy      575 AGACGGGCTGCCACTTTCGACGCGCTGGGCTCGCGCTGTTTGAATGTCACGGTGACCACT 634
Db      633 ACATGAAGACTCACTTCGATGCTTGGGCGCAGCAAGGGCATGACTCT--TGGTAGCCACT 689
Qy      635 ACTACCAGATCGTTGCAACGGAGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 692
Db      690 ACTACCAGATTCGCTTACCGAGGATTACTTCTCCACCGGTTCTGCGTCTATCACTGT 747
```

RESULT 7

```
US-10-213-990-65
; Sequence 65, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 65
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(666)
US-10-213-990-65
```

```
Query Match      22.8%; Score 224.6; DB 5; Length 666;
Best local Similarity 61.5%; Pred. No. 4.5e-61;
Matches 413; Conservative 0; Mismatches 249; Indels 9; Gaps 3;
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```
Qy      31 ATGTCGGCTTTACCCCGTTGCCCTTGCGGCTTAGCCCGCACTGGGGCCCTGCGCTTC 90
Db      1 ATGCTCATCTCTTCTCTCGTTTCGCTGCTCCACCGTTGCTGGCGTGAAGTACA 60
Qy      91 CCGG---CAGGGAATGCGACGAGCTGAAAAGCAGACAGAACCCCACTCGAGGGC 147
Db      61 CCGGCTCGAGCAATACGTTGAGCTAGCCAGCGCAGCTCAACAGCTCAAGTGGC 120
Qy      148 TGGCAGATGTTATTACTATTCCTGTTGAGTGAAGCGTGAAGCGGCAAGCCAGTACAC 207
Db      121 ACGAATAACGGCTACTACTCTCTTGAGACCGACGCGCGGCAAGTGAAGTACAC 180
Qy      208 AACCTGGAAGCGGCACTACGAGATCACTGGGAGATGGCGGTAACTCTGCTGGTGA 267
Db      181 AACGGCAATGGCGGCCAGTATCAGGTGAGTGAACAACATGCGGCACTTGTGCTGG 240
Qy      268 AAGGGCTGGAACCCCGGCTGAAACGCAAGCCATCCACTTTGAGGGTGTTCAGGCCA 327
Db      241 AAGGGCTGGAACCCGGCC--AGCGAAGAAAGCGTCACTCAAGCGGCTCTGCGAGACC 297
Qy      328 AACGGCAACAGCTACCTTGCGTCAAGGTTGAGACCGCAACCGGCTGTGAGTATTAC 387
Db      298 AGCGAAGAGGCTACTCTCGTGAAGGCTGAGACGACGATCGGCTGTGGAATTCTAC 357
Qy      388 ATGTCGAGAACTTTGGCACTATGATCCTTCTCCGCTGCTACCGATAGAACTGTC 447
Db      358 ATGTCGAGAGTTACGGCTCTATGATGACCTCCACGGGAGCCACCATCTCGGCACTGC 417
Qy      448 GAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACCACTCGGCTCAAGCAAGCACTAGCATC 507
Db      418 GAGAGCGAGCGGGCCACGTAACAACCTTTACAAGACGACGCGGCAAGAAATGCGCGTCCATC 477
```

```
Qy      508 GACGGCAACCAAACTTCGACCAATACTGTCGGTCCGCCAGGACAAAGCCGACGCGGT 567
Db      478 CAGGCAAGGCTACTTTTGACAGTACTGTCGGTTCGAACTTCGACCCGGCAGAGTGA 537
Qy      568 ACCGTCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGCTGTTGAATGTAACGGT 627
Db      538 ACTGTAGACAGCAAGAACCACTTTGATGCGTGAGAAATGCGGCTCTGCAATT---GGGG 594
Qy      628 GACCACTACTACAGATCGTTGCAACGGAGGCTACTTCAGCAGCGGCTATGCTCGCATC 687
Db      595 AACTTGACTATATGATGTTGCGACGAGGGGTACCAAGCAGCAGCGGCTCTGCTACTATC 654
Qy      688 ACCGTTGCTGA 698
Db      655 ACTGTTCTTGA 665
```

RESULT 8

```
US-10-213-990-68
; Sequence 68, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 68
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(705)
US-10-213-990-68
```

```
Query Match      22.7%; Score 223; DB 5; Length 705;
Best local Similarity 60.5%; Pred. No. 1.5e-60;
Matches 411; Conservative 0; Mismatches 250; Indels 18; Gaps 2;
```

```
Qy      29 TGATGTCGGCTTTACCCCGTTGCCCTTGCGGCTTAGCCCGCACTGGGGCCCTGCGCT 88
Db      23 TGCTGGCGTCTCGGCCATTGAGCTCTGCTGCGCCCGCGCAACCCGAGCACTCTCT 82
Qy      89 TCCCGGAGGAATGCGACGAGCTGAAAAGCAGACAAACCCCACTCGAGGGCT 148
Db      83 TCAATGAGACTGCTTTCATGAGTTGCTGAGCGCGCGCGCAACCCCAAGCTTCAACGGCT 142
Qy      149 GGCAGATGTTATTACTATTCCTGTTGAGTGAAGGTTGAGCGGCAAGCCAGTACACCA 208
Db      143 GGAACAAGGCTACTACTACTCTTCTGAGTGAATGGCGGCGGCAAGTGAAGTACACCA 202
Qy      209 ACCGTGAAGCGGCACTCAAGATCAGCTGGGGAGATGGCGGTAACTCTCGGTGGA 268
Db      203 ATGGCGCGGCTGCTCGTACTTCGTTCACTGAGGAAAGTGGGCACTTTGTGCTGGA 262
Qy      269 AGGGCTGGAACCC-----CGGCTGAAACGCAAGAGCCATCCACTTTGAGG 313
Db      263 AGGGCTGGAACCCCTGGAAGCGCTAGGTAACGAGCTTTAAGTAACCATCACTACGAG 322
Qy      314 GTGTTTACAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGAGCCGCAACCCGC 373
Db      323 GCAGCTTCAACCCAGCGGCAATGGCTACCTGCGTGTCTACGGCTGAGCAACCAACCCCT 382
Qy      374 TGGTCGATATTACATCGTCGAGAACTTTGACACTATGATCCTTCTCGGTGCTACCG 433
Db      383 TGATGAGTACTAGTGTGAGTGTGATGATGATACAAACCCGCGAGCGGCTACCT 442
```

QY 434 ATCTAGAACTGTGAGTGCAGCGGTAGCATCTATGACTCGGCAAGACCACTCGCGTCA 493
DB 443 TCAGGGGCACTGTCAACACCGGCGGTGCACTTACAATCTACACGCGCGCTCGCTACA 502
QY 494 ACCGACCTAGCATGACGCGGCAACCAACTTCGACCAATACTGTCGGTCCGCCAGGACA 553
DB 503 ATGCTCCCTCCATCGAAGGCAACCAAGACCTTCAACCCAGTACTGTCGTGCGCACTTCCA 562
QY 554 AGCGACCAAGCGGTACCGCTCCAGACGCGGCTGCCACTTCGACCGCTGGGCTCGCGCTGTT 613
DB 563 AGCGTACCGGCGGCACTGTACCATGCGCAACCACTTCAACGCGCTGAGAGCACTGGGCA 622
QY 614 TGAATGTCAACGCTGACCACTACTACAGATCGTTGCAACGAGGCGTACTTCAGCAGCG 673
DB 623 TGAA---CCTGGAACTCAACAACCTACAGATTGTGCGCACTGAGGCTTACCAAGACGCG 679
QY 674 GCTATGCTCGCATCACCGT 692
DB 680 GATCTGCTTCCATCACTGT 698

RESULT 9

US-09-770-621-1
Sequence 1, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M neyl, Arja
APPLICANT: Vehmanper, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. US20010024815A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-09-770-621-1

Query Match 20.1%; Score 197.2; DB 3; Length 1375;
Best Local Similarity 58.6%; Pred. No. 4e-52;
Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;

QY 35 TCGGCTTACCCCGTTGCCCTTGCGGCTTAGCCCGCACTGGGCGCTGCGCTTCCCGG 94
DB 349 TCGGCTCCGGCGCATGTCACCAAGTGCCTTGCCCTGGCACTCGCCATCGCGGTGCGC 408
QY 95 CAGGAATGCCACGAGCTCGAAAAGCGACAGACACCCCACTCGAGGGCTGGCAGC 154
DB 409 TCGTCCCGGCGACGCGCCCGGACACCAACCAATCAACCAAGACCGGTAACGACA 468
QY 155 ATGTTATTACTATTCTGTTGAGTGAAGTGAAGGCGGCGGCGGCGGCGGCGGCGGCGG 214
DB 469 ACCGCTACTTCTACTCTGTTCTGGAACGACGCGCGCGGCGGCGGCGGCGGCGGCGG 528
QY 215 AAGCGGCACTTACGAGATCACTGGGAGATGGCGGTAACCTCGTGGTGAAGGCGCT 274
DB 529 CGGGCGGCACTACAGACCTCTGCGGGAACACCGGAACTTCTGCGCGGCGGCGGCGGCT 588
QY 275 GGAACCCCGGCGCTGAAACGAGACCATCCACTTTGAGGGTGTTCACAGCAACGCGCA 334
DB 589 GGTCCACCGG---GGAGCGGCGGACGTAACCTTCAACCGCTTCAACCGCTGCGGTA 645
QY 335 ACAGTACTTGGCGTCTACGCTTGAGCCGCAACCGGCTGCTGAGTATTACATCGTGC 394
DB 646 ACCGCTACTCAGCTCTTACGCTTGAGCAGCAAGAACCGGCTGCTGAGTACTACATCGT 705
QY 395 AGAATTGGACACCTATGATCTTCTCCGCTGCTACCATCTAGAACTGTGAGTGGC 454
DB 706 AGAGTGGGGCACTTACCGGCGGCAAC---GGACCTTCAAGGGCACCGTCAACACCG 759
QY 455 ACCGTACATCTATGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATCGACGCA 514
DB 760 ACCGGGAACGTACGACATCTAGAGACCTGGCGGTACAAACCGCTCATCGAGGCA 819
QY 515 CCCAAACCTTGAACCAATCTGTCGTCGCGCAGGACAGGACGACGCGGTACCGTCC 574
DB 820 CCGGACCTTCCAGCAGTCTTGAGCGTCCGCGCAGAGGAGGACGCGGACCATCA 879
QY 575 AGACGGCTGCACTTGAAGCGCTGGGCTGCGCTGCTGTTGAATGTCAACGTTACCACT 634
DB 880 CCATCGGCAACCACTTGAAGCGCTGGGCGCGCGCGGATGAA---CTGGGACGCGACG 936
QY 635 ACTACCAATCTGTCAGACGAGGCTACTTACAGACGCGGTATGCTGCATCACCGTGG 694
DB 937 ACTACCAATCTGTCAGACGAGGCTACTTACAGACGCGGTATGCTGCATCACCGTGG 996
QY 695 CTGACGTGGGCTAAGACGTAACCTGGTG 722
DB 997 GCGAGGTGGCAACCCCGCAACCCCGG 1024

RESULT 10

US-10-286-993-1
Sequence 1, Application US/10286993
Publication No. US20030148453A1
GENERAL INFORMATION:
APPLICANT: Mantyla, Arja
APPLICANT: Paloheimo, Marja
APPLICANT: Lantto, Raija
APPLICANT: Fagerstrom, Richard
APPLICANT: Lahtinen, Tarja

```
/ APPLICANT: Suominen, Pirkko
/ APPLICANT: Vehmanpera, Jari
/ TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
/ TITLE OF INVENTION: Fungi
/ FILE REFERENCE: 1716.0340004
/ CURRENT APPLICATION NUMBER: US/10/286,993
/ CURRENT FILING DATE: 2002-08-13
/ PRIOR APPLICATION NUMBER: US/09/120,804
/ PRIOR FILING DATE: 1998-07-23
/ PRIOR APPLICATION NUMBER: PCT/FI97/00037
/ PRIOR FILING DATE: 1997-01-24
/ PRIOR APPLICATION NUMBER: US 08/590,563
/ PRIOR FILING DATE: 1996-01-26
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 1375
/ TYPE: DNA
/ ORGANISM: Actinomadura flexuosa (Strain: DSM43186)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (303)..(1337)
/ OTHER INFORMATION: Product= AM35 xylanase
US-10-286-993-1
```

```
Query Match      20.1%; Score 197.2; DB 6; Length 1375;
Best Local Similarity 58.6%; Pred. No. 4e-52;
Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;
```

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QY      35 TCGGCTTTACCCCGCTTGCCCTTGCGCGCTTACCGCGACTGGGGCCCTTGCCCTCCCG 94
DB      349 TCGGCTCCGGCGCATCGTCACAGTGGCTTGGCCCTGGCACTGCCATCGCGGTGCGC 408
QY      95 CAGGAATGCCACGAGCTCGAAAAGGACAGACAACCCCACTCGAGGGCTGGCAG 154
DB      409 TGCTGCCCGGACGGCCCGCCGACACCACTACCCAGAACAGACCGGGTACGACA 468
QY     155 ATGTTATTACTATTCTCTGTGAGTACGGTGGAGCGGCAAGCCACGTACACCACTGG 214
DB     469 ACGGCTACTTCTACTCTGTTCTGGACCGACGCGCCCGGACCGTCTCATGACCTTCACT 528
QY     215 AAGCGGCACTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAAGGCT 274
DB     529 CGGGCGGACGTACAGCACCCTGCGGGAACACCGGAACTTCTGCGCGGCAAGGGCT 588
QY     275 GGAACCCCGGCTGAACGCAAGACCACTTTCAGGGTGTTCACGACCAAGGCA 334
DB     589 GGTCACCGG---GGAGCGGCGGACGCTGACTCAACAGCCTCTTCAACCCGTCGGGTA 645
QY     335 ACAGCTACTTGGCGTCTACGGTTGACCCGCAACCCGCTGGTCAAGTATTACATCTCG 394
DB     646 ACGGCTACTTCAAGCTCTACGGCTGACAGGAACCCGCTGCTGAGTACTACTATCTGTCG 705
QY     395 AGAATTGGCACTATGATCTTCTCTCGGCTGCTACCGATCTAGGAATGTGGAATGTGAGTGG 454
DB     706 AGAGCTGGGGCACTACCGGCCACCC-----GGCACTACAGGGGCAACCGTCAACCG 759
QY     455 ACGGTAGCATCTATGACTCGGCAAGACCACTGCGTCAAGGCACTAGCATCGAGGCA 514
DB     760 ACGGGGGAAGTACGACATCTACGAGACTGGCGGTACAAAGCGCGCTCATCGAGGGCA 819
QY     515 CCCAAACCTTTCGACCAATACTGTCGTCGCGGACAGACAGCGCAACGCGGTACCGTCC 574
DB     820 CCCGACCTTTCGACAGTCTGAGCGTCCGGGACAGAGCGGACAGCGGCACTCA 879
QY     575 AGAGGGGTGCACTTGCAGCGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACT 634
DB     880 CCATCGGCAACCACTTGCAGCGCTGGGCGCGCGCGCATGAA---CTGGGCAAGCAAG 936
QY     635 ACTACGAGATCTTGCAACGAGGGGCTTTCAGCAGCGGCTATGCTGCATCAACCGTTG 694
DB     937 ACTACGAGATCATGGCGACCGAGGGGCTTACAGAGCAGCGGTAGCTCCACCGTCTCATCA 996
```

```
QY      695 CTGACGTGGGCTAAGACGTAACTGCTG 722
DB      997 GCGAGGTGGCAACCCCGGCAACCCGGG 1024
```

RESULT 11

```
US-10-213-990-67
/ Sequence 67, Application US/10213990
/ Publication No. US20030082595A1
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Bo
/ APPLICANT: Bussey, Howard
/ APPLICANT: Storms, Reg
/ APPLICANT: Roemer, Terry
/ TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
/ TITLE OF INVENTION: ENZYMES AND METHODS OF USE
/ FILE REFERENCE: 10182-019-999
/ CURRENT APPLICATION NUMBER: US/10/213,990
/ PRIOR FILING DATE: 2002-08-05
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 67
/ LENGTH: 739
/ TYPE: DNA
/ ORGANISM: Aspergillus
US-10-213-990-67
```

```
Query Match      19.4%; Score 190.6; DB 5; Length 739;
Best Local Similarity 57.8%; Pred. No. 4e-50;
Matches 412; Conservative 0; Mismatches 249; Indels 52; Gaps 2;
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QY      29 TGATGTCGCTTTTACCCCGTTGCCCTTGCGGCTTACCGCGACTGGGCGCTGGCCT 88
DB      23 TGCTGGGCTGCTCCGCCATGAGCTCTGCTGCCCGCGTGAACCCGAGCAACCTCGT 82
QY      89 TCCCGGAGGAATGCCACGAGCTCGAAAAGGACAGACAACCCCACTTGGAGGGCT 148
DB      83 TCAATGAGACTGCTCTTCAATGAGTTGCTGAGCGCGCGGACCCCAAGCTTCAACCGCT 142
QY     149 GGCACGATGTTATTACTATTCTGTGAGTGAAGTGAAGCGGACGAGGCAAGCTACACCA 208
DB     143 GGAACAAGGCTACTACTACTCTTCTGTGACTGATGGCGGCGGACGATGACTACACCA 202
QY     209 ACCTGGAAGCGGCACTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGA 268
DB     203 ATGCGCGGCTGCTGCTGCTGCTGCTCACTGAGAGAACGTGGCACTTGTCTGGTGA 262
QY     269 AGGCTGGAACCCCGGCTG----- 288
DB     263 AGGCTGGAACCTTGAAGCGTAACTACCGAGCTTGTCAAGCTCGGATGTCAGACT 322
QY     289 -----AACGCAAGACCATCCACTTTGAGGGTGTTCACAGCCAAAGGCAACAGC 339
DB     323 GTGGCTGACAGAGTAGAACCATCACTACGAGGCACTTCAACCCGAGGCAATGGC 382
QY     340 TACCTTGGGCTTACCGTTGACCCGCAACCCGCTGCTGAGTATTACATCTGCGAAG 399
DB     383 TACCTGGCTGTCTACGGCTGACCAACCAACCCCTTGAATTGACTACTAGTTGTGAGTGC 442
QY     400 TTGGAACCTATGATCTTCTCTCGGTGCTACCGATCTAGGAATGTGAGTGGAGCGGT 459
DB     443 TATGTATATACAAACCCCGGACGCGGTACTCTTCAAGGGCACTGTCAACAGCGGT 502
QY     460 AGCATCTATGACTCGGCAAGACCACTGCGGTCAAGCACTAGCATGACGCAACCA 519
DB     503 GGCATTAACAACATCTACAGGCGCGTTCGTACATATGCTCCCTCATCGAAGGACCAAG 562
QY     520 ACCTTGACCAATACTGTCGTCGCGGCAAGCAAGCGCAACGCGGTACCGTCAAGAG 579
DB     563 ACCTTCAACCACTACTGTCGTGTGCGCACCTCCAAAGCTACCGGCGGCACTGTACCATG 622
QY     580 GGTGCACTTGCAGCGCTGGGCTGCGCTGTTGAATGTCAACGGTACCACTACTAC 639
```

Db 623 GCCAACCACTTCAACGCCCTGGAGCAGACTGGGCATGAA---CCTGGAACTTCACACTAC 679
Qy 640 CAGATCGTTGCAACGAGGGCTACTTACAGCGGCTATGCTCGCATCACCGT 692
Db 680 CAGATTGCGCCACTGAGGGTTACAGACAGCGGATGCTTCCATCACTGT 732

RESULT 12

US-10-213-990-64

; Sequence 64, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; NUMBER OF SEQ ID NOS: 2002-08-05
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 712
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-64

Query Match 18.4%; Score 181.2; DB 5; Length 712;
Best Local Similarity 57.7%; Pred. No. 4.1e-47;
Matches 412; Conservative 0; Mismatches 253; Indels 49; Gaps 3;

Qy 31 ATGTCGCTTTACCCCGTTGCGGCTTACCGCGACTGGGGCCCTGCGCTTC 90
Db 1 ATGTCCTACTCTCTCTCTGTTGCGCTGCTCCACCGTTGCTGCGTACTAGTACA 60
Qy 91 CCGG---CAGGGAATGCCACGAGCTCGAAAGCAGACAGCAACCCCACTCGAGGGC 147
Db 61 CCGGCTCGAGCAATACGTTGAGCTAGCCAAAGCGCAGCTCAAGCTCTCAGACTGGC 120
Qy 148 TGGCAGCATGTTATTACTATTCCTGTTGAGTGAACGGTGAAGCGCAGCCACTACAC 207
Db 121 ACGAATAACGGCTACTACTCTCTTGGACCGACGGCGGCCAGGTGACCTACACC 180
Qy 208 AACCTGGAAGCGGCACTACGAGATCAGTGGGAGATGGCGGTAACCTCGTGGTGA 267
Db 181 AACGGCAATGGCGGCCAGTATCAGGTGCACTGGAACAACCTGGCGCACTTGTGCTGGG 240
Qy 268 AAGGCTGGAACCCCGGCTGAACGCA----- 294
Db 241 AAGGCTGGAACCCCGGCGCAGCGAAGATAGCTCTCTCTGCTGTTAGTTCAAGC 300
Qy 295 -----AGAGCCATCCACTTTGAGGTTTACCAGCCAAAGGCAACAGCTACT 344
Db 301 TAATGATTCAAGAGGGTCACTACAGCGGCTCTGCGACAGCGGAAACGGCTACT 360
Qy 345 TGGGTTCTACGTTGGAACCGCAACCGCTGTTGAGTATTAATCGTGAAGACTTGG 404
Db 361 CTCCGTGTACGGCTGGAACGACCAAGTCCGCTGTTGAATTCATCGTGAAGATTGG 420
Qy 405 CACCTATGATCTTCTCTCCGGTCTACCGATTAAGAACTGTGAGTGGCAGCGTACAT 464
Db 421 CTCTATGACCCCTCTCAAGGAGCCACCCATCTCGGCAACCGTCAAGAGCGGCGCAC 480
Qy 465 CTATGACTCGGCAAGCACTCGCGTTCAAGCACTAGCATGACGGCAACCAAACTT 524
Db 481 GTACAACCTCTACAAGACGACGCGAAGATGCGCGTCCATCAAGGCAAGGCTACTT 540
Qy 525 CGACCAATACTGTCGGTCCGCGCAGACAGCAAGCGCACAGCGGTACCGTCCAGACGGGCTG 584
Db 541 TGACCAAGTACTGTCGGTTCGGAAGTTCGCAACGGCAGAGTGAAGTGTGACGAGAAAGA 600

Qy 585 CCACTTCAGCGCCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACTACTACAGAT 644
Db 601 CCACTTTGATGCGTGAAGAAATGCGGCTGCAATT---GGGAACTTTGACTATATGAT 657
Qy 645 CGTTGCAACGAGGGCTACTTACAGACGGGCTATGCTCGCATCACCGTTGCTGA 698
Db 658 TGTTCGACGAGGGGTACCAAGACAGCGGCTGCTACTATCACTGTTCTTA 711

RESULT 13

US-10-213-990-71

; Sequence 71, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; NUMBER OF SEQ ID NOS: 2002-08-05
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(942)
US-10-213-990-71

Query Match 16.8%; Score 165.4; DB 5; Length 942;
Best Local Similarity 59.3%; Pred. No. 5.6e-42;
Matches 340; Conservative 0; Mismatches 221; Indels 12; Gaps 3;

Qy 126 GACACCCCACTCGAGGGCTGGCAGATGTTATTACTATTCCTGTTGAGTGAACGG 185
Db 99 GATCAGCAGCAGCAGCAGCAGCAACAAATGGCTACTATTCCTTCTGACCAACGG 158
Qy 186 TGGAGCGGAGCCACGTACACCAACCTGGAAGCGGCACCTACGAGATCAGTGG---- 241
Db 159 TGCCGATCAGTGCAATATATAGTGTGCTGTTGGCAATATAGTGAACGTTGGCGAA 218
Qy 242 --GAGATGCGGTAACTCGTGGTGAAGAGGCTGGAACCCCGCTGAACGCAAGAC 299
Db 219 CCAGAACGTTGTTACTTACTGTGGAGAGGCTGGAATCCAGG--GAGTGAACATGA 275
Qy 300 CATCACTTTGAGGGTATTACCAACCAACGCAACAGCTACTTGGGCTACGTTG 359
Db 276 CATTAACCTTCTGCGAGCTTCAATCCTCCGAAATGCTTACCTGTCGTATGATG 335
Qy 360 GACCCGCAACCCGCTGTCGATTTACATCGTCGAGAACTTGGCACTATGATCCTTC 419
Db 336 GACTACCAACCCCTAGTGAATATACATCTCTGAGAACTATGGCAATTCAATCCTGG 395
Qy 420 CTCCGTTGCTACCGATCTAGGAATGTCGAGTGGCAGCGGTAGCATCTATCGACTG 479
Db 396 CTGGGCAATGACGCAAGGGCAGCGTCAACGAGTGAATCCACTACGACATCTATGA 455
Qy 480 GACCACTGCGGTCAACGCACTAGCATGACGGCACCACCAACCTTGACCAATATGCTG 539
Db 456 GACCAACAGGTCAACAGCCTTGCATGTCGGCAGCGGCACCTTCAACCAATATGCTG 515
Qy 540 GGTCCGCGAGCAAGCGCAGCGGTACCGTCCAGAGCGGCTGCCACTTGAACGCTG 599
Db 516 CATCCGCGCAAAACAAGCGATCAGGGGCAAGTCAACCGCGAATCACTTCAAGGCTG 575
Qy 600 GGCTGCGCTGTTGATGTCAACGGTGAACCACTACTACAGATCGTTGCAACGAGGG 659
Db 576 GGCTAGTCTGGGGATGAA---CCTGGGTACCACTATCACTATGATTTCCACTGAGGG 632

Qy 660 CTACTTCAGCAGCGCTATGCTGCATCACCGT 692
Db 633 ATATGAGCAGCGGTACTCTGCACCATCACTGT 665

RESULT 14

US-11-018-645-21
; Sequence 21, Application US/11018645
; Publication No. US20050208178A1
; GENERAL INFORMATION:
; APPLICANT: Bauer, Michael
; APPLICANT: Bedford, Michael
; APPLICANT: Pulliam, Derrick
; TITLE OF INVENTION: Microbially Expressed Xylanases and Their Use as Feed Additives
; TITLE OF INVENTION: Uses
; FILE REFERENCE: 70357WOPCT
; CURRENT APPLICATION NUMBER: US/11/018,645
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: 60/531,404
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: XYL1A1E
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(978)
US-11-018-645-21

Query Match 15.8%; Score 155.2; DB 10; Length 978;
Best Local Similarity 56.8%; Pred. No. 1.1e-38;
Matches 327; Conservative 0; Mismatches 243; Indels 6; Gaps 2;

Qy 130 ACCCCCACTCGAGGGCTGGCAGCATGTTATTACTTCTCTGGAGTACGGTGA 189
Db 19 ACGTGAGCCAGACGGGACCAACAAGCAATTACTTTCTGTAAGAACAGTCCG 78
Qy 190 GCGCAGCCACGTACACCAACCTGGAAGCGGCACACTACGAGATCAGCTGGGAGATGGC 249
Db 79 GGCACGGTGAATCTTGATGTATGCGAATGGCCGCTATACCTCCACTGAGGGGCATC 138
Qy 250 GGTAACTCTCGTGGTGGAAAGGCTGGAACCCCGGCTGAAAGCAAGAGCCATCCATT 309
Db 139 AACAACTGGGTGGGGCGGCAAGGGCTGGGCTACCGGCTCCAGCCACAGATCAGCTACTCC 198
Qy 310 GAGGGTGTTCACAGCCAAACGGCAACAGTACCTTGGGCTTACGGTTGACCCGCAAC 369
Db 199 GGCACGTTCAATTGCGCG--GGCAACGGTTACCTGGCCTGTATGGCTGACCAACAAT 255
Qy 370 CCGCTGGTCAAGTATTACATCGTCGAAACTTTGGCACTATGATCCTTCTCCGGTGT 429
Db 256 CCATTGGTCAAGTACTACATCGTCGACAGCTGGGGTACTTACCGTCCGCGGGGCGGCAG 315
Qy 430 ACCGATCTAGGAAGTGTGAGTGGCAGCGGTAGCATCTATGACTCGGCAAGCACTGCG 489
Db 316 GGTTCATGGGCAAGGTAGTTCGACAGGGGGGCAAGTACGATGACCGGCAAGCGC 375
Qy 490 GTCAACGCACTAGCATGACGCGCAACCAACCTTCCACCAATATGCTGCTCCGCGCCAG 549
Db 376 GTGAACCAAGCCATCATCATCGGCAAGCCACGTTTACCAAGTACTGAGCGGTGCGGCGAG 435
Qy 550 GACAAGCGCAACGCGGTACCGTCCAGACGGGCTGCCACTTGACGCGCTGGGCTGCGGT 609
Db 436 TCGAAGCGCGTGGGCGGCAACCAATCATGCGCAACCAATTTCAACGCTGGGCGACGCTG 495
Qy 610 GGTTCGATGTCACGCGTGAACCACTATACAGATCGTTGCAACGAGGGGCTACTTCAGC 669
Db 496 GGCATGAA---CCTGGGCGAGCAAACTACAGGTCAATGGCCACCGAGGGTTACCAAGAGC 552

Qy 670 AGCGGCTATGCTCGCATCACCGTTGCTGACGTGGC 705
Db 553 AGCGGAGCTCCGACATCACCGTGACCGAAGGTGGC 588

RESULT 15

US-10-213-990-70
; Sequence 70, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-70

Query Match 15.0%; Score 147.2; DB 5; Length 1002;
Best Local Similarity 62.2%; Pred. No. 4.1e-36;
Matches 249; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

Qy 293 CAAGAGCCATCCACTTTGAGGGTGTTCACGCAACCGCAACAGCACTACCTTGGGCTCT 352
Db 329 CTAGTGAATTAATCTTCTGTGGCAGCTTCAATCTTCCGAAATGCTTACTGTCCGTGT 388
Qy 353 ACGGTGGAACCGCAACCGCTGTGAGTATTAATCTGTCGAACTTTGGCACTATG 412
Db 389 ATGATGGAATACCAACCCCTAGTGAATATCAATCTTCGAGAACTATGGCAGTTACA 448
Qy 413 ATCTTCTCTCGGTGCTACCGATCTAGAACTGTGAGTGGCAGGTAGCATCTATGAC 472
Db 449 ATCTGCTCTGGGATGAGCAACAAGGCACCTTCAACAGCATGATCACTACGACA 508
Qy 473 TCGCAAGAACCACTCGGCTCAACGCACTAGCATGCAAGGCAACCAACCTTGCACCAAT 532
Db 509 TCTATGAGCAACCAACAGTCAACGACCTTCAATGCTGGCAGCGGCACTTCAACCAAT 568
Qy 533 ACTGGTGGTCCGCGCAGCAAGCGCACAGCGGTACCGTCCAGACGGGCTGCCACTTGG 592
Db 569 ACTGGTCCATCCGCCAACAAGCGATCCAGCGCAAGTCAACCAACCGGAATCACTTCA 628
Qy 593 ACGCTGGGCTCGCGTGGTGAATGTCAACGCTGACCACTACTACAGATGCTTGCAA 652
Db 629 AGGCTGGGCTAGTGTGGGATGAA---CCTGGGTACCATTAATCAATGATTTTCCA 685
Qy 653 CGGAGGCTACTTCAAGCAGCGGTATGCTGCATCAACCGT 692
Db 686 CTGAGGATATGAGAGCAGCGGTACTCTGACCATCACTGT 725

Search completed: February 11, 2006, 23:51:27
Job time : 1025.32 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:37:15 ; Search time 314.228 Seconds
(without alignments)
2812.856 Million cell updates/sec

Title: US-09-467-368-1
Perfect score: 983
Sequence: 1 TCGGCCGACGCTCTTGCAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
12: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	585	59.5	588	11	US-11-170-653-9 Sequence 9, Appli
2	202.2	20.6	1008	7	US-10-517-939-231 Sequence 231, App
3	197.2	20.1	1375	11	US-11-108-163B-1 Sequence 1, Appli
4	190.2	19.3	663	11	US-11-108-163B-5 Sequence 5, Appli
5	190.2	19.3	906	11	US-11-108-163B-4 Sequence 4, Appli
6	187	19.0	663	11	US-11-108-163B-3 Sequence 3, Appli
7	187	19.0	906	11	US-11-108-163B-2 Sequence 2, Appli
8	186.2	18.9	1059	7	US-10-517-939-225 Sequence 225, App
9	185	18.8	1047	7	US-10-517-939-165 Sequence 165, App
10	170	17.3	1074	7	US-10-517-939-199 Sequence 199, App
11	170	17.3	1137	7	US-10-517-939-255 Sequence 255, App
12	165.8	16.9	1041	7	US-10-517-939-169 Sequence 169, App
13	165.6	16.8	1044	7	US-10-517-939-221 Sequence 221, App
14	165.4	16.8	1299	7	US-10-517-939-177 Sequence 177, App
15	161.6	16.4	1083	7	US-10-517-939-217 Sequence 217, App
16	160.8	16.4	1044	7	US-10-517-939-195 Sequence 195, App
17	160.8	16.4	1083	7	US-10-517-939-183 Sequence 183, App
18	156.2	15.9	1047	7	US-10-517-939-253 Sequence 253, App
19	150.8	15.3	1065	7	US-10-517-939-215 Sequence 215, App
20	150.6	15.3	1071	7	US-10-517-939-233 Sequence 233, App
21	150.2	15.3	1041	7	US-10-517-939-159 Sequence 159, App

22	146.4	14.9	1047	7	US-10-517-939-299	Sequence 299, App
23	141.8	14.4	1077	7	US-10-517-939-181	Sequence 181, App
24	131.2	13.3	1047	7	US-10-517-939-161	Sequence 161, App
25	128	13.0	1029	7	US-10-517-939-219	Sequence 219, App
26	127.8	13.0	747	7	US-10-517-939-227	Sequence 227, App
27	124	12.6	1695	7	US-10-517-939-317	Sequence 317, App
28	119.2	12.1	642	11	US-11-214-413-31	Sequence 31, Appl
29	118	12.0	669	7	US-10-517-939-167	Sequence 167, App
30	116.4	11.8	1086	7	US-10-517-939-211	Sequence 211, App
31	114.8	11.7	1068	7	US-10-517-939-205	Sequence 205, App
32	109.2	11.1	1020	7	US-10-517-939-153	Sequence 153, App
33	108.4	11.0	633	7	US-10-517-939-197	Sequence 197, App
34	107.2	10.9	636	7	US-10-517-939-197	Sequence 207, App
35	106.8	10.9	555	7	US-10-517-939-251	Sequence 251, App
36	95.4	9.7	1983	7	US-10-517-939-353	Sequence 353, App
37	94.2	9.6	570	7	US-10-517-939-189	Sequence 189, App
38	93.4	9.5	1068	7	US-10-517-939-163	Sequence 163, App
39	92.4	9.4	1338	7	US-10-517-939-367	Sequence 367, App
40	91.8	9.3	570	7	US-10-517-939-377	Sequence 377, App
41	91.4	9.3	678	7	US-10-517-939-171	Sequence 171, App
42	91	9.3	645	7	US-10-517-939-157	Sequence 157, App
43	91	9.3	1053	7	US-10-517-939-191	Sequence 191, App
44	90.2	9.2	570	7	US-10-517-939-375	Sequence 375, App
45	89.8	9.1	1077	7	US-10-517-939-369	Sequence 369, App

ALIGNMENTS

RESULT 1
US-11-170-653-9
; Sequence 9, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Thermomyces lanuginosus
US-11-170-653-9

Query Match 59.5%; Score 585; DB 11; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.9e-148; Indels 0; Gaps 0;
Matches 585; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	124	CAGACACCCCACTCGAGGCTGGACGATGTTATTCTATTCCTGTGAGTGAC	183
DB	4	CAGACACCCCACTCGAGGCTGGACGATGTTATTCTATTCCTGTGAGTGAC	63
QY	184	GGTGAAGGCGAGGCGACGTACCAACTGGAAGGCGCACTACGAGATCAGCTGGGA	243
DB	64	GGTGAAGGCGAGGCGACGTACCAACTGGAAGGCGCACTACGAGATCAGCTGGGA	123
QY	244	GATGGCGTTAAGCTCGTGGTGAAGGCTGGAACCCCGCTGAACGCAAGCCATC	303
DB	124	GATGGCGTTAAGCTCGTGGTGAAGGCTGGAACCCCGCTGAACGCAAGCCATC	183

```
QY 304 CACTTGAGGGTGTTCACGACCAACGGCAACAGCTTACCTTGGGTCTACGGTTGGACC 363
DB 184 CACTTGAGGGTGTTCACGACCAACGGCAACAGCTTACCTTGGGTCTACGGTTGGACC 243
QY 364 CGCAACCCGCTGTGAGATATTAATCGTCGAGAACTTTGGCACTTATGATCTTCTCC 423
DB 244 CGCAACCCGCTGTGAGATATTAATCGTCGAGAACTTTGGCACTTATGATCTTCTCC 303
QY 424 GGTGCTACCGATCTAGAACTGTGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACC 483
DB 304 GGTGCTACCGATCTAGAACTGTGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACC 363
QY 484 ACTCGCTCAACGCACTAGCATCGACCCAAACCTTGCACCAATATGTTGGTGC 543
DB 364 ACTCGCTCAACGCACTAGCATCGACCCAAACCTTGCACCAATATGTTGGTGC 423
QY 544 CGCCAGGACAAGCGCACCGCGGTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCT 603
DB 424 CGCCAGGACAAGCGCACCGCGGTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCT 483
QY 604 CGCGCTGTTGATGTCAACGGTGAACCACTACTACCAAGTGTGCAACGGAGGGCTAC 663
DB 484 CGCGCTGTTGATGTCAACGGTGAACCACTACTACCAAGTGTGCAACGGAGGGCTAC 543
QY 664 TTCAGCAGCGGCTATGCTCGCATCACCGTGTGACGTGGGCTAA 708
DB 544 TTCAGCAGCGGCTATGCTCGCATCACCGTGTGACGTGGGCTAA 588
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RESULT 2

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US-10-517-939-231
; Sequence 231, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 56462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Bacteria
US-10-517-939-231
```

```
Query Match 20.6%; Score 202.2; DB 7; Length 1008;
Best Local Similarity 59.1%; Pred. No. 5.7e-45;
Matches 386; Conservative 0; Mismatches 258; Indels 9; Gaps 2;
```

```
QY 67 GCCGCGACTGGGCGCTTCCCGGAGGAATGCCAGGAGCTCGAAAGCGACAG 126
DB 73 GTCCGCTGGCGGCTCGCGCGTGAATGTCGGGCAACGCCGACGCGGACAGGCTC 132
QY 127 ACAACCCCACTCGGAGGGCTGCGACGATGTTATTACTATTCTGTGTGAGTACGCT 186
DB 133 GTCAACGACCAACGAGGCGGACCAACGAGGCTACTACTCTGTTCTGACCGACAGC 192
QY 187 GGAGCGCAGGCGGACGTAACCAACCTGGAAGCGGCGACCTACGAGATCAGCTGGGAGAT 246
DB 193 CAGGCGACCGTCTCATGAACATGGGCTCGGCGGTCAGTACAGCACTCGTGGCGCAAC 252
```

```
QY 247 GCGGTAACCTCGTCGGTGAAGGGCTGGAACCCCGGCTGAACGCAAGCCATCCAC 306
DB 253 ACCGGCAACTTCGTCCGGGCAAGGGCTGGGCCAACGGCGCGCCGGA---CCGTGACG 309
QY 307 TTGAGGGTGTTCACGACCAACGCGCAACAGCTTACCTTGGGTCTACGGTTGACCCGC 366
DB 310 TACTCGGGCAGCTTCAACCCCTCCGGCAACGCGTACTGGCGCTTACGAGTGAAGTGC 369
QY 367 AACCCGCTGTGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCTTCTCCGGT 426
DB 370 AACCCGCTGTGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCTTCTCCGGT 427
QY 427 GCTACCGATCTAGGAATGTGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACCACT 486
DB 428 ---AGTCAAGGCGCACCGTCAACGACGACGGGCGCACTACGACATCTTCAAGACGACC 483
QY 487 CGCGTCAACGCACTAGCATCGACGCGCAACCAACCTTGCACCAATAGTGGTCCGCGC 546
DB 484 CGCGTCAACGCACTAGCATCGACGCGCAACCAACCTTGCACCAATAGTGGTCCGCGC 543
QY 547 CAGGACAAGCGCACCGGTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCTCGC 606
DB 544 CAGGACAAGCGCACCGGCGGACCATCAACGCGCAACCACTTGCAGCGCTGGGCTCGC 603
QY 607 GCTGTTGATGTCAACGGTGAACCACTACTACCAAGTGTGCAACGGAGGGCTACTTC 666
DB 604 GCGGAGTCCGCTCGGCACTTACGCTACTACATGATCATGCGCACCGAGGGCTAACG 663
QY 667 AGCAGCGGCTATGCTCGCATCACCGTGTGACGTGGGCTAAGACGTACTG 719
DB 664 AGCAGCGGCACTTCCAGCATCAACGTGCGGCGGACCGGCGCGGCGCAACGCG 716
```

RESULT 3

```
US-11-108-163B-1
; Sequence 1, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Raij
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
; FILE REFERENCE: 1716.03400B/MAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1375
; TYPE: DNA
; ORGANISM: Nonomuraea flexuosa
; FEATURE:
; OTHER INFORMATION: Nf xyn11A nucleotide sequence (AJ508952), the coding region is
US-11-108-163B-1
```

```
Query Match 20.1%; Score 197.2; DB 11; Length 1375;
Best Local Similarity 58.6%; Pred. No. 1.4e-43;
Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;
```

```
QY 35 TCGGCTTAACCCCGTTCCTTGGCGGCTTAGCCGCGACTGGGCGCTTCCCGG 94
DB 349 TCGGCTTCGGCGCATCGTACCAAGTGCCTTGCCTTGCCTGCACTCGCCATCGCGGTGCGC 408
```



```
OY 95 CAGGGAATGCCACGGAGCTCGAAAACGACAGAACCCCACTCGGAGGCTGGCAG 154
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 409 TGCTGCCGGCAGCGCCACGCGGACACCAACCATCACCAAGAACGAGCCGGTACGACA 468
OY 155 ATGTTATTACTATTCTCTGTGTGAGTGAACGGTGAAGCGGACCGACATACCAACCTGG 214
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 469 ACCGCTACTTCTACTCTGTTCTGGAACGACGCGCCCGGACCGTCTCATGACCTCCACT 528
OY 215 AAGCGGCACTACGAGATCAGTGGGAGATGCGGTAACCTCGTGGTGAAGGGCT 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 529 CGGGCGGACGTACAGACACCTCGTGGCGGAACACCGGAACCTCGCGCGGACAGGGCT 588
OY 275 GGAACCCCGGCTGAACGCAAGCCATCCACTTTGAGGTTGTTTACAGCCAAACGCA 334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 GGTCCACCGGC--GACGCGGACCGTGAACCTACAAACGCTCTTCAACCCGTCGGGTA 645
OY 335 ACAGCTACTTGGCGGTCTACCGGTTGAACCCGCAACCCGCTGGTGAATATTACATCGTCG 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 646 ACCCTACTTCAACGCTCTACCGCTGGACCAAGAACCCGCTCGTGAAGTACTACATCGTCG 705
OY 395 AGAAGTTGGACCTATGATCCTTCTCGGTGCTACCGATCTAGGAAGTGTGAGTGG 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 706 AGAGCTGGGCACTACCGGCCCAAC-----GGCACTTCAAGGGCACCGTCAACCAACG 759
OY 455 ACCGTAGCATCTACGACTCGGCAAGCACTCGCGTCAAGCAAGCACTAGACGAGGCA 514
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 ACCGCGGACGTACGACATCTACGAGACCTGGCGGTACAGCGCGCGTCCATGAGGGCA 819
OY 515 CCCAAACCTTCGACCAATACCTGTCGGTCCGCGGACAGACAGCGCACCGGTAACCGTCC 574
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 820 CCGGACCTTCCAGCAGATTCTGAGCGTCCGGCAGAGAGCGGACCAAGCGGCAACCATCA 879
OY 575 AGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGGTGTTGAATGCAACGGTGAACCACT 634
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 880 CCATCGGCAACCACTTCGACGCGCTGGGCGCGCGCGGCAAGAA--CCTGGGACGCGACG 936
OY 635 ACTACCATGATCGTTGCAACGGAGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTG 694
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 937 ACTACCATGATCATGGCGACCGAGGGCTAACAGAGCAGCGGTAGCTCCACCGTCTCATCA 996
OY 695 CTGACGTGGGCTAAGACGTAACTGGTG 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 997 GCGAGGTGGCAACCCCGGCAACCCCGG 1024
```

RESULT 4
US-11-108-163B-5
; Sequence 5, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:

```
; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Raij
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
; FILE REFERENCE: 1716.034000B/MAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Nonomuraea flexuosa
; FEATURE:
; OTHER INFORMATION: am24*, like am24 but 9 codons are changed in the sequence like in
```

; OTHER INFORMATION: am35* (See Example 10)
US-11-108-163B-5

Query Match 19.3%; Score 190.2; DB 11; Length 663;
Best Local Similarity 61.2%; Pred. No. 8.6e-42;
Matches 363; Conservative 0; Mismatches 218; Indels 12; Gaps 3;

```
OY 130 ACCCCCACTCGAGGCTGGCAGCATGTTATTACTATTCTGTGTGAGTGAACGGTGA 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 ACCAGAACGAGACCGGCTACGACAAACGGCTACTTCTACTCGTCTGAGCGACGCCCC 72
OY 190 GCGCAGCCACGTACACCAACCTGGAAGCGGCACTACGAGATCAGCTGGGAGATGGC 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 GGCACGCTCTCATGACCTTCCACTCGGCGGCACTACAGCACCTCGTGGCGCAACACC 132
OY 250 GGTAACTCTGTCGTGGAAGGGCTGGAACCCCGCCTGAACGCAAGACCATCACTTT 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 GGCACCTTCGTGCGCGGCAAGGGCTGTCCACCGGC--GGCCGCGCACCGTCACTAC 189
OY 310 GAGGTGTTTACAGCCAAACGGCAACAGCTACCTTCCGGTCTACGGTTGACCCGCAAC 369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 AACGCTCTCTCAACCCGTCGGGTAAACGCTTCACTCAAGCTTACGGCTGGAACAGGAAC 249
OY 370 CCGCTGTGAGTATTACATGCTCGAAGAACTTTGGCACTTATGATCCTTCTCCGGTCT 429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 CCGCTGTGAGTACTACATGCTGAGAGCTGGGGCACTAACCGGCCAAC-----GGC 303
OY 430 ACCGATCTAGGAACCTGTGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGCACTCGC 489
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 ACCTCAAGGGCACCGTCAACCAACGAGCGGCAAGTACGACATCTAGAGACCTGGCGG 363
OY 490 GTCAAGCACTAGCATCGACGGCACCCAAACCTTGAACCAATACCTGTCGTCGCCAG 549
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 TACAACGCGCGGTCCATCGAGGGGACCCGACCTTCAAGCAGTTCTGAGGTCGCCGAG 423
OY 550 GACAGCGCACCAAGCGGTACCGTCCAGACGGGCTGCCACTTCGACGCTGGGCTCGCGCT 609
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 CAGAGCGGACCAAGCGGCACTACCATTCGGCAACCACTTCGACGCTGGGCGCCGCC 483
OY 610 GGTGGAATGTCAACGGTGAACCACTACTACAGATGTTGCAACGGAGGCTACTTACG 669
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 GGCATGAA--CCTGGGACGCCACGACTACAGATCATGCGACCGAGGGCTACCAAGAC 540
OY 670 AGCGCTATGCTCGCATCAACCGTGTGCTGACGTGGGCTAAGACGTAACTGGTG 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 AGCGGTAGCTCCACCGTCTTCATCAGCGAGGTGGCAACCCCGCAACCCCGG 593
```

RESULT 5
US-11-108-163B-4
; Sequence 4, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:

```
; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Raij
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
; FILE REFERENCE: 1716.034000B/MAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 906
; TYPE: DNA
```

```
; ORGANISM: Nonomuraea flexuosa
; FEATURE:
; OTHER INFORMATION: am35*, like am35 but 9 codons are changed in the sequence. See
; OTHER INFORMATION: Example 10 (the changes do not alter the encoded amino acid
; OTHER INFORMATION: sequence)
US-11-108-163B-4
```

```
Query Match      19.3%; Score 190.2; DB 11; Length 906;
Best Local Similarity 61.2%; Pred. No. 9.6e-42;
Matches 363; Conservative 0; Mismatches 218; Indels 12; Gaps 3;
```

```
QY 130 ACCCCCACTCGAGGCTGGCAGATGTTATTACTTCTGTGTGAGTGAAGGTGA 189
DB 13 ACCCAGAACGACCGGCTACGACACGGCTACTTCTACTGTTCTGACCGACGCCCC 72
QY 190 GCGCAGGCCACGTACACCAACCTGGAAGCGGCACCTACGAGATCAGCTGGGAGATGGC 249
DB 73 GGCACCGTCTCCATGACCTCCACTCGGGCGGACGTAAGCACTCGTGGCGCAACACC 132
QY 250 GGTAACTCTGCTGGTGGAAAGGCTGGAACCCCGCTGAACGCAAGACCACTTCTT 309
DB 133 GGCACCTCTGCTGGCGGCAAGGGCTGTCTCCACCGGC---GGCGCGCACCGTCACTAC 189
QY 310 GAGGGTGTTTACCAAGCCAAACGGCAACAGCTACCTTGGCTTACGGTTGACCCGCAAC 369
DB 190 AACGCTCTTCAACCCGCTGGGTAAAGCTTACCTCAGCTCTTACGGCTGACCAAGAAAC 249
QY 370 CCGCTGTGAGTATTACATCTGTCGAAACTTTGGCACCTATGATCCTTCTCCGCTGCT 429
DB 250 CCGCTGTGAGTATTACATCTGTCGAAAGCTGGGCACCTACCGGCCAACCC---GGC 303
QY 430 ACCGATCTAGGAACCTGTGAGTGCAGCGGTAGCATCTATGCACTCGGCAAGACCACTGCG 489
DB 304 ACCTACAAGGGCACCGTCAACACCGACGGCGCACGTAAGCATCTACGAGACCTGGCGG 363
QY 490 GTCAACGCACTAGCATGACGGGCAACCAACTTGCACCAATACTGTCGGTCCGCCAG 549
DB 364 TACAACGGCGCGTCCATCGAGGGCACCCGGAACCTTCCAGCAGTTCGAGCGTCCGGCAG 423
QY 550 GACAAGCGCACGCGGTACCGTCCAGACGGGCTGCCATTGCAAGCCTGGGCTCGCGCT 609
DB 424 CAGAAAGCGGACGACGGGACCACTACCACTCGGCAACCACTTTCGACGCTGGGCCCGGCC 483
QY 610 GGTGTAATGTCAACGGTGACCACTACTACAGATCGTTGCAACGGAGGGCTACTTTCAGC 669
DB 484 GGCATGAA---CCTGGGACGCCACGACTTACGATCATGGGCAACGAGGGCTACCAAGAC 540
QY 670 AGCGGCTATGCTGCATCACCGTGTGCTGACGTGGCTAAGACGTAACTGTGTG 722
DB 541 AGCGGTAGCTCCACCGTCTCCATCAGCAGGGGTGGCAACCCCGGCAACCCGGG 593
```

RESULT 6

```
US-11-108-163B-3
; Sequence 3, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Raij
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; FILE REFERENCE: 1716.034000B/MAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; NUMBER OF SEQ ID NOS: 25
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Nonomuraea flexuosa
; FEATURE:
; OTHER INFORMATION: am24, shortened form of am35, includes a STOP codon
US-11-108-163B-3
```

```
Query Match      19.0%; Score 187; DB 11; Length 663;
Best Local Similarity 60.9%; Pred. No. 6.3e-41;
Matches 361; Conservative 0; Mismatches 220; Indels 12; Gaps 3;
```

```
QY 130 ACCCCCACTCGAGGCTGGCAGATGTTATTACTTCTGTGTGAGTGAAGGTGA 189
DB 13 ACCCAGAACGACCGGCTACGACACGGCTACTTCTACTCTGTTGACCGACGCCCC 72
QY 190 GCGCAGGCCACGTACACCAACCTGGAAGCGGCACCTACGAGATCAGCTGGGAGATGGC 249
DB 73 GGCACCGTCTCCATGACCTTCCACTCGGGCGGACGTAAGCACTCGTGGCGCAACACC 132
QY 250 GGTAACTCTGCTGGTGGAAAGGCTGGAACCCCGCTGAACGCAAGACCACTTCTT 309
DB 133 GGCACCTCTGCTGGCGGCAAGGGCTGTCTCCACCGGC---GGACGGCGCACCGTGAACCTAC 189
QY 310 GAGGGTGTTTACCAAGCCAAACGGCAACAGCTACTTGGCTTACGGTTGACCCGCAAC 369
DB 190 AACGCTCTTCAACCCGCTGGGTAAAGCTTACCTCAGCTCTTACGGCTGACCAAGAAAC 249
QY 370 CCGCTGTGAGTATTACATCTGTCGAAACTTTGGCACCTATGATCCTTCTCCGCTGCT 429
DB 250 CCGCTGTGAGTATTACATCTGTCGAAAGCTGGGCACCTACCGGCCAACCC---GGC 303
QY 430 ACCGATCTAGGAACCTGTGAGTGCAGCGGTAGCATCTATGCACTCGGCAAGACCACTGCG 489
DB 304 ACCTACAAGGGCACCGTCAACACCGACGGCGCACGTAAGCATCTACGAGACCTGGCGG 363
QY 490 GTCAACGCACTAGCATGACGGGCAACCAACTTGCACCAATACTGTCGGTCCGCCAG 549
DB 364 TACAACGGCGCGTCCATCGAGGGCACCCGGAACCTTCCAGCAGTTCGAGCGTCCGGCAG 423
QY 550 GACAAGCGCACGCGGTACCGTCCAGACGGGCTGCCATTGCAAGCCTGGGCTCGCGCT 609
DB 424 CAGAAAGCGGACGACGGGACCACTACCACTCGGCAACCACTTTCGACGCTGGGCCCGGCC 483
QY 610 GGTGTAATGTCAACGGTGACCACTACTACAGATCGTTGCAACGGAGGGCTACTTTCAGC 669
DB 484 GGCATGAA---CCTGGGACGCCACGACTTACGATCATGGGCAACGAGGGCTACCAAGAC 540
QY 670 AGCGGCTATGCTGCATCACCGTGTGCTGACGTGGGCTAAGACGTAACTGTGTG 722
DB 541 AGCGGTAGCTCCACCGTCTCCATCAGCAGGGGTGGCAACCCCGGCAACCCGGG 593
```

RESULT 7

```
US-11-108-163B-2
; Sequence 2, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Raij
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; FILE REFERENCE: 1716.034000B/MAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
```

```
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Nonomurea flexuosa
; FEATURE:
; OTHER INFORMATION: am35, Nf xyn11A coding region for the mature Nf xyn11A (AM35)
; OTHER INFORMATION: protein
US-11-108-163B-2
```

```
Query Match      19.0%; Score 187; DB 11; Length 906;
Best Local Similarity 60.9%; Pred. No. 7e-41;
Matches 361; Conservative 0; Mismatches 220; Indels 12; Gaps 3;
```

```
QY 130 ACCCCCACTCGAGGGCTGGACGAGTTATTACTATTCTGTGGAGTGACGGTGA 189
DB 13 ACCCAGAACGACCGGGTACGACACGGCTACTTCTACTCGTTCTGACCGACGGCCC 72
QY 190 GCGCAGGCCACGTACACCAACCTGGAAGGGGCACTACGAGATCAGCTGGGAGATGCG 249
DB 73 GGGACCGTCTCATGACCTCCACTCGGGGGGCACTACAGCACTCGTGCGGAACCC 132
QY 250 GGTAACCTCGTGGTGAAGGGGCTGAAACCCGGGCTGAACGCAAGACCATCACTT 309
DB 133 GGGAACTTCGTGCGCGGCAAGGGCTGTCCACCGGC--GGACGGCGGACCGTGAACCTAC 189
QY 310 GAGGGTGTTTACAGCCCAACGGCAACAGTAACTTGGCGTCTACGGTTGAGCCCGCAAC 369
DB 190 AAGCCTCTCTCAACCCGTCGGGTAAACGCTTACCTCAGCCTTACGGCTGAGCAGGAAC 249
QY 370 CCGCTGTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCTTCTCCGGTCT 429
DB 250 CCGCTGTCGAGTACTACATCGTCGAGAGCTGGGGCACCTACCGGCCCCACC-----GGC 303
QY 430 ACCGATCTAGGAAGTGTGAGTGCAGCGGTAGCATCTATGCACTGGCAAGACCACTGCG 489
DB 304 ACCTACAAAGGCAACCGTCAACCAACCGGCGGCAAGTACGACATCTTACGAGACCTGGCGG 363
QY 490 GTCAACGCACTAGCATCGACGCGACCCAAACCTTGCACCAATACTGTCGTCGCGCAG 549
DB 364 TACAACGCGCGCTCCATCGAGGGCAACCGGACCTTCCAGCAGTTCTGAGCGTCCGGCAG 423
QY 550 GACAAGCGCACCGCGTACCGTCCAGACGGGCTGCCACTTGCACGCTGGGCTCGCGCT 609
DB 424 CAGAAGCGGACCGGCGGCAACCATCACTCGGCAACCACTTGCACGCTGGGCGCGCGC 483
QY 610 GATTGAATGTCAACGGTGACCACTACTACAGATCGTTGCAAGGAGGCTACTTCAAC 669
DB 484 GGCATGAA--CTGGGCGAGCCAGCACTACAGATCATGGCGAAGGAGGCTACCAAGC 540
QY 670 AGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAGACGTAACTGCTG 722
DB 541 AGCGTAGCTCCACCGTCTCCATCAGCGAGGGTGGCAACCCGCGCAACCCGGG 593
```

RESULT 8

US-10-517-939-225

```
; Sequence 225, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Bateghalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517, 939
```

```
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-225
```

```
Query Match      18.9%; Score 186.2; DB 7; Length 1059;
Best Local Similarity 60.2%; Pred. No. 1.2e-40;
Matches 346; Conservative 0; Mismatches 223; Indels 6; Gaps 2;
```

```
QY 130 ACCCCCACTCGAGGGCTGGACGATGTTATTACTATTCTGTGGAGTGACGGTGA 189
DB 88 ACGTCCAGCGGAGCGGCGACCAACAGGGCCACTACTATTCTTCTGGAAGCACAGTGGC 147
QY 190 GCGCAGGCCACGTACACCAACCTGGAAGGGGCACTACGAGATCAGCTGGGAGATGCG 249
DB 148 GGCACCGTCACTTCTGATGTACGGAACGGCGCTACACTTCAACTGAGCGGCAATC 207
QY 250 GGTAACCTCGTGGTGAAGGGGCTGAAACCCGGGCTGAACGCAAGACCATCACTT 309
DB 208 AACAAGTGGTGGGCGGCAAGGGCTGGCAGACCGGCTCAGCGCGGA---CGATCAGCTAC 264
QY 310 GAGGGTGTTTACAGCCCAACGGCAACAGTAACTTGGCGTCTACGGTTGAGCCCGCAAC 369
DB 265 TCGGGCTCGTTCAACTACCCGCGAATGTTATCTCACCTGTACGGTTGACCAACCAAT 324
QY 370 CCGCTGTCGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCTTCTCCGGTCT 429
DB 325 CCATGATCGAGTACTACATCGTCGAGCAACTGGGGCACGTACCGGCGCGGAGGCTCG 384
QY 430 ACCGATCTAGGAAGTGTGAGTGCAGCGGTAGCATCTATGCACTGGCAAGACCACTGCG 489
DB 385 GGCTACATGGGCAAGGTGACGAGCGAGCGGCGCACTACGACGTCTATCGCACCGACGCG 444
QY 490 GTCAACGCACTAGCATCGACGCGACCCAAACCTTGCACCAATACTGTCGTCGCGCAG 549
DB 445 GTAAACCAAGCTTCCATCATCGGCAACCGAGCTTCTATCAATACTGAGCGTGGCCAG 504
QY 550 GACAAGCGCACAGCGGTACCGTCCAGACGGGCTGCCACTTGCACGCTGGGCTCGCGCT 609
DB 505 CAGAAGCGGACCGGCGGACCATCAACCGGCAATCACTTGCACGCTGGGCGCGCATAC 564
QY 610 GATTGAATGTCAACGGTGACCACTACTACAGATCGTTGCAAGGAGGCTACTTCAAC 669
DB 565 GGAATGAA---CTCGGCAACCCCAACTACAGATCATGGCGAAGGAGTTACCAAGC 621
QY 670 AGCGGCTATGCTCGCATCACCGTTGCTGACGTGGG 704
DB 622 AGCGCAGTTCCGACATCACCGGTGAGCGAGGGCGG 656
```

RESULT 9

US-10-517-939-165

```
; Sequence 165, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Bateghalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
```

```
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PCT/US03/19153
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 165
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-165
```

```
Query Match      18.8%; Score 185; DB 7; Length 1047;
Best Local Similarity 60.6%; Pred. No. 2.6e-40;
Matches 340; Conservative 0; Mismatches 215; Indels 6; Gaps 2;
```

```
QY 145 GGCTGCACGATGTTATTACTATTCCTGGTGAAGTGAAGGAGCGAGCGCACTGAC 204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 97 GGCACCAACAAGGCTTCTACTATTCTGTCGACCGAGCGGCTGCTCCGTGACGTTTC 156

QY 205 ACCAACCTGGAAGCGGACCTACGAGATCAGCTGGAGATGGCGGTAACTCGTCGT 264
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 157 TGCCTGCAATCCGCGCGGCGCTACACTCCAGCTGAGCAATGTCGAAACTGGTCGGT 216

QY 265 GGAAGGGCTGGAACCCCGGCTGAACGCAAGAGCCATCCATTGAGGTTTACCAG 324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 217 GGCAGGGGCTGGCAGACCGGCGCGCGC---CGCAACATCAACTATTCGGGAGCTTCAAT 273

QY 325 CCAACGGCAACAGCTACCTTGGCGTTACGGTTGACCCCGCAACCCGCTGTCAGTAT 384
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 274 CCCTCGGGTAACGGCTACCTGCGCGTCTATGGCTGACCAGCAATCCCTGTGTGAGTAC 333

QY 385 TACATCGTCGAGACTTGGCACCTATGATCCTTCCGTGCTACCGATCTAGAACT 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 334 TACATCGTCGACACTGGGGTACCTATCGTCCACCGGGTGGCAGGATTCATGGGACG 393

QY 445 GTGAGTGCAGGTAAGTACATCTATGACTCGGCAAGACCACTGCGTCAACGCACTAGC 504
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 394 GTGTGACGAGTGGGGGCACTACGAGCTTACCGCAGCAAGGGTCAACGCGCCTCC 453

QY 505 ATGACGGCAACCAACCTTCGACCAATAGTGTGCTCGCGCAAGACAAGCGCAACGAC 564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 454 ATTCAAGGGCAACGCACTTCTACCAAGTATGAGCGTTCCGCACTCGAAGCGCAACGGT 513

QY 565 GGTACCGTCCAGACGGGCTGCCACTTTCGACGCGCTGGGCTCGCGCTGTTGAATGTCAAC 624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 514 GGAACCATCTCCACCGGCAACCAATTTGACGCGCTGGGCGAGCTTCGGCATGAA--CTTG 570

QY 625 GGTGACCACTACTACAGATCGTTGCAACGAGGGCTACTTTCAGCAGCGGCTATGCTGC 684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 571 GGAACCTTCAATTACAGATCGTGGCGACGAGGGCTACCAAGACGCGCAATTCGAC 630

QY 685 ATCACCGTGTGCTGACGTGGGC 705
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 631 ATCACGGTGAGCGATGGCGGC 651
```

```
RESULT 10
US-10-517-939-199
; Sequence 199, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
```

```
; APPLICANT: Blum, David
; APPLICANT: Besehalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PCT/US03/19153
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 199
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-199
```

```
Query Match      17.3%; Score 170; DB 7; Length 1074;
Best Local Similarity 57.5%; Pred. No. 2.9e-36;
Matches 368; Conservative 0; Mismatches 260; Indels 12; Gaps 3;
```

```
QY 59 CGGCTTAGCCCGGCACTGGGGCCCTGGCCTTCCCGGCAAGGAATGCCAGGAGCTGAAA 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 26 CGGGCAGGCGCGCGCGTCCGCGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 85

QY 119 AGCGACAGAC-----AACCCTCACTCGAGGGCTGGCAAGATGTTATTACTATTCCT 172
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 ATGCGCAAACTGTCATCAGCTGAGGCCAGACGGGCAACCAACGCAACTACTTTTTCGT 145

QY 173 GGTGAGTGAACGGTGGAGCGGCGCAAGCTACACCAACTGGAAGCGGCGCACTACGAGA 232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 146 TCTGGAAGACAGCCCGGCGAGCGTGAACCTTCTGATGTACTCCGGCGCGCTACACGT 205

QY 233 TCAGCTGGGAGATGGCGTAACTCTGCTGGTGAAGAGGCTGGAACCCCGGCTGAACG 292
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 206 CCAACTGAGCGGCATCAACAACTGGGTGGCGGCAAGGGCTGGCAGACGGGCTGCTCC 265

QY 293 CAAGAGCATCCACTTTGAGGGTGTACAGCCAAAGGCAACAGTAACTTGGGCTCT 352
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 GCAACGCTCTACTCCGGCAGCTTCAATTGCGCG---GGTAAAGGCTACCTGAGGCTCT 322

QY 353 ACGTTGACCCCGCAACCCGCTGTCGAGTATTACATCGTCAAGAACTTTGGCACTATG 412
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 ACGGCTGACCAACCAATCCGCTCATCGAGTACTACATCGTCAACAACTGGGGCAGTATC 382

QY 413 ATCTTCTCTCCGCTGCTACCGATCTAGGAACGTGTCAGTGGCAGCGGTAGCATCTATGAC 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 GTCCCGCGGCTGGCAGGGCTTCAATGGGCAAGTGAACCGACGCGGCGCAAGTACGACA 442

QY 473 TCGCAAGACCACTCGCGTCAACGCACTAGCATGACGCGCAACCAACCTTCGACCAAT 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 TCTATCGACGCAACGAGGTCAACAGCCGTGATCATCGGCAACCGGCTTACAGAT 502

QY 533 ACTGTCGTCGCGCAGAGCAAGCGCAACGCGTACCGTCCAGACGGGCTGCACTTCG 592
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 503 ACTGAGCGTCCGCGCAGTCAAGCGCAACCGGCGCAACCAACGCGCAACCACTTCA 562

QY 593 ACGCTGGGCTCGCGCTGTTGATGTCAACGCTGACCACTACTACAGATCGTTGCA 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 563 ATGCTGGGCGAGCCTCGGCATGAA---CTGGAGACAGCAACTACCAAGTGATGGCCA 619

QY 653 CGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 620 CCGAGGGCTACAGAGCAGCGGCGCTCCGACATCACCGGT 659
```

```
RESULT 11
US-10-517-939-255
; Sequence 255, Application US/10517939
```

```
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-255
```

```
Query Match      17.3%; Score 170; DB 7; Length 1137;
Best Local Similarity 57.5%; Pred. No. 3e-36;
Matches 368; Conservative 0; Mismatches 260; Indels 12; Gaps 3;
```

```
OY 59 CGGCCTTAGCCGCGACTGGGGCCCTGCTCCGCGAGGGAATGCCAGGAGCTGAAA 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 89 CGGGCAGGCGCGCGCTGCGCGCGCTGCTGCTTCCGCGCTTACATGCGCGCGA 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 119 AGGCACAGAC-----AACCCCAACTGGAGGGCTGGCAGATGTTATTACTTCT 172
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 149 ATGCGCAACCTGCATCAGCTGAGCGCAGACGGGCACCAACACGCACTACTTTCGT 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 173 GGTGAGTGAAGGTGGAAGCGCAGCGCAAGTACCAACCTGGAAGCGGCACCTACGAGA 232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 209 TCTGAAAGACAGCCCGGCGCAGGTGAATCTTGATGATCTCCGGCGCGCTACAGT 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 233 TCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAGGGCTGGAACCCCGGCTGAAAG 292
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 269 CCAACTGGAGCGGCATCAACAACCTGGGTGGCGGCAAGGGCTGGCAGACGGGCTGCTCC 328
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 293 CAAGAGCCATCACTTTGAGGGTGTACCAAGCAACCGGCAAGCTACCTTGGGCTCT 352
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 329 GCACCGTCTCTACTCCGCGCAGCTTCAATTGCGCG--GGTAAAGGCTACCTGACGCTCT 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 353 ACGGTTGACCGGCAACCCGCTGCTGAGTATTACATGCTGAGAACTTGGACCTATG 412
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 386 ACGGCTGACCAACCAATCCGCTCATGAGTACTACATGCTGCACACTGGGCACTATC 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 413 ATCCTTCTCGGTGCTACCGATCTAGGAATGTGAGTGCAGCGGTAGCATCTATCGAC 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 446 GTCCGCGGGGTGCGCAGGGCTTCAATGGGCAAGTGAACACCGGCGGCAAGTACGACA 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 473 TCGGCAAGACCACTGCGCTCAACGCACTAGCATGACGGGCAACCAACTTGCACCAAT 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 506 TCTATCGACGCAACGGGTCAACCAAGCTGATCATCGGCAACGGGAGCTTCTACCAAT 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 533 ACTGTCGGTCCGCGCAGGCAAGCGCAAGCGGTACCGTCCAGACGGGCTGCCACTTGG 592
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 566 ACTGAGCGTGGCGAGTGAAGCGCAAGCGGCGGCAACATCAACGCGCAACCACTTCA 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 593 ACGCTGGGCTCGCGCTGTTGAATGTCACCGGTACCACTACTACAGATGTTGCAA 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 626 ATGCTGGGCGCAAGCTTGGCATGAA---CTGGGACAGCAACTACAGGTGATGGCCA 682
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 653 CGGAGGCTACTTCAAGCAGCGGCTATGCTCGCATCACCGT 692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
DB 683 CCGAGGGCTACCAAGACGAGCGGCAAGCTCCGACATCACGCT 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 12
US-10-517-939-169
; Sequence 169, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 169
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-169
```

```
Query Match      16.9%; Score 165.8; DB 7; Length 1041;
Best Local Similarity 56.8%; Pred. No. 3.9e-35;
Matches 346; Conservative 0; Mismatches 257; Indels 6; Gaps 2;
```

```
OY 97 GGAATGCCACGAGCTCGAAAAGCGACAGACAAACCCCACTCGGAGGCTGGCAGAT 156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 52 GGCATTAACCGCGCGCAGGCGGAACCTGCATCATCTTCCAGCCAGACCGGTACCAAC 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 157 GGTATTACTATTCTGCTGAGTGAAGGTGAGCGGAGCGCAGCGTACACCACTGGA 216
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 112 GGCACTACTTTCTTCTGGAAGAGACAGCCCGGTACCGTCAACTTCTGATGTATGCC 171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 217 GCGGCACTACGAGATCAGCTGGGAGATGGCGGTAACTCGTGGTGAAGGGCTGG 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 172 AATGGGCGCTACACCTCCCACTGAGCGGCATCAACAATGGGTGGCGGCAAGGCTGG 231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 277 AACCCGCGCTGAACGCAAGGCCATCCACTTTGAGGGTGTACCAAGCCAAAGGCAAC 336
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 232 CAGACGGGCTCCAAACCGCAGGTGACTACTCC--GGTTCGTCAATTGCCCCGCAAT 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 337 AGCTACTTGGGCTTACCGTTGGAACCGCAACCCGCTGGTGAATATTACATGTCGAG 396
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 289 GGTATCTACCTTGTACGGAATGACCAAGATCAATGATGAGTACTACATGTCGAC 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 397 AACTTGGCACTATGATCTTCTCCGCTGCTACGATCTAGAACTGTGAGTGGAC 456
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 349 AGTGGGCACTATGACCGCGCGGCGGCAAGGCTTATGGGCAACCGTCAACAGCAT 408
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 457 GGTAGCATCTATGACTGGGCAAGACCACTGCGTCAAGCACTAGACGAGCGCAC 516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 409 GCGGCACTATGACATCTACCGCAGCAGCGGCTGAACCAAGCTTCAATCGGCAAC 468
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 517 CAACCTTGCACCAATATCTGCTCGCTCCGCAAGCAAGCGCAACGCGGTACCTCCAG 576
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 469 GCCACGTTCTACAGTACTGAGCGGTGCGGCAAGTGAAGCGGCTGGCGGCAAGATCAC 528
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 577 ACGGCTGCCACTTGAAGCGCTGGGCTGCGGCTGTTGAATGTCACCGTGAACCACTAC 636
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


Db 529 ACGGCCAACCACTTCAACGCTGGGCCACGCTGGGATGAA---CCTGGGCCAGACAAC 585
Qy 637 TACCAGATCGTTGCCAACGGAGGGCTACTTACGACGGCGTATGCTGCATCAACCGTTGCT 696
Db 586 TACCAGATCGTTGCCAACGGAGGGTTACAGAGCAGTGGCAGCTCCGACATCAACCGTGACC 645
Qy 697 GACGTGGGC 705
Db 646 GAGGCGGC 654

RESULT 13

US-10-517-939-221
; Sequence 221, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-221

Query Match 16.8%; Score 165.6; DB 7; Length 1044;
Best Local Similarity 58.0%; Pred. No. 4.5e-35;
Matches 332; Conservative 0; Mismatches 234; Indels 6; Gaps 2;
Qy 134 CCAACTCGAGGCTGGCAGATGTTATTACTATTCCTGGTGGAGTGACGGTGGAGCGC 193
Db 89 CCAGCCAGACCGGACCAACAAGCAATTATTTTCATTCTGGAAGAACAACCCGGGCA 148
Qy 194 AGGCCACGTACACCAACTGGAAGCGGCACTACAGATCAGCTGGGGAGATGGCGGTA 253
Db 149 CGGTGACCTTCTGCAATGATGCCAACGGCGGCTACACCTCCAACTGGAGCGGCATCAACA 208
Qy 254 ACCTCGTGGTGAAGGGCTGGAAACCCCGGCTGAACGCAAGAGCCATCCACTTTGAGG 313
Db 209 ACTGGGTGGTGGCAAGGGCTGGCAGACCGGCTCGAATCGCAGGTGAACCTACTCCGGTT 268
Qy 314 GTGTTTACCAAGCCAAACGGCAACAGCTTACCTTGGCTTACCGTTGGAACCCGCAACCGC 373
Db 269 CGTTCAACTCGC---CGGCAACGGCTACTCTACCTGTACGGGTGAGCCAGAAATCCGC 325
Qy 374 TGGTCGAGTATTACATCGTCGAGAACTTTGGCACTATGATCCTTCCGTTCCGTTACCG 433
Db 326 TGATCGAGTACATCGTCGACAGTTGGGCAATTATCGACCGCCGCGGCAAGGCT 385
Qy 434 ATCTAGAACTGTGAGTGCAGCGTAGCATCTATCGACTCGCAAGACCACTCGGCTCA 493
Db 386 TCATGGGACCGTGACGACCGGCGGCACTACGACATCTATCGCAAGCGCGCTGA 445
Qy 494 ACGCACCTAGCATCGACGGCAACCAACCTTGCACCAATCTGGTGGTCCGCCAGGACA 553
Db 446 ACCAGCCTTCCATCATCGGCAACCGGACGTTCTTACAGTACTGGAGCGTGGGCAGTGCA 505

Qy 554 AGCGCACCAAGCGGTACCGCTCCAGACGGGCTGCCACTTGACGCGCTGGGCTCGCGCTGTT 613
Db 506 AGCGCGTGGGGGCGACCATCAACACCGCCAACTTCAATGCTTGGCGGACGCTGGGCA 565
Qy 614 TGAATGTCAACGGTGACCACTACTACAGATCGTTGCAACGGAGGGCTACTTCAGCAGCG 673
Db 566 TGAA---CCTGGCGCAGCAACTACAGGTGATGGCCACCGAGGTTACAGAGCAGCG 622
Qy 674 GCTATGCTCGCATCACCGTGTGACGTGGC 705
Db 623 GCAGCTCCGACATCACCGGTGACCGAAGCGGC 654

RESULT 14

US-10-517-939-177
; Sequence 177, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-177

Query Match 16.8%; Score 165.4; DB 7; Length 1299;
Best Local Similarity 56.3%; Pred. No. 5.5e-35;
Matches 351; Conservative 0; Mismatches 266; Indels 6; Gaps 2;
Qy 70 GCGACTGGGGCCCTTGGCCTTCCCGCAGAGGAATGCCACGGAGCTCGAAAAGCGACAGACA 129
Db 28 GCGATTGCTGCGCGCAGACACTAGCGGTGGCGACTGTTCCAAATCGCTCATGCGCAACGCTT 87
Qy 130 ACCCCCACTCGGAGGGCTGGCAGATGTTATTACTATTCTGTGAGTGAAGGTGA 189
Db 88 AGCTCAATGCCACTGGAACCCAGAAATGTTACTACTATTGTTTGAAGATTCCGGT 147
Qy 190 GCGAGGCCAGTACACCAACTGGAAGCGGCACTACAGATCAGCTGGGGAGATGGC 249
Db 148 AAGCCACCATGACACTCGGTGCGGTGGAATACTATCTTCATCTCTGGAACAGCAGCACT 207
Qy 250 GGTAACTGTCGTTGGTGAAGGGCTGGAACCCCGGCTGAACGCAAGAGCCATCCACTTT 309
Db 208 AACAACTGGGTGGCGGTAAAGGCTGATGCCGG---TACTCGGCGCACAGTCACTTAT 264
Qy 310 GAGGTGTTTACAGCCAAACGGCAACAGTACCTTGGGCTTACGGTTGACCCGCAAC 369
Db 265 TCGGGCAGTTATAGCGCGAGTGAACCAAGCTACTCGCACTTACGGCTGAGCTGCAAC 324
Qy 370 CCGTGGTGAATTTACATCGTCGAGAACTTTGGCACTTATGATCTTCTCCGGTCT 429
Db 325 CCGTGATGAATATTATCATTTGTGAAAACCTGGTCAATTACATCTGCGTCCGGCGCA 384

QY	430	ACCGATCTAGGA	CTGTGAGTGC	GCCAGCGGTAGCATCTATGCACTGGGCAAGACCATTCCG	489	
Db	385	ACGAATTATGGACTGTCA	TATTGACGGCAGCACCTTACCAGCTGGGCCGCAACGG	444		
QY	490	GTCAACGCACCTAGCATGC	AGCGCACCCAACTTCGACCAATACTGTCCGTCGCCAG	549		
Db	445	GTTAATCAGCCATCTATTGA	AGGACGGCCACGTTCTACCAATACTGAGTGTCGCCAA	504		
QY	550	GACAAGCGCACCGCGGTACC	GTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGCT	609		
Db	505	AACAAGCGCACCGCGGAACGATTA	TATTGAGCGCATTTGCATG	CATGGGCTGCTGTG	564	
QY	610	GTTTGAATGTCAA	CGGTGACCACTACTACCA	GATCGTTGCCAACGAGGGCTACTTCAGC	669	
Db	565	GGCTTGAAA	--CCTGGGGA	CTCAGGATTA	TTCAGATTATGGCGCACCGAGGGCTAC	621
QY	670	AGCGGCTATGCTCGCATC	ACCGT	692		
Db	622	AGCGGCCAGTCCA	TATTCACGGT	644		

RESULT 15

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US-10-517-939-217
; Sequence 217, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517, 939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389, 299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-217

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Query Match	16.4%;	Score 161.6;	DB 7;	Length 1083;
Best Local Similarity	56.8%;	Pred. No. 5.4e-34;		
Matches 359;	Conservative	0;	Mismatches 264;	Indels 9;
				Gaps 3;

OY		130	ACCCCCAACTCGGAGGGGCTGGCAGCATGGTTATTACTATTCCTGTGGAGTGA	189
Db		100	ACGTCCAGCCAGACGGGCACCACAACGGGAACTACTTTTCGTTCTGAAAAGACAGCCG	159
OY		190	GCGCAGGCCACGTACAACCAACTGGAAAGCGGCCA CCTACGAGATCAGCTGGGGAGATGGC	249
Db		160	GGCACGGTGAACTTCTGCATGTACCCGAA TGGCCGCTACACCTCGAACTGGAGCGCATC	219
OY		250	GGTAACCTCGTCGGTGGAAAAGGGCTGGAACCCCGGCCTGAACGCAAGCCATCCACTTT	309
Db		220	AACAAC TGGGTGCGCGCGCAAGGGCTGTGCA CCGGCTCAGC --- CGCACCGTCAGCTAT	276
OY		310	GAGG GTGTTTACAGCCAAACGGCAACAGCTACCTTGC GGTCTACGGTTGACCCGCAAC	369
Db		277	TGGG CAGCTTCAAATTCCGCCCGCAACGGGTACCTGACTCTTACAGGGGTGACCAACCAAC	336
OY		370	CCGCTGGTCGAGTATTACATCGTCGAGA CTTTGGCACCCTATGATCCTTCCCTCCGGTCT	429

Db 337 CCGCTCATCGAGTACTACATCGTCGAGAACTGGGGTAACTACCGCCCCGGGGCGGCCAG 396

QY 430 ACCGATCTAGGAAGTGTGAGTGGGACGGTAGCATCTTATCGACTCGGCAAGACCACTCGC 489

Db 397 GGGTACATGGGAGCCGTCAATTCGACGGGGCGACCTATGACATCTACCGGACTTTCGG 456

QY 490 GTCAACGCACCTAGCATCGACGGCA---CCCAACCTTGCACCAATACTGTGCGTCCG 546

Db 457 GACAACCAAGCCCTGCATCACGGGCACTCCTGCACTTCAACAGTACTGAGCGTGGCG 516

QY 547 CAGGACAAGCCCAACCAAGCCGTACCGTCCAGACGGGGTCCACTTCGACGCGCTGGGCTCGC 606

Db 517 CAGTCCAAGCGCAGCAGCGGCACCATCAACCAAGGCCAATCACTTCGGGCGTGGAAACAGC 576

QY 607 GCTGTTTGAATGTCAACGGGTGACCACTACTACCAGATCGTTGCCAACGGAGGGTACTTC 666

Db 577 CTGGCATGAA---CCTGGGCCAGCACAACTACCAGGTCAATGGCCACCGAGGGTTAACAG 633

QY 667 AGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGGCTAAGACGTAACCTGTGGTGA 726

Db 634 AGCAGCGGCAAGCTCCGACATCACGCTCACGGAAAGCGGCGGCGGACAGCAATGTGGC 693

QY 727 TCTCGGAGGCAACAGCCCAAGATGTCTGAG 758

Db 694 AGCAGCAACGGCGGCAGCAGCAATGGCGGCAG 725

Search completed: February 11, 2006, 22:06:15
Job time : 316.228 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:13:38 ; Search time 3493.06 Seconds
(without alignments)
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Title: US-09-467-368-1_COPY_31_705

Perfect score: 675
Sequence: 1 ATGTCGCGCTTTACCCCGT.....TCACCGTTGCTGACGTGGGC 675

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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10: gb_sts:*
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14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	100.0	983	6	AR044575 Sequence
2	675	100.0	983	6	AR157660 Sequence
3	582	86.2	588	6	AX244978 Sequence
4	559	82.8	2460	15	TLU54436 Sequence
5	262.4	38.9	89019	15	BX842624 Neurospor
6	243.6	36.1	786	15	TRU24191 Trichoderma
7	240.6	35.6	1039	15	HIXYU1 X76047 H.involens
8	239	35.4	1123	6	I65436 Sequence 3
9	239	35.4	1123	6	BD006885 Aspergill1
10	230.8	34.2	841	15	AY156910 Trichoder
11	228.2	33.8	672	15	AY320048 Trichoder
12	214.6	31.8	2202	15	AF246830 Fusarium
13	214	31.7	928	15	TV1012718 Trichoder
14	213	31.6	912	15	AK110604 Oryza sat
15	211.4	31.3	696	15	AY648860 Gibberell
16	206.2	30.5	678	15	AY536639 Aspergill1
17	205	30.4	1195	6	E28868 Xylanase ge
18	205	30.4	1195	6	E28869 Xylanase ge

19	204.4	30.3	816	15	AF490982 Aspergill1
20	204.4	30.3	843	15	AY551187 Aspergill1
21	203.4	30.1	576	1	AJ292317 Streptomy
22	203	30.1	696	6	CQ786060 Sequence
23	201.2	29.8	300800	1	SCO939112 Streptomy
24	201	29.8	2208	15	CEMXB2 D49851 Chaetomium
25	200.2	29.7	1623	15	APB14BXYL 268891 A.pisi endo
26	199.8	29.6	1767	1	SPXYL1 X9851 Streptomyce
27	199.6	29.6	3173	1	AB110644 Streptomy
28	199.6	29.6	4398	1	STMXLNB M64552 Streptomyce
29	199.4	29.5	1640	15	CCLXYLANAS L13596 Cochliobous
30	198.4	29.4	851	6	A62443 Sequence 5
31	198.4	29.4	949	15	AJ863566 Gibberell
32	198	29.3	1008	1	AF194025 Streptomy
33	196.8	29.2	687	15	AY575961 Gibberell
34	196.2	29.1	1375	1	APL508952 Nonomurae
35	196.2	29.1	1375	6	AR274543 Sequence
36	196.2	29.1	1375	6	AR369734 Sequence
37	196.2	29.1	1375	6	AR441840 Sequence
38	194.8	28.9	2015	15	CEMXA1 D49850 Chaetomium
39	194.6	28.8	695	15	CNS01CPS AL115832 Botrytis
40	191.6	28.4	1020	15	TRXYN1GNA X69573 T.reesei xy
41	190	28.1	1015	6	AR055687 Sequence
42	190	28.1	1075	15	S67387 xln2=endoxy
43	188.2	27.9	514	6	E28872 Xylanase ge
44	187.8	27.8	2196	1	U01242 Thermomonos
45	187.8	27.8	3204	1	AY795559 Thermobif

ALIGNMENTS

RESULT 1
AR044575
LOCUS AR044575 983 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5817500.
ACCESSION AR044575
VERSION AR044575.1 GI:5966040
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 983)
AUTHORS Hansen,P.Kamp., Wagner,P., Mullertz,A. and Knap,I.Helmer.
TITLE Animal feed additives
JOURNAL Patent: US 5817500-A 1 06-OCT-1998;
FEATURES
source location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match	Best Local Similarity	Score	DB	Length
Matches 675;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGTCGCGCTTTACCCCGCTTGCGGCTTAAGCGGCGACTGGGGCCCTGGCCTTC	60	
DB	31	ATGTCGCGCTTTACCCCGCTTGCGGCTTAAGCGGCGACTGGGGCCCTGGCCTTC	90	
QY	61	CCGGCAGGAATGCCACGGAGCTCGAAAAAGCAGACACAACCCCAACTCGGAGGGCTGG	120	
DB	91	CCGGCAGGAATGCCACGGAGCTCGAAAAAGCAGACACAACCCCAACTCGGAGGGCTGG	150	
QY	121	CACGATGTTATTACTATTCTGTGTGAGTGACGGTGAGCGGACGACGACCAACCAAC	180	
DB	151	CACGATGTTATTACTATTCTGTGTGAGTGACGGTGAGCGGACGACGACCAACCAAC	210	
QY	181	CTGAAGCGCGCACCTACGAGATCAGCTGGGAGATGGCGGTAACTCGTGGTGAAG	240	
DB	211	CTGAAGCGCGCACCTACGAGATCAGCTGGGAGATGGCGGTAACTCGTGGTGAAG	270	
QY	241	GGCTGAACCCCGGCGCTGAACGCAAGACCATCACTTTGAGGGTGTTTACCAAGCCAAC	300	

Db 271 GGGTGAACCCCGGCTGAACGCAAGAGCCATCCACTTTGAGGGTGTTCACAGCCAAAC 330
Qy 301 GGGCAACAGCTACCTTGGCGGTCTACGGTTGACCCCGCAACCCGCTGTCGAGTATTACATC 360
Db 331 GGGCAACAGCTACCTTGGCGGTCTACGGTTGACCCCGCAACCCGCTGTCGAGTATTACATC 390
Qy 361 GTGGAAGAACTTTGGCACTATGATCCTTCCCTCCGGTGCTACCGATCTAGGAAGTGTGAG 420
Db 391 GTGGAAGAACTTTGGCACTATGATCCTTCCCTCCGGTGCTACCGATCTAGGAAGTGTGAG 450
Qy 421 TGGCAGCGTAGCATCTATCGAAGTGGCAAGACCACTCGCGTCAACGCACTAGCATCGAC 480
Db 451 TGGCAGCGTAGCATCTATCGAAGTGGCAAGACCACTCGCGTCAACGCACTAGCATCGAC 510
Qy 481 GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACAGCGGTACC 540
Db 511 GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACAGCGGTACC 570
Qy 541 GTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGTGGTTGAATGTCAACGGTGAC 600
Db 571 GTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGTGGTTGAATGTCAACGGTGAC 630
Qy 601 CACTACTAACAGATCGTTGCAACGGAGGGCTACTTCAGACGCGGTATGCTCGCATCAC 660
Db 631 CACTACTAACAGATCGTTGCAACGGAGGGCTACTTCAGACGCGGTATGCTCGCATCAC 690
Qy 661 GTTGCTGACGTGGGC 675
Db 691 GTTGCTGACGTGGGC 705

RESULT 2
AR157660 983 bp DNA linear PAT 17-OCT-2001
LOCUS AR157660
DEFINITION Sequence 1 from patent US 6245546.
ACCESSION AR157660
VERSION AR157660.1 GI:16218623
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 983)
AUTHORS Hansen, P., Kamp, P., Mullertz, A. and Knap, I. Helmer.
TITLE Animal feed additives
JOURNAL Patent: US 6245546-A 1 12-JUN-2001;
FEATURES
source 1. .983
/organism="Unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 675; DB 6; Length 983;
Best Local Similarity 100.0%; Pred. No. 4.8e-130;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCGGCTTACCCCGCTTGCCCTTGCGGCTTAGCCGCGACTGGGGCCCTGGCCTTC 60
Db 31 ATGTCGGCTTACCCCGCTTGCCCTTGCGGCTTAGCCGCGACTGGGGCCCTGGCCTTC 90
Qy 61 CCGGCAAGGAATGCCAGGAGCTCGAAAGGACAGACAACCCCACTCGGAGGGCTGG 120
Db 91 CCGGCAAGGAATGCCAGGAGCTCGAAAGGACAGACAACCCCACTCGGAGGGCTGG 150
Qy 121 CACGATGTTATTAATTTCTCTGTGTGAGTGAAGGTGAGCGGCAAGCTACACCAAC 180
Db 151 CACGATGTTATTAATTTCTCTGTGTGAGTGAAGGTGAGCGGCAAGCTACACCAAC 210
Qy 181 CTGGAAGGCGGCACTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAG 240
Db 211 CTGGAAGGCGGCACTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAG 270
Qy 241 GGCTGGAACCCCGGCTGGAACGCAAGAGCCATTCATTGAGGGTGTTCACAGCCAAAC 300

Db 271 GGGTGAACCCCGGCTGAACGCAAGAGCCATTCACCTTGAGGGTGTTCACAGCCAAAC 330
Qy 301 GGGCAACAGCTACCTTGGCGGTCTACGGTTGACCCCGCAACCCGCTGTCGAGTATTACATC 360
Db 331 GGGCAACAGCTACCTTGGCGGTCTACGGTTGACCCCGCAACCCGCTGTCGAGTATTACATC 390
Qy 361 GTGGAAGAACTTTGGCACTATGATCCTTCCCTCCGGTGCTACCGATCTAGGAAGTGTGAG 420
Db 391 GTGGAAGAACTTTGGCACTATGATCCTTCCCTCCGGTGCTACCGATCTAGGAAGTGTGAG 450
Qy 421 TGGCAGCGTAGCATCTATCGAAGTGGCAAGACCACTCGCGTCAACGCACTAGCATCGAC 480
Db 451 TGGCAGCGTAGCATCTATCGAAGTGGCAAGACCACTCGCGTCAACGCACTAGCATCGAC 510
Qy 481 GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACAGCGGTACC 540
Db 511 GGCACCCAAACCTTCGACCAATACTGGTCGGTCCGCCAGGACAAGCGCACAGCGGTACC 570
Qy 541 GTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGTGGTTGAATGTCAACGGTGAC 600
Db 571 GTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGTGGTTGAATGTCAACGGTGAC 630
Qy 601 CACTACTAACAGATCGTTGCAACGGAGGGCTACTTCAGACGCGGTATGCTCGCATCAC 660
Db 631 CACTACTAACAGATCGTTGCAACGGAGGGCTACTTCAGACGCGGTATGCTCGCATCAC 690
Qy 661 GTTGCTGACGTGGGC 675
Db 691 GTTGCTGACGTGGGC 705

RESULT 3
AX244978 588 bp DNA linear PAT 28-SEP-2001
LOCUS AX244978
DEFINITION Sequence 9 from Patent WO0166711.
ACCESSION AX244978
VERSION AX244978.1 GI:15859703
KEYWORDS
SOURCE Thermomyces lanuginosus
ORGANISM Thermomyces lanuginosus
REFERENCE 1
AUTHORS Sibbesen, O. and Sorensen, J.F.
TITLE Xylanase variants having altered sensitivity to xylanase inhibitors
JOURNAL Patent: WO 0166711-A 9 13-SEP-2001;
FEATURES
source 1. .588
/organism="Thermomyces lanuginosus"
/mol_type="unassigned DNA"
/db_xref="taxon:5541"

Query Match 86.2%; Score 582; DB 6; Length 588;
Best Local Similarity 100.0%; Pred. No. 1e-110;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 CAGACAACCCCAACTCGGAGGGCTGGCAAGATGTTATTAATTTCTGTGTGAGTGAAC 153
Db 4 CAGACAACCCCAACTCGGAGGGCTGGCAAGATGTTATTAATTTCTGTGTGAGTGAAC 63
Qy 154 GGTGAGCGGAGGCACTACACCAACTGGAAGGCGGCACTACGAGATCAGCTGGGGA 213
Db 64 GGTGAGCGGAGGCACTACACCAACTGGAAGGCGGCACTACGAGATCAGCTGGGGA 123
Qy 214 GATGCGGTAACTCTGCTGGTGAAGGCGTGAACCCCGGCTGAACGCAAGAGCCATC 273
Db 124 GATGCGGTAACTCTGCTGGTGAAGGCGTGAACCCCGGCTGAACGCAAGAGCCATC 183
Qy 274 CACTTTGAGGGTGTTCACAGCCAAACGCAACAGCTACCTTGGGCTTACGGTTGAGCC 333
Db 184 CACTTTGAGGGTGTTCACAGCCAAACGCAACAGCTACCTTGGGCTTACGGTTGAGCC 243

QY 334 CGCAACCCGCTGTGAGTATTACATCGTCGAACTTTGGACCTATGATCCTTCCTCC 393
|||||
Db 244 CGCAACCCGCTGTGAGTATTACATCGTCGAACTTTGGACCTATGATCCTTCCTCC 303
QY 394 GGTGCTACCGATCTAGGAATGTGAGTCCGAGTAGCATCTATCGACTCGGCAAGACC 453
|||||
Db 304 GGTGCTACCGATCTAGGAATGTGAGTCCGAGTAGCATCTATCGACTCGGCAAGACC 363
QY 454 ACTCGGCTCAACGCACTAGCATCGACGGCAACCAACTTCGACCAATACTGTCGGTC 513
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Db 364 ACTCGGCTCAACGCACTAGCATCGACGGCAACCAACTTCGACCAATACTGTCGGTC 423
QY 514 CGCCAGACAAGCGCAACGCGTACCGCTCAGACGGGCTGCCACTTCGACGCGCTGGCT 573
|||||
Db 424 CGCCAGACAAGCGCAACGCGTACCGCTCAGACGGGCTGCCACTTCGACGCGCTGGCT 483
QY 574 CGCGCTGTTGAAATGTCAACGCGTGACCACTACTACAGATCGTTGCAACGAGGGCTAC 633
|||||
Db 484 CGCGCTGTTGAAATGTCAACGCGTGACCACTACTACAGATCGTTGCAACGAGGGCTAC 543
QY 634 TTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGC 675
|||||
Db 544 TTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACGTGGC 585

RESULT 4
TLU35436 2460 bp DNA linear PLN 15-NOV-2001
LOCUS TLU35436 Thermomyces lanuginosus endo-beta-1,4-D-xylanase precursor (xyna)
DEFINITION gene, complete cds.
ACCESSION U35436
VERSION U35436.1 GI:2737877
KEYWORDS
SOURCE Thermomyces lanuginosus
Thermomyces lanuginosus
ORGANISM Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
REFERENCE 1 (bases 1 to 2460)
AUTHORS Schlacher,A., Holzmann,K., Hayn,M., Steiner,W. and Schwab,H.
TITLE Cloning and characterization of the gene for the thermostable
xylanase Xyna from Thermomyces lanuginosus
JOURNAL J. Biotechnol. 49 (1-3), 211-218 (1996)
PUBMED 8879171
REFERENCE 2 (bases 1 to 2460)
AUTHORS Schlacher,A., Holzmann,K., Hayn,M., Steiner,W. and Schwab,H.
TITLE Direct Submision
JOURNAL Submitted (06-SEP-1995) Institute of Biotechnology, SFB
Biocatalysis, TU-Graz, Petergasse 12,, Graz 8010, Austria
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Best Local Similarity 86.4%; Pred. No. 5.6e-106;
Matches 675; Conservative 0; Mismatches 0; Indels 106; Gaps 1;
QY 1 ATGTCGGCTTTACCCCGTTGCCCTTGCGGCTTAGCCGCACTGGGGCCCTGGCCTTC 60
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QY 61 CCGCAGGAATGCCACGAGCTCGAAAGCAGACAGAACCCCACTCGAGGGCTGG 120
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QY 435 CTATGACTCGGCAAGACCACTCGGTCAACGCACTAGCATGACGGCAACCAACCTT 494
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QY 495 CGACCAATACTGTCGTCGCGCAGACAAGCGCAACGCGGTACCGTCCAGACGGGCTG 554
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QY 675 C 675
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Db 1845 C 1845

RESULT 5
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LOCUS BX842624 89019 bp DNA linear PLN 17-APR-2005
DEFINITION Neurospora crassa DNA linkage group I BAC clone B10D6.
ACCESSION BX842624
VERSION BX842624.1 GI:38566913
KEYWORDS
SOURCE
ORGANISM
Neurospora crassa
Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE
AUTHORS
1 Schulte,U., Aign,V., Hoheisel,J., Brandt,P., Fartmann,B.,
Holland,R., Nyakatura,G., Mewes,H.W. and Mannhaupt,G.
Unpublished
2 (bases 1 to 89019)
German Neurospora genome,project.
REFERENCE
AUTHORS
TITLE Direct Submission
JOURNAL
Submitted (26-NOV-2003) MIPS, Institut fuer Bioinformatik,
GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,
Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:
G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute
of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf,
E-mail: ulrich-schulte@uni-duesseldorf.de
BAC clone 10D6 (strain OR74A) is available at the Fungal Genetic
Stock Center, http://www.fgsc.net
Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
http://www.mwgdna.com
Information on performance of analysis and a more detailed
annotation of this entry and other sequences can be viewed at:
http://mips.gsf.de/proj/neurospora.
FEATURES
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Query Match	38.9%; Score 262.4; DB 15; Length 89019;
Beet local similarity	65.3%; Pred. No. 1.7e-44;
Matches 418; Conservative 0; Mismatches 216; Indels 6; Gaps 2;	
24 CCTTGGCGCCCTTACGCCGACTGGGGCCCTGGCCCTCCCGGACAGGAATGCCACGGAGCT	83
39342 CCTCCTCGGCGCTGCGCGGTGCGCTCGCTATGCGCTTCAACGCCACCGAGTTCTCTGAGCT	39283
84 CGAAAAGCGACAGACAACCCCAACTCGGAGGGCTGGCAGCATGTTACTATTCTCTG	143
39282 CGCCGAGCGTGGCGGTACCCCGACGACCGGCTTCAACAACGGCTTCTACTACTCTT	39223
144 GTGAGTGACCGTGGAGCGCAGGCCACCTGACCAACCTGGAAGCGGACCTACGAGAT	203

Db	39222	CTGGACCCGCAACACGGCGGCAATGTCAACTACGCCCAACGGCGCCAGCGGCTTACTCTGT	39163
Qy	204	CAGCTGGGAGATGGCGGTAACTTCGTGGTGAAAGGGCTGGAACCCCGGCTGAACGC	263
Db	39162	GAACTGGAGAAACGCGCGCAACTTTGTGCGCCGGAAGGGCTGGAACCCCGGTTGC--GC	39106
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Qy	324	CGGTTGACCCGCAACCCCGCTGGTGCAGTATTACATCGTGAGAACTTGGCACTATGA	383
Db	39045	CGGCTGGACTCGCAACCCGCTTGTGAGTACTAGTCGTGAGAACTTTGGCTCCTACAA	38986
Qy	384	TCCTTCCTCCGGTGTCTACCGATCTAGGAACGTGCGAGTCCGACGGTAGCATCTAGCAT	443
Db	38985	CCCTTCGTGGGGCGGCCCAACGCTCTCGGATCCGTCTACACCGACGGCTCCACTACGACAT	38926
Qy	444	CGGCAAGACCACTCGCGCTCAACGCACCTAGCATGACGGCACCCCAACCTTCGACCAATA	503
Db	38925	CTACAAGACCAACCGCTTACAACGACCGCTCATTTGACGGCACCCGCACTTCAACCACTA	38866
Qy	504	CTGCTCGGTCCGCCAGACAGACGCCACCGGTACCGTCCAGACGGGCTGCCACTTGA	563
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Qy	564	CGCCTGGGCTCGCGCTGTTTGAATGTCAACGGTGAACCACTACTACAGATCGTTGCAAC	623
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Qy	624	GGAGGGCTAATTACAGACGGGCTATGCTCGCATCACCGTT	663
Db	38748	TGAGGGATACCAAGACAGATGCTCTGCCCATCACCGTT	38709
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LOCUS	TRU24191	786 bp	mRNA linear PLN 25-MAR-1997
DEFINITION	Trichoderma reesei beta-xylanase (XYN2) mRNA, complete cds.		
ACCESSION	U24191		
VERSION	U24191.1	GI:780815	
KEYWORDS			
SOURCE			
ORGANISM	Hypocrea jecorina		
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.		
REFERENCE			
AUTHORS	1 (bases 1 to 786)		
TITLE	la Grange,D.C., Pretorius,I.S. and van Zyl,W.H.		
JOURNAL	Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in Saccharomyces cerevisiae Appl. Environ. Microbiol. 62 (3), 1036-1044 (1996)		
PUBMED	8975597		
REFERENCE	2 (bases 1 to 786)		
AUTHORS	van Zyl,W.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-APR-1995) Willem H. van Zyl, University of Stellenbosch, Microbiology, Victoria street, Stellenbosch, 7600, South Africa		
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ORIGIN

Query Match	36.1%;	Score 243.6;	DB 15;	Length 786;
Best Local Similarity	61.7%;	Pred. No. 2.1e-40;		
Matches	406;	Conservative 0;	Mismatches 249;	Indels 3; Gaps 1;
OY	5	TCGGCTTTACCCCGCTTGCCCTTGCGGCTTAGCCGCGACTGGGGCCCTGGCCCTCCCGG	64	
Db	115	TCACCTCCCTCCTCGCCGGCGCTCGCCGCATCTCGGGCGCTTGCGCCGCTCCCGCCCGG	174	
OY	65	CAGGAATGCCACGGAGCTCGAAAACGACAGACAACCCCAACTCGGAGGGCTGGCAG	124	
Db	175	AGTTCGAACCCGTGGCTGTGAGAACGCCAGACGATTGACCCCGGCACGGGCTCAACA	234	
OY	125	ATGTTATTACTATTCTCTGTGAGTGAAGGTGAGCGCAGGCCACGTACACCAACTGG	184	
Db	235	ACGGCTACTTCCACTCGTACTGMAAGATGGCCACGGCGCGTGACGTACACCAATGGTC	294	
OY	185	AAGCGGCACCTACGAGATCAGCTGGGGAGATGGCGTAACTCTGTCGTGGAAGGGCT	244	
Db	295	CCGGCGGGCAGTCTCCGTCAACTGGTCCAACCTCGGCACTTTGTTCGGCGCAAGGAT	354	
OY	245	GGAACCCCGGCTGAACGCAAGACCACTTCACTTGAGGCTTTTACCAACCAACGGCA	304	
Db	355	GGCAGCCCGGCAACCAAGACAGGTATCAACTTCTCGGGCAGCTACAAACCCCAACGGCA	414	
OY	305	ACAGCTACTTGGCGGTCTACGGTTGGAACCCGCAACCCGCTGGTCAAGTATTACATCGTCG	364	
Db	415	ACAGCTACTCTCCGTGTACGGCTGGTCCGCAACCCCTGATCGAGTACTACATCGTCG	474	
OY	365	AGAACTTTGGCACTATGATCTTCTCCGCTGCTACCCGATCTAGGAATGTTCAGTGGCG	424	
Db	475	GGAACCTTTGGCACTTACCAACCCGCTCAACGGCGCCACCAAGCTGGGCGAGTCACTCCG	534	
OY	425	ACGGTAGCATCTATCGACTCGCAAGCACTCGCGTCAACGCACTAGCATCGAGGCA	484	
Db	535	ACGGCAGCGTCTACGACATTTACCGCAGCAGCGCGTCAACCAAGCCGTCATCATCGGCA	594	
OY	485	CCCAACCTTGCACCAATATCTGTCGGTCCGCCAGGACAAGCGCACGCGTACCGTCC	544	
Db	595	CCGCCACCTTTTACCACTAGTACTGTCGGTCCGCCGCAACCAACCGCTCGAGCGGCTCCGTC	654	
OY	545	AGACGGGCTGCCACTTTCGACGCGCTGGGCTCGCGCTGTTGATGTCAACGCTGACCACT	604	
Db	655	ACACGGCGGAACCACTTCAACGCGTGGGCTCAGCAAGGCGCTGACGCT--CGGACGATGG	711	
OY	605	ACTACCAAGATCGTTGCAACGGAGGGCTTCTCAGCAGCGGCTATGCTCGCATCACCGT	662	
Db	712	ATTACCAAGATGTGGCCGTGAGGGTTACTTTAGCTCTGGCTCTGCTTCCATCACCGT	769	

RESULT 7
HIXYL1
LOCUS HIXYL1 1039 bp mRNA linear PLN 18-APR-2005
DEFINITION H. insolens XYL1 mRNA for endoglucanase.
ACCESSION X76047
VERSION X76047.1 GI:505260
KEYWORDS endoxylanase; xyl1 gene.
SOURCE Humicola insolens
ORGANISM Humicola insolens
REFERENCE 1 (bases 1 to 1039)
AUTHORS Dalboege,H. and Hansen,H.P.H.

TITLE A novel method for efficient expression cloning of fungal enzyme
genes
JOURNAL Mol. Gen. Genet. 243 (3), 253-260 (1994)
PUBMED 8190078
REFERENCE 2 (bases 1 to 1039)
AUTHORS Dalboege,H.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1993) H. Dalboege, Manager GeneExpress, Novo Nordisk A/S, Symbion, Fruebjergvej 3, 2100 Copenhagen OE, DENMARK
FEATURES
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ORIGIN

Query Match 35.6%; Score 240.6; DB 15; Length 1039;
Best Local Similarity 64.6%; Pred. No. 8.4e-40;
Matches 392; Conservative 0; Mismatches 209; Indels 6; Gaps 2;

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Db	178	CTGGCAACGGCTACTTCTACTCTGTGTGTCGCGACGGCGGAGGCCAAGTTCAGTACAC	237	
OY	177	CAACTGGAAGCGGCACCTACGAGATCAGCTGGGGAGATGGCGTAACTCTGTCGTGG	236	
Db	238	CAACCTGAGGGGACCGGCTACAGGTCAAGTGGCGTAAACCGCAACTTCTGTCGTGG	297	
OY	237	AAAGGCTGGAACCCCGGCTGAACGCAAGACCATCACTTTGAGGGTGTTCAGACC	296	
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OY	297	AAACGGCAACAGCTACCTTGGGCTTACGGTTGGAACCGCAACCCGCTGGTCAAGTATA	356	
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OY	357	CATCGTCAGAACTTTGGCACCTATGATCCTTCTCCGGTGTCTAACGATCTAGGACTGT	416	
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OY	417	CGAGTGCAGCGTAGCATCTATGACTCGGCAAGACCACTCGCTCAACGCACCTAGCAT	476	
Db	475	CTATACCGAGCGCGATCAGTATGACATTTTGTGAGCACCCGCTTCAACCAAGCCACGAT	534	
OY	477	CGACGGCAACCAACTTGCACCAATACTGGTGGTCCGCGCAGGACAAGCGCACACCGG	536	
Db	535	CGACGGCACCCGAGCGTTCAGACGACTGTCTATCCGCAAGAACAGCGTGTGAGG	594	
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Db 652 CCAGCACTACTACCAAGTGTGTCGCCACCGAGGGCTACCAAGACAGTGGCGAGTCCGACAT 711

Qy 657 CACCGTT 663

Db 712 CTATGTT 718

RESULT 8

LOCUS 165436 1123 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 3 from patent US 5667990.

ACCESSION 165436

VERSION 165436.1 GI:2482006

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1123)

AUTHORS Berka,R.Michael., Yoder,W., Takagi,S. and Boomnathan,K.Cheltier.

TITLE Aspergillus expression system

JOURNAL Patent: US 5667990-A 3 16-SEP-1997;

FEATURES

source 1.1123

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ORIGIN

Query Match 35.4%; Score 239; DB 6; Length 1123;

Best Local Similarity 64.4%; Pred. No. 1.8e-39;

Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

Qy 57 CTTCCCGCAGGGAATGCCAGGAGCTGAAAAGCAGACAGCAACCCCACTCGAGGG 116

Db 197 CGTTCCTCGGACAACCTGACGCGCCCTTCAAGCTCGACAGGTGACCCCAACGGCAGAGG 256

Qy 117 CTGCAAGATGTTATTACTATTCTGTTGAGTGAACGGTGGAGCGCAGGCCAGTACAC 176

Db 257 CTGGCAACAAGGCTACTTCTACTCGTGTGTCGCAAGCGGAGGCCAGGTTCACTACAC 316

Qy 177 CAACCTGGAAGCGCGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACTCTCGGTGG 236

Db 317 CAACCTGAGGGCAGCGGCTACGAGTCAAGTGGCGTAAACCGGCAACTTCGTGGTGG 376

Qy 237 AAAGGCTGGAACCCCGGCTGAACGCAAGAGCCATCCATTGAGGGTGTTCACAGCC 296

Db 377 TAAGGTTGGAACCCGGG--AACCGGCGCAGATCAACTAAGCGGCTACTTCAACCC 433

Qy 297 AAACGGCAAGCTACCTTGCGGTACGGTTGACCCGCAACCGGTGTCAGTATTTA 356

Db 434 CCAGGGCAAGGCTACCTGCGGTACGGCTGACCCGCAACCGGTCTGTCAGTACTA 493

Qy 357 CATCGTGAAGACTTTGGCACTATGATCCTTCTCCGGTGTACCGATCTAGAACTGT 416

Db 494 TGTCAATGAGTCGTACGGCAGCTACATCCCGGAGCCAGGCTCAGTACAAGGGCACATT 553

Qy 417 CGAGTCCGACGGTAGCATCTATCGACTCGGCAAGACCACTGCGCTCAAGCAGCTAGCAT 476

Db 554 CTATACCGAGCGCGATCAGTATGACATCTTGTGAGCACCCGCTTACAACCAAGCCAGCAT 613

Qy 477 CGACGGCACCAAACTTGCAGCAATATGTCGTGTCGCGCAGGACAGCAAGCGCAGCGG 536

Db 614 CGACGGCACCCGAGCGTTCAGAGCAGTACTGTCTATCCGCAAGAAACAAGCGTGTGGAAG 673

Qy 537 TACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCTCGGCTGTTGAATGTCAACGG 596

Db 674 CTGGTCAACATGCAAGAACCACTTCAACGCGTGGCAGCAGCAGGAATGCCGCT---CGG 730

Qy 597 TGACCACTACTACCAAGATCGTTGCAACGGAAGGCTACTTCAAGCAGCGGCTATGCTCGCAT 656

Db 731 CCAGCACTACTACCAAGTGTGCGCCACCGAGGGCTACCAAGACAGTGGCGAGTCCGACAT 790

Qy 657 CACCGTT 663

Db 791 CTATGTT 797

RESULT 9

BD006885

LOCUS BD006885 1123 bp DNA linear PAT 31-JAN-2002

DEFINITION Aspergillus expression system.

ACCESSION BD006885

VERSION BD006885.1 GI:18635256

KEYWORDS JP 2001025393-A/2.

SOURCE Humicola insolens

ORGANISM Humicola insolens

REFERENCE 1 (bases 1 to 1123)

AUTHORS Berka,R.M., Yoder,W., Takagi,S. and Boomnathan,C.C.

TITLE Aspergillus expression system

JOURNAL Patent: JP 2001025393-A 2 30-JAN-2001;

COMMENT

OS Humicola insolens

PN JP 2001025393-A/2

PD 30-JAN-2001

PF 17-MAY-2000 JP 2000185449

PR 01-DEC-1993 US 08/161675

PI RANDY M BERKA,WENDY YODER,SHINOBU TAKAGI,

PI CARAPAPAN CHETVER BOOMINAZAN

PC C12N15/09,C12N1/15,C12P21/02/(C12N15/09,C12R1:66),(C12N15/09,PC C12R1:685)

PC (C12N15/09,C12R1:69),(C12N1/15,C12R1:66),(C12P21/02,C12R1:66),PC C12N15/00,C12R1:66),(C12N15/00,C12R1:685),(C12N15/00,PC C12R1:69)

CC

FEH Key

FT CDS (126).(806).

location/Qualifiers

source 1.1123

/organism="Humicola insolens"

/mol_type="genomic DNA"

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ORIGIN

Query Match 35.4%; Score 239; DB 6; Length 1123;

Best Local Similarity 64.4%; Pred. No. 1.8e-39;

Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

Qy 57 CTTCCCGCAGGGAATGCCAGGAGCTGAAAAGCAGACAGCAACCCCACTCGAGGG 116

Db 197 CGTTCCTCGGACAACCTGACGCGCCCTTCAAGCTCGACAGGTGACCCCAACGGCAGAGG 256

Qy 117 CTGCAAGATGTTATTACTATTCTGTTGAGTGAACGGTGGAGCGCAGGCCAGTACAC 176

Db 257 CTGGCAACAAGGCTACTTCTACTCGTGTGTCGCAAGCGGAGGCCAGGTTCAGTACAC 316

Qy 177 CAACCTGGAAGCGCGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACTCTCGGTGG 236

Db 317 CAACCTGAGGGCAGCGGCTACCAAGTCAAGTGGCGTAAACACCGGCAACTTCGTGGTGG 376

Qy 237 AAAGGCTGGAACCCCGGCTGAACGCAAGAGCCATCCATTGAGGGTGTTCACAGCC 296

Db 377 TAAGGTTGGAACCCGGG--AACCGGCGCAGATCAACTAAGCGGCTACTTCAACCC 433

Qy 297 AAACGGCAAGCTACTTGCAGTACGGTTGACCCGCAACCGGTGTCAGTATTTA 356

Db 434 CCAGGGCAAGGCTACTTGCAGTACGGCTGACCGGCAACCGGTCTGTCAGTACTA 493

Qy 357 CATCGTGAAGACTTTGGCACTATGATCCTTCTCCGGTGTACCGATCTAGAACTGT 416

Db 494 TGTCAATGAGTCGTACGGCAGCTACATCCCGGAGCCAGGCTCAGTACAAGGGCACATT 553

OY	417	CGAGTGCACGGGTAGCATCTATTCGACTCGGCAGAACCACCTGCCGTCAACGCACCTTAGCAT	476
Db	554	CTATTACCGACGGCGGATCAGTATGACATCTTTGTGAGCACCCGGCTAACACCAGCCCAGCAT	613
OY	477	CGACGGCACCCCAAACCTTGACAACATACTGTGGTCCGCCAAGACAAGCGCACCAAGCGG	536
Db	614	CGACGGCACCCCGACGTTCCAGCAGTA CTGTTATCCGAAGAA CAAGCGTGTGGAGG	673
OY	537	TACCGTCCAGACGGGCTGCCACTTGACGCGCTGGGCTCGCGCTGTTGATGTCAACGG	596
Db	674	CTCGGTCAACATGCAGAACCACTTCAACGCGTGGCAGCAGCAGCGAATGCCGCT--CGG	730
OY	597	TGACCACTACTACCAGATCGTTGCCAACGGAGGGCTACTTCAGCAGCGGCTATGCTCGCAT	656
Db	731	CCAAGCACTACTACCAAGGTCTGTGCCACCGAGGGCTACCAAGCAGTGGCGAGTCCGCAT	790
OY	657	CACCGTT 663	
Db	791	CTATGTT 797	

RESULT	10		
AY156910			
LOCUS	841 bp	mRNA	linear
DEFINITION	Trichoderma sp.	Sy xylanase mRNA,	complete cds.
ACCESSION	AY156910		
VERSION	AY156910.1	GI:26514829	

SOURCE ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales;
Trichoderma.

REFERENCE	
AUTHORS	
TITLE	
1	(bases 1 to 841)
Min, S. Y., Kim, B. G. and Ahn, J. -H.	
Purification, Characterization, and cDNA Cloning of Xylanase from	

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 841)

AUTHORS Min, S. Y., Kim, B. G. and Ahn, J. -H.
TITLE Direct Submission
JOURNAL Submitted (30-SEP-2002) Forest a

University, 1 Hwayang-Dong, Kwangjin-Gu, Seoul 143-701, South Korea

Location/Qualifiers

1. .841

source

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1. 841
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60. 722
CDS

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ORIGIN

Query Match	34.2%;	Score 230.8;	DB 15;	Length 841;
Best Local Similarity	60.8%;	Pred. No. 9.3e-38;		
Matches 395;	Conservative	0;	Mismatches 252;	Indels 3;
				Gaps 1;

24 CCTTGGGCGCTTAGCCGCGACTGGGGCCCTGGCCTTCCCGGAGGAATGCCACGAGCT 83

Db 80 CCTGCCGGCTTTGCGCGCTGTGCCGAGTCCTGTCCGCTCCTACTGAAGACGTGCAAGT 139

84 CGAAAGCGACAGACAACCCCACTCGAGGGCTGGCAGATGTTACTATTCTG 143

Db 140 CGAAAGCGTCAGGTCATTGGCCCCGGCACTGGCTTCAACAACGGCTACTACTCGTA 199

QY 144 GTGGAGTGACCGGTGAGCGGCAGGCCACGTACACCACCTGGAAAGCCGCACTACGAGAT 203
| | | | | | | | | | | | | | | | | | | | |
Db 200 CTGGAACGACGGCCATGCCGCGTGACTTACACCAACGCGCTGGCGGCTCATTACGCGT 259
| | | | | | | | | | | | | | | | | | | | |

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QY      204  CAGCTGGGAGATGGCGGTAACTCGTGGGTGAAAGGGCTGGAACCCCGGCTGAACGC 263
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Db      260  CACTGGGCCCACTCGGGCACTTGTGGGAGGCAAGGATGGAACCCGGGCAAGCAC 319

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DY 264 AAGGCCATCCACTTTGAGGGTGTTCACAGCCAAACGGCAACAGCTACCTTGCGGTCTA 323
||| |||
Db 320 CAGAACCATTCACTTCTCCGGCAGCTACAGCCCCAACGACAACAGCTACTCTCCGCTTA 379

Figure S8.

Dy
324 CCGTTGACCCGCCAACCCGCTGTGAGTATTATCATCGTAGAACCITTTGGACCTATGA 383

Db
380 CGGCTGTCCAAGAACCCTGCATTCAGTACTACATTGTGAGAACTTTGGACCTACAA 439

[illegible]

QY 444 CGGCAAGACCACTCGCGTCAACGCACCTAGCATCGACGGCACCCAAACCTTCGACCATA 503
| | | | | | | | | | | | | | | |
Db 500 TTACCGCAGCGCAGCGCGGTCAACCGACCGGTCCATCATCGGACGCGCCACCTTTTACCACTA 559

QY 504 CTGCTCGGTCGCCAGGACCAAGCGGTACCGTCCAGACGGGCTGCCACTTGA 563
|||||
Db 560 CTGCTCGGTCGCCAGGACCAAGCGGTACCGTCCAGTGGGCAACCACTTCA 619
|||||

OY
Db

564 CGCCTGGGCTCGCGCTGTGTTGAATGCACGGTGACCCTACTACCAGATCGTTCAC 623
||||| ||||| ||||| ||||| |||||
620 TGGCTGGCGCAATCTCGGCTGACGCT---GGACAGCTGGACTACCAGATTATGCCGT 676
||||| ||||| ||||| ||||| |||||

DY 624 GAGGGCTACTTCAGCAGCGGCTATGCTGCATCACCGTGTGACGTGG 673
| | | | | | | | | | | | | | |
Db 677 GAGGGATATTTCAGCTCTGGCAGGCCAACAATTAACTCAGCTAGGTGG 726
| | | | | | | | | | | | | | |

RESULT 11
AY320048

LOCUS	AV320048	672 bp	mRNA	linear	PLN 14-JUL-2003
DEFINITION	Trichoderma viride strain YNUCC0183 endo-1,4-beta-xylanase mRNA, complete cds.				
ACCESSION	AV320048				

VERSION	AY320048.1	GI:32481056
KEYWORDS	.	
SOURCE	Trichoderma viride	
ORGANISM	Trichoderma viride	

SOURCE ORGANISM	Trichoderma viride
Trichoderma viride	
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma; Trichoderma viride species complex.	

REFERENCE
AUTHORS
1 (bases 1 to 672)
Li, W. P., Zhang, Q., Liao, C. L., Zhou, J. G., Yang, Y. H., Liu, W. J. and Yang, Z. W.

JOURNAL
REFERENCE
Trichoderma viride YNUCC0183
Unpublished
2 (bases 1 to 672)

TITLE Yang, Z. W.
JOURNAL Direct Submission
Submitted (10-JUN-2003) Key Laboratory of Industrial Microbiology

FEATURES
Fermentation Technology of Yunnan, School of Life Science, Yunnan University, 2 North Road, Green Lake, Kunming, Yunnan 650091, China
Location/Qualifiers

Source

/organism="Trichoderma viride"

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1. 672

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ORIGIN

Query Match	33.8%;	Score 228.2;	DB 15;	Length 672;
Best Local Similarity	60.6%;	Pred. No. 3.3e-37;		
Matches	393;	Conservative	0;	Mismatches 253; Indels 3; Gaps 1;
Qy	15	CCCCGTGCGCTTGGCGCCTTAGCCGCACTGGGGCCCTGGCCCTCCCGGCAAGGAATGC	74	
Db	21	CCTCGCCGCTTCGTGCTGTACCGGAGTTCTGTCCGCTCCCACTGAGAACGTGAGGT	80	
Qy	75	CACGGAGCTCGAAAGCGCAGACAACCCCAACTCGAGGGCTGGCAGCATGTTATTA	134	
Db	81	CGTGAAGTGAAGAGCGCCAGAGATTGGCCCCGCACTGGCTTCAACAACGGCTACTA	140	
Qy	135	CTATTCCTGTGAGTGACGGTGAAGCGCAGCCAGTACCAACCTGGAAGCGGCAC	194	
Db	141	CTACTGTAAGTGAAGATGGCCATTCCGGCGTGACATACCAACGAGTGTGGCGGCTC	200	
Qy	195	CTACGAGTCAAGTGGGAGATGGCGGTAACTCGTCCGTGGAAAGGGCTGAAACCCCGG	254	
Db	201	ATTGAGCGTCAACTGGGCAAACTGGGCAACTTTGTCCGAGGCAAGGATGAAACCCCGG	260	
Qy	255	CCTGAACGCAAGAGCCATCCACTTTGAAGGTGTTTACAGCCAAACGGCAACGCTACCT	314	
Db	261	CAGCAGCTCCAGGGTCATCAACTTCTCTGGCAGCTACAACCCCAACGGCAATAGCTACCT	320	
Qy	315	TGCGGTCTACGGTTGGAACCCGCAACCCGCTGTGCGATTAATCATGTCGAGAACTTTGG	374	
Db	321	CTCAGTCTATGCTGTGTCMAAGAACCTCTCATGAGTACTATCATGTTGAACCTTTGG	380	
Qy	375	CACCTATGATCCTTCTCCGCTGTAACGATCTAGGAATGTGAGTGCAGCGTAGCAT	434	
Db	381	AACTCAACACCATCGACCGGCAACCAAGCTGGCGAGGTGACCTTGACGGCAGCGT	440	
Qy	435	CTATGCACTCGGCAAGACCACTGCGTCAACGCACTAGCATCGACGGCAACCAACCTT	494	
Db	441	CTACGACATCTACCGCAGCAGAGTCAACCAAGCTTCCATCATCGGAACGCCCACTT	500	
Qy	495	CGACCAATACTGCTCGGTCCGCCAAGACAAGCGCACGCGGTACCGTCCAGACGGGCTG	554	
Db	501	TTACCACTACTGCTGTCTCGCGCAACCAACGCTCCAGCGGCTCGGTACGGTTGCGAA	560	
Qy	555	CCACTTCGACGCGCTGGGCTCGCGCTGTTGAATGTCAACGGTGACCACTACTACAGAT	614	
Db	561	CCACTTCAACGCGTGGCGCAACTGGGCTTGA---CCCTGGGAACCTTGAGTACAGAT	617	
Qy	615	CGTTCGAACGAGGCTACTTCAAGCAGCGGCTATGCTGCATCACCGTT	663	
Db	618	CATTGCCGTGAGGCTACTTAGCTCTGTAAACGCCCAATTAAAGTT	666	

RESULT 12
AF246830 2202 bp DNA linear PLN 20-FEB-2002
LOCUS AF246830
DEFINITION Fusarium oxysporum f. sp. lycopersici xylanase 5 protein (xyl5)
ACCESSION AF246830
VERSION AF246830.1 GI:13491872
KEYWORDS
SOURCE
ORGANISM Fusarium oxysporum f. sp. lycopersici
Fusarium oxysporum f. sp. lycopersici
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
Fusarium oxysporum complex.
REFERENCE
1 (bases 1 to 2202)

AUTHORS Gomez-Gomez, B., Isabel, M., Ronceño, G., Di Pietro, A. and Hera, C.
TITLE Molecular characterization of a novel endo-beta-1,4-xylanase gene
JOURNAL from the vascular wilt fungus Fusarium oxysporum
PUBMED Curr. Genet. 40 (4), 268-275 (2001)
REFERENCE 11795847
AUTHORS 2 (bases 1 to 2202)
TITLE Hera, C., Gomez-Gomez, B. and Roncero, M.
JOURNAL Direct Submission
Submitted (17-MAR-2000) Departamento de Genética, Universidad de
Cordoba, Avda. San Alberto Magno s/n, Cordoba 14071, Spain
FEATURES
source location/Qualifiers
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CDS

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ORIGIN

Query Match	31.8%;	Score 214.6;	DB 15;	Length 2202;
Best Local Similarity	64.7%;	Pred. No. 2e-34;		
Matches	377;	Conservative	0;	Mismatches 159; Indels 47; Gaps 2;
Qy	132	TTACTATTCTGTGTGAGTGACGGTGAAGCGCAGGCCACGTACACCAACTTGAAGCGG	191	
Db	870	TGACTTTATATAGTGAGTGATGGCGGTGCCGATGCCACTTACACCAACGCTGAGGAGG	929	
Qy	192	CACCTACGAGATCAGTGGGAGATGGCGGTAACTCTGTCGGTGAAGGGCTGAACCC	251	
Db	930	TTCTTACTCCATGAGTGAAGATGCGCGCAAGTGTGCTGGTGAAGGTTGTTCTCC	989	
Qy	252	CGGCTGAAC-----GCAAGA	267	
Db	990	TGGAAGGCGCGTTAGTACACATAAGCTTACATGCGCCCTGTGTAATACCTGTAGA	1049	
Qy	268	GCCATCCACTTTGAGGGTGTTCACAGCCAAACGGCAACAGCTACCTTGGCTTACGGT	327	
Db	1050	ACCATCTGTACGAGGAGAGTACAAGCCCAACGGCAACAGCTACTCTCTGTCTACGGT	1109	
Qy	328	TGACCCGCAACCCGCTGCTGAGTATTACATGTCGAGAACTTTGGCACTATGATCCT	387	
Db	1110	TGACCCGCAACCCCTCTGCTGCAATACATACATGTCGAGTCTTGGTACTTACAACCCC	1169	
Qy	388	TCTCCGGTGTACCGATCTTAGAAGTGTGCGAGCGTAGCATCTATCGACTCGGC	447	
Db	1170	TCCAGCGGTGTACCAAGAGGACCGTTGAGGCGGATGCGACGACCTACGACATCTTC	1229	
Qy	448	AAGACCACTGCGTCAACGCACCTAGCATGACGGCAACCAACCTTGACCAATACTGG	507	
Db	1230	GAGACCACTGCGACCAACGCCCTTCAATGCAACGCTACTGACACCTTCAAGCACTACTGG	1289	
Qy	508	TGCGTCCGCCAGACAAAGCGCAACGCGTACCGTCCAGACGGGCTGCCACTTGACGCC	567	
Db	1290	TCTGTTCCGCAAGACACCGCTCTACTGCGACGGTGCACACTGCTTTCATTTCGATGCC	1349	
Qy	568	TGGGCTCGCGTGTGTAATGTCAACGGTGAACCACTACTACGAGATGTTGCAACGGAG	627	

Db	1350	TGGAGAGAGCCCGGCATGAAGCT--CGGTACTACGACTACCAAGATCCTGCTACTGAG	1406
Oy	628	GGCTACTTCAGCAGCGGCTATGCTCGCATCACCGTTGCTGACG	670
Db	1407	GGTTACTTCAGCAGCGGATCGTCCCATGACCGTCTGTGAGG	1449
RESULT 13			
TVI012718			
LOCUS	TVI012718	928 bp	mRNA linear PLN 15-APR-2005
DEFINITION	Trichoderma viride mRNA for endo-1,4-beta-xylanase.		
ACCESSION	AJ012718		
VERSION	AJ012718.1	GI:6434132	
KEYWORDS	endo-1,4-beta-xylanase.		
SOURCE	Trichoderma viride		
ORGANISM	Trichoderma viride		
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma; Trichoderma viride species complex.		
REFERENCE			
AUTHORS	1	Furman-Matarasso, N., Cohen, E. and Avni, A.	
TITLE		Mutations in the Active Site of the Ethylene Inducing Xylanase Elicitor Inhibits the b-1-4-Endoxylanase Activity But Not the Elicitation Activity	
JOURNAL	Unpublished		
REFERENCE	2	(bases 1 to 928)	
AUTHORS		Avni, A.	
TITLE		Direct Submission	
JOURNAL		Submitted (10-NOV-1998) Avni A., Plant Sciences, Tel-Aviv University, Tel-Aviv, 69978, ISRAEL	
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	/EC_number="3.2.1.8"		
ORIGIN			
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Best Local Similarity	60.2%;	Pred. No. 2.9e-34;	
Matches	390;	Conservative 0;	Mismatches 255; Indels 3; Gaps 2;
Oy	15	CCCCGTGCCCCTTGGCGCCTTAGCCCGCACTGGGGCCCTTGCCCTCCCGCAGGGAATGC	74
Db	83	CCTGCGAGGCTTCGTGCTGTATCCGGAGTTCTGTCCGCTCCCACTGAGACCGTGAAGGT	142
Oy	75	CACGGAGCTCGAAAAGCGACAGACAACCCCAACTCGGAGGCTGGCAGCATGTTATTA	134
Db	143	CGTGACGTGGAGAGCGCCAGACGATTGGCCCGGCACTGGCTTCAACAACGGCTACTA	202
Oy	135	CTATTCCTGGTGAAGTGAAGCGTGAAGCGCACGCTACACCACTGGAAGCGGCAAC	194
Db	203	CTACTCCTACTGGAACGATGGCCATTCGCGCGTGACATACACCAACGCTGCGCGCTC	262
Oy	195	CTACGAGATCAGCTGGGAGATGCGGTAACTCTGCTGTGGAAGGCTGGAACCCGG	254

Db	263	ATTCAAGCTCAACTGGGCAAACTCGGGCAACTTGTTCGAGGCAAGGATGGAACCTCGG	322	
Oy	255	CCTGAACGCAAGAGCCATCCACTTTGAGGGTGTATTACCAAGCCAAACGGCAACAGTACCT	314	
Db	323	CAGCAGCTCCAGAGTCATCAACTTCTCTGGCAGCTACAAACCCCAACGGCAACAGTACCT	382	
Oy	315	TGGGCTTACGGTTGGACCCCGCAACCCGCTGGTCGAGTATTACATCGTTCAGAACTTTGG	374	
Db	383	CTCAGTCTATGCTGTGTCCAGAAGAACCCCTCATCGAGTACTACATTGTTGAGAACTTTGG	442	
Oy	375	CACCTATGATCCTTCTCCGGTGTACTACCGATCTAGGAACCTGTGAGTGGCAGCGTAGCAT	434	
Db	443	AACCTAACACCCATCGACTGGCACCAACCAAGCTGGGTGAGTGACCTTGACGGCAGCGT	502	
Oy	435	CTATCGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATGACGCGCAACCCAAACCTT	494	
Db	503	CTACGACATCTACCGCACGACGAGTCAACCAAGCCTTCATCATCGGAACGGCCACCTT	562	
Oy	495	CGACCAATACTGTGTCCGTCGCCGCAAGACCAAGCCAGCGGTACCGTCCAGACGGGCTG	554	
Db	563	TTACCACTACTGTTCTGTCCGCCGCAACCA-CGCTCCAGCGGCTCGGTACCGTTGCCAA	621	
Oy	555	CCACTTCGACGCGCTGGGCTCGCGCTGTTGATGTCAACGCGTGACCACTACTACCAAGT	614	
Db	622	CCACTTCCAACGCGTGGCGCAACCTGGGCTTGA--CTCTGGAACTTGGACTTACCAAGT	679	
Oy	615	CGTTGCAACGAGGGCTACTTTCAGACGCGGCTATGCTGCATCACCGT	662	
Db	680	CATTGCCGTGAGGGGCTACTTTAGCTCTGTTAGCAAGCCCAACATTAAAGT	727	
RESULT 14				
AK110604		912 bp	mRNA linear PLN 24-JUL-2003	
LOCUS	AK110604			
DEFINITION	Oryza sativa (japonica cultivar-group)	cDNA clone:002-168-G08, full insert sequence.		
ACCESSION	AK110604			
VERSION	AK110604.1	GI:32995813		
KEYWORDS	FLI_CDNA; oligo capping.			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group)			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryza.			
REFERENCE				
AUTHORS	1	The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team; Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nilkura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN; Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.		
TITLE		Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice		
JOURNAL		Science 301 (5631), 376-379 (2003)		
PUBMED		12869764		
REFERENCE				
AUTHORS	2	(bases 1 to 912)		
	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,			

Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoaka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
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FEATURES
source
1. .912
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Best Local Similarity 62.8%; Pred. No. 4.6e-34;
Matches 365; Conservative 0; Mismatches 210; Indels 6; Gaps 2;
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QY 262 GCAAGACCATCCACTTTGAGGTTGTTACCAAGCCAAACGGCAACAGCTACTTGGGTC 321
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DB 396 TACGGCTGACCCGCAACCCCGCTGCTGAGTACTAGTATGAGAACTACGGCAGCTAC 455
QY 382 GATCTTCTCCGCTGCTGCTACCGATCTAGAACTGTGAGTGGACGGTAGACTATTCGA 441
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DB 636 AACGAGTGGCTTAAGTATGCAATGA---CTTGGTCAAGCACTTACTACCAATTGTGCT 692
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RESULT 15
AY648860 696 bp mRNA linear PLN 05-AUG-2005
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCES
Hatsch,D., Phalip,V. and Jeltsch,J.-M.
The xylanases of *Gibberella zeae*
Unpublished
2 (bases 1 to 696)
Hatsch,D., Phalip,V. and Jeltsch,J.-M.
Direct Submission
Submitted (09-JUN-2004) Laboratoire de Phytopathologie, UMR 7100 - IIR 85 - ESBS -UIP, Boulevard Sebastien Brant - BP10413, Illkirch-Graffenstaden, Alsace 67412, France

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ORIGIN

Query Match 31.3%; Score 211.4; DB 15; Length 696;
 Best Local Similarity 62.3%; Pred. No. 1e-33;
 Matches 367; Conservative 0; Mismatches 216; Indels 6; Gaps 2;

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QY     134 ACTATTCCTGGTGGAGTGAAGGTGAGCGCAGGCAAGTACCAACTGGAAGCGGCA 193
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DB     161 TCTACTCTTGGTGTCTGATGTTGGTGTATGCTCAGTACCGTATGGTGAAGGACGCC 220
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QY     314 TTGCGGTCTACGGTTGAGCCCGCAACCGCTGTGAGTATTACATCGTCGAACTTTG 373
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QY     374 GCACCTATGATCTCTCCGCTGCTACCGATCTAGGAATGTGAGTGCAGCGGTAGCA 433
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DB     398 GTTCTTACAACCCCGGAGCGCTCAGACCGAGGTACGTTACACCGAGGTGACA 457
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Search completed: February 11, 2006, 20:54:07
 Job time : 3495.06 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:07:17 ; Search time 422.587 Seconds
(without alignments)
10645.530 Million cell updates/sec

Title: US-09-467-368-1_COPY_31_705

Perfect score: 675

Sequence: 1 ATGTCGCGCTTTACCCCGT.....TCACCGTTGCTGACGTGGGC 675

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: Geneseqn1990s:*
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- 4: Geneseqn2001as:*
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- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	675	100.0	983	2	AAT40742 Aat40742 Xylanase
2	675	100.0	983	2	AAT43010 Aat43010 Endo-1,4-
3	582	86.2	588	5	AAS13813 Aas13813 DNA encod
4	371.6	55.1	678	4	AAD17927 Aad17927 Thermomyc
5	239	35.4	1123	2	AAQ74098 Aaq74098 Humicola
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7	224.6	33.3	666	10	ABQ80362 Abq80362 A. fumiga
8	221.6	32.8	705	10	ABQ80364 A. fumiga
9	205	30.4	1195	2	AAZ28864 Aaz28864 Streptomy
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12	203	30.1	696	12	ADL23221 Adl23221 A. niger
13	201.2	29.8	1008	12	ADJ35015 DNA encod
14	198.4	29.4	851	2	AAT63044 Aat63044 Aspergill
15	196.2	29.1	1375	2	AAX90405 Actinomad
16	196.2	29.1	1375	2	AAT64930 Aat64930 Actinomad
17	194.2	28.8	822	2	AAV29598 Aav29598 DNA seque
18	190	28.1	1015	2	AAQ54775 Aaq54775 T. reesei
19	190	28.1	1015	2	AAV81332 Aav81332 T. reesei

20	189.2	28.0	739	10	ABQ80363 Abq80363 A. fumiga
21	187.8	27.8	1273	2	AAQ90388 Aaq90388 Xylanase
22	186.2	27.6	1059	12	ADJ35009 DNA encod
23	185	27.4	1047	12	ADJ34949 DNA encod
24	183.4	27.2	1057	2	AAO03405 Aaq03405 Streptomy
25	181.8	26.9	1281	2	AAT71585 Aat71585 Chaetomiu
26	181.2	26.8	712	10	ABQ80361 Abq80361 A. fumiga
27	171.8	25.5	572	2	AAQ43458 Aaq43458 Sequence
28	170	25.2	1074	12	ADJ34983 Adj34983 DNA encod
29	170	25.2	1137	12	ADJ35039 DNA encod
30	168.4	24.9	675	2	AAQ36563 Aaq36563 Endo-xyla
31	165.8	24.6	1041	12	ADJ34953 DNA encod
32	165.6	24.5	1044	12	ADJ35005 DNA encod
33	165.4	24.5	942	10	ABQ80366 Abq80366 A. fumiga
34	165.4	24.5	1299	12	ADJ34961 Adj34961 DNA encod
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36	164	24.3	516	2	AAQ28828 Aaq28828 Recombina
37	160.8	23.8	1044	12	ADJ34979 DNA encod
38	160.8	23.8	1083	12	ADJ34967 DNA encod
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40	159	23.6	1581	2	AAQ69150 Aaq69150 Aspergill
41	156.2	23.1	1047	12	ADJ35037 DNA encod
42	153.6	22.8	2439	12	ADL23220 A. niger
43	150.8	22.3	1065	12	ADJ34999 DNA encod
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ALIGNMENTS

RESULT 1	
AAT40742	
ID	AAT40742 standard; CDNA; 983 BP.
XX	
AC	AAT40742;
XX	
DT	21-MAY-1997 (first entry)
XX	
DE	Xylanase coding sequence.
XX	
KW	Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermoascus;
KW	Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia;
KW	Byssochlamys; Paecilomyces; animal feed additive; in-vivo breakdown;
KW	plant cell wall; growth rate; feed conversion; ss.
XX	
OS	Thermomyces lanuginosus.
XX	
FH	Key
FT	CDS
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FT	/product= "xylanase"
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PN	W09623062-A1.
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PD	01-AUG-1996.
XX	
PF	26-JAN-1996; 96WO-DK000046.
XX	
PR	26-JAN-1995; 95DK-00000094.
XX	
PA	(NOVO) NOVO-NORDISK AS.
XX	
PI	Hansen PK, Wagner P, Muellertz A, Knap IH;
XX	
DR	WPI; 1996-454790/45.
DR	P-PSDB; AAW01112.
XX	
PT	Fungal xylanase preps. for use as animal feed additives - and DNA
PT	construct for producing recombinant Thermomyces xylanase.
XX	
PS	Claim 5; Page 45-46; 69pp; English.
XX	

CC This sequence represents the coding sequence for the xylanase from
CC Thermomyces lanuginosus strain DSM 4109. The encoded xylanase, and
CC xylanases derived from Humicola, Thermascus, Chaetomium, Mucor,
CC Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssoschlamus or
CC Paecilomyces strains can be used in the monocomponent xylanase
CC preparations of the invention. The xylanase preparations and the
CC recombinant Thermomyces xylanase are useful as animal feed additives,
CC which promote in-vivo breakdown of plant cell wall material and thus
CC improve digestibility, growth rate and/or feed conversion
XX
SQ Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 675; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.6e-174;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGGCTTTACCCCGGTTGCCCTTGCGGCTTAGCCCGCACTGGGGGCGCTGCTTC 60
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QY 181 CTGGAAGGCGGCACCTACGAGATCACTGGGGAGATGGCGGTAACTCGTCGGTGAAG 240
DB 211 CTGGAAGGCGGCACCTACGAGATCACTGGGGAGATGGCGGTAACTCGTCGGTGAAG 270
QY 241 GGTGGAACCCCGGCTGAAACGCAAGACCATCCACTTTGAGGGTGTACCAGCCAAAC 300
DB 271 GGTGGAACCCCGGCTGAAACGCAAGACCATCCACTTTGAGGGTGTACCAGCCAAAC 330
QY 301 GGCACAGCTAAGCTTGCGGTCTACGGTTGGAACCGCAACCCGCTGTGAGTATTACATC 360
DB 331 GGCACAGCTAAGCTTGCGGTCTACGGTTGGAACCGCAACCCGCTGTGAGTATTACATC 390
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DB 391 GTCGAGAAGCTTTGGACCTATGATCCTTCCTCGGTGCTACCGATCTAGGAAGTTCGAG 450
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DB 451 TCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGGTCACGCACTAGCATCGAC 510
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RESULT 2
ID AAT43010 standard; cDNA; 983 BP.
XX AAT43010;
AC AAT43010;
XX 16-OCT-2003 (revised)
DT 22-FEB-1997 (first entry)

XX Endo-1,4-beta-D-xylanase gene.
DE
XX
XX Endo-1,4-beta-D-xylanase; xylanase; Thermomyces lanuginosus;
KW Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae; yeast;
KW flour; baking; dough; ss.
XX
OS Thermomyces lanuginosus; (strain DSM 4109).

XX
FH Key Location/Qualifiers
FT 5'UTR 1..30
FT CDS /+tag= a
FT /tag= 31..708
FT /product= "Endo-1,4-beta-D-xylanase"
FT /note= "EC-3.2.1.8"
FT 3'UTR 709..983
FT /+tag= c

XX W09632472-A1.
XX
XX 17-OCT-1996.
XX
XX 11-APR-1996; 96WO-DK000171.
XX
XX 11-APR-1995; 95DK-00000435.
XX
XX (NOVO) NOVO-NORDISK AS.

XX Jorgensen OB, Si JQ, Jakobsen TS;
XX
XX WPI; 1996-477123/47.
XX P-PSDB; AAW05187.

PT Bread improving additive contg. xylanase from Thermomyces - and opt.
PT alpha-amylase, increases volume, improves anti-staling properties etc.
XX
XX Claim 7; Page 30-31; 41pp; English.

XX The sequence encodes an endo-1,4-beta-D-xylanase from Thermomyces
XX lanuginosus (Humicola lanuginosa), which may be used as a bread-
XX improving additive. The enzyme may be expressed recombinantly from a
XX plasmid pYES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed),
XX and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour,
XX optionally along with other enzymes (amylase, maltogenase, lipase,
XX cellulase, hemicellulase, pentosanase, glucose-oxidase, laccase,
XX protease and/or peroxidase). The enzyme combines particularly well with
XX amylolytic enzymes, and may be used to improve baking properties of flour
XX and/or dough, by increasing volume and improving texture, flavour, crumb
XX softness, freshness and anti-staling properties, while improving dough
XX machinability and stability. (Updated on 16-OCT-2003 to standardise OS
XX field)

SQ Sequence 983 BP; 225 A; 272 C; 277 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 675; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 2.6e-174;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGGCTTTACCCCGGTTGCCCTTGCGGCTTAGCCCGCACTGGGGGCGCTGCTTC 60
DB 31 ATGTCGGCTTTACCCCGGTTGCCCTTGCGGCTTAGCCCGCACTGGGGGCGCTGCTTC 90
QY 61 CCGGCAAGGAATGCCACGAGCTCGAAAAAGCAGACAGAACCCCACTCGGAGGGCTGG 120
DB 91 CCGGCAAGGAATGCCACGAGCTCGAAAAAGCAGACAGAACCCCACTCGGAGGGCTGG 150
QY 121 CACGATGGTTATTACTATTCTGTGGAGTGACGGGTGAGCGCAGGCCACGTACCAAC 180
DB 151 CACGATGGTTATTACTATTCTGTGGAGTGACGGGTGAGCGCAGGCCACGTACCAAC 210
QY 181 CTGGAAGGCGGCACCTACGAGATCACTGGGAGATGGCGGTAACTCGTCGGTGAAG 240

Db 211 CTGAAGCGGCACTTAGAGATGAGTGGGAGATGGCGGTAACTCGTCGGTGAAG 270
Qy 241 GGCTGAACCCCGGCTGAACGCAAGAGCCATCCATTGAGGGTGTATTACCAAGCAAAAC 300
Db 271 GGCTGAACCCCGGCTGAACGCAAGAGCCATCCATTGAGGGTGTATTACCAAGCAAAAC 330
Qy 301 GGCAACAGCTACCTTGGGCTACCGGTGAGCCCGCAACCCGCTGTCGAGTATTACATC 360
Db 331 GGCAACAGCTACCTTGGGCTACCGGTGAGCCCGCAACCCGCTGTCGAGTATTACATC 390
Qy 361 GTCGAGAATTGGCACTATGATCTCTCCGGTGTCTACCGATCTAGGAACGTGAG 420
Db 391 GTCGAGAATTGGCACTATGATCTCTCCGGTGTCTACCGATCTAGGAACGTGAG 450
Qy 421 TGGACGGTAGCATCTATGACTGGGAGAGACCACTCGCTCAACGCACCTAGCATCGAC 480
Db 451 TGGACGGTAGCATCTATGACTGGGAGAGACCACTCGCTCAACGCACCTAGCATCGAC 510
Qy 481 GGCACCCAAACCTTCGACCAATATGTCGGTCCGCGCAGAGCAAGCGCACCGGTACC 540
Db 511 GGCACCCAAACCTTCGACCAATATGTCGGTCCGCGCAGAGCAAGCGCACCGGTACC 570
Qy 541 GTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAC 600
Db 571 GTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAC 630
Qy 601 CACTACTACAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGTCTGCATCAC 660
Db 631 CACTACTACAGATCGTTGCAACGGAGGGCTACTTCAGCAGCGGCTATGTCTGCATCAC 690
Qy 661 GTTGCTGACGTGGGC 675
Db 691 GTTGCTGACGTGGGC 705

RESULT 3

AA513813
ID AA513813 standard; DNA; 588 BP.
XX
AC AA513813;
XX
DT 18-DEC-2001 (first entry)
XX
DE DNA encoding Thermomyces lanuginosus xylanase A.
XX
KM Xylanase A; plant cell wall; baking; cereal; starch production; wood;
KW wood pulp bleaching; hemicellulose; arabinoxylan; foodstuff; bread; ds.
XX
OS Thermomyces lanuginosus.
XX
PN WO200166711-A1.
XX
PD 13-SEP-2001.
XX
PF 08-MAR-2001; 2001WO-1B000426.
XX
PR 08-MAR-2000; 2000GB-00005585.
XX 27-JUN-2000; 2000GB-00015751.
XX
PA (DANI-) DANISCO AS.
XX
PI Sibbesen O, Sorensen JF;
XX
DR WPI, 2001-596834/67.
XX
XX
PT Novel variant xylanase polypeptide or its fragment useful for degrading
PT or modifying plant cell wall, comprises amino acid modifications such
PT that the polypeptide has altered sensitivity to xylanase inhibitor.
XX
PS Disclosure; Page 64; 70pp; English.
XX
CC The invention relates to a variant xylanase polypeptide (I) or its
CC fragment having xylanase activity, comprising one or more amino acid

CC modifications such that (I) or its fragment has an altered sensitivity to
CC a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or
CC its coding sequence (II) is useful for degrading or modifying plant cell
CC wall or for processing a plant material by contacting the plant cell wall
CC or plant material with (I) or (II). (I) is useful for modifying plant
CC materials, and in baking, processing cereals, starch production,
CC processing wood and enhancing the bleaching of wood pulp. (I) is useful
CC for altering the viscosity derived from the presence of hemicellulose or
CC arabinoxylan in a solution or system comprising plant cell wall material.
CC (I) is useful for preparing a foodstuff such as bread, pretzels,
CC tortillas, cakes, cookies, biscuits or crackers. The present sequence
CC represents the coding sequence of Thermomyces lanuginosus xylanase A as
CC described in the method of the invention
XX

SQL Sequence 588 BP; 131 A; 178 C; 168 G; 111 T; 0 U; 0 Other;

Query Match 86.2%; Score 582; DB 5; Length 588;
Best Local Similarity 100.0%; Pred. No. 6.1e-149;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 CAGACAAACCCCACTCGAGGGCTGGACAGATGTTATTACTATTCTGTGGAGTGAC 153
Db 4 CAGACAAACCCCACTCGAGGGCTGGACAGATGTTATTACTATTCTGTGGAGTGAC 63
Qy 154 GGTGAGCGCAGGCGCACGTACCAACCTGGAAGGCGGCACTACGAGATCAGCTGGGGA 213
Db 64 GGTGAGCGCAGGCGCACGTACCAACCTGGAAGGCGGCACTACGAGATCAGCTGGGGA 123
Qy 214 GATGCGGTTAACCTCGTCGGTGGAAAAGGGCTGGAACCCCGGCTGAAACGCAAGACCATC 273
Db 124 GATGCGGTTAACCTCGTCGGTGGAAAAGGGCTGGAACCCCGGCTGAAACGCAAGACCATC 183
Qy 274 CACTTGAGGGGTGTTTACCAAGCCAAACGGCAACAGCTACTTGCGGTCTACGGTTGACC 333
Db 184 CACTTGAGGGGTGTTTACCAAGCCAAACGGCAACAGCTACTTGCGGTCTACGGTTGACC 243
Qy 334 CGCAACCCGCTGTGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCTTCCTCC 393
Db 244 CGCAACCCGCTGTGAGTATTACATCGTCGAGAACTTTGGCACCTATGATCTTCCTCC 303
Qy 394 GGTGTAACCATCTAGGAATGTCGAGTGCAGCGGTAGCATCTATGACCTGGCAAGACC 453
Db 304 GGTGTAACCATCTAGGAATGTCGAGTGCAGCGGTAGCATCTATGACCTGGCAAGACC 363
Qy 454 ACTCGGCTCAACGCACCTAGCATCGACGGCAACCCAAACCTTCGACCAATATCTGTCGGTC 513
Db 364 ACTCGGCTCAACGCACCTAGCATCGACGGCAACCCAAACCTTCGACCAATATCTGTCGGTC 423
Qy 514 CGCCAGAGCAAGCGCACCGGCTACCGTCCAGACGGGCTGCCACTTCGACGCTGGGCT 573
Db 424 CGCCAGAGCAAGCGCACCGGCTACCGTCCAGACGGGCTGCCACTTCGACGCTGGGCT 483
Qy 574 CGGCTGTTTGAATGTCAACGGTGACCACTACTACAGATCGTTGCAACGAGGGCTTAC 633
Db 484 CGGCTGTTTGAATGTCAACGGTGACCACTACTACAGATCGTTGCAACGAGGGCTTAC 543
Qy 634 TTCAAGACGGGCTATGCTCGCATCACCGTTGCTGACGTGGGC 675
Db 544 TTCAAGACGGGCTATGCTCGCATCACCGTTGCTGACGTGGGC 585

RESULT 4

AA017927
ID AA017927 standard; DNA; 678 BP.
XX
XX
AC AA017927;
XX
DT 10-DEC-2001 (first entry)
XX
DE Thermomyces lanuginosus codon optimised xylanase gene.
XX
KW Xylanase; Pichia cell; heterologous nucleotide; codon optimisation; ds.
XX

OS Thermomyces lanuginosus.
OS Synthetic.
XX WO200166693-A1.
XX PD 13-SEP-2001.
XX PF 09-MAR-2001; 2001WO-DK000154.
XX PR 10-MAR-2000; 2000DK-00000392.
XX PR 15-MAR-2000; 2000DK-00000419.
XX PA (NOVO) NOVOZYMES AS.
XX PI Takagi S, Terui Y, Tsutsumi N, Taira R;
XX DR WPI; 2001-582273/65.
XX PT Novel Pichia cell useful for producing polypeptide of interest, comprises
PT a copy of heterologous nucleotide sequence encoding polypeptide of
PT interest.
XX PS Claim 14; Page 38-39; 61pp; English.
XX CC The invention relates to a Pichia cell comprising at least one copy of
CC heterologous nucleotide sequence encoding a polypeptide of interest,
CC where the codon usage of the sequence has been adjusted to match the
CC preferred codon usage of P. methanolica. The invention also relates to a
CC method for producing high yields of heterologous codon optimised
CC polypeptide in a Pichia cell. The Pichia cell is useful for producing a
CC polypeptide of interest, where the polypeptide is encoded by a nucleotide
CC sequence heterologous to P. methanolica. The present sequence is
CC Thermomyces lanuginosus codon optimised xylanase gene which is the
CC heterologous DNA used in the invention
XX SQ Sequence 678 BP; 180 A; 89 C; 152 G; 257 T; 0 U; 0 Other;

Query Match 55.1%; Score 371.6; DB 4; Length 678;
Best Local Similarity 72.0%; Pred. No. 2.2e-91;
Matches 485; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 1 ATGTCGGCTTTACCCCGTGGCCCTTACGCCGCACTGGGGCCCTGCTTC 60
DB 1 ATGTTGGTTTACTCCAGTTGCTTTAGCTGCTTAACTGCTGCTTTAGCTTTC 60

QY 61 CCGGCAAGGAATGCCAGGAGCTCGAAAAGCAGACACACCCCACTCGAGGGCTGG 120
DB 61 CCAGCAGGTAATGCTACTGAATTAGAAAAAGACAAACAACTCCAAATTCTGAAGTTGG 120

QY 121 CACGATGGTTATTAATCTATTCCTGGTGAGTGACGGGTGAGCGGACGACGATACCAAC 180
DB 121 CATGATGGTTATTAATCTATTCCTGGTGAGTGAGGTGCTCAAGCTACTTATTAATAAT 180

QY 181 CTGAAGCGGCACTACGAGATCAGCTGGGAGATGCGGTAACTCTGCTGGTGAAG 240
DB 181 TTGAAGGTGTAACCTATGAATTTCTGGGGTGATGCTGTAATTTAGTTGTTGTA 240

QY 241 GGCTGAACCCCGCCCTGAACGCAAGCCATCCACTTTGAGGGTTTACCAAGCAAC 300
DB 241 GGTGGAATCCAGGTTTAAATGCAAGAGCTATTCATTTGAAGGTGTTTATCAACCAAT 300

QY 301 GGCAACAGCTACTTGGCGGTCTACGGTTGGAACCCGCAACCCGCTGGTCAAGTATTAATC 360
DB 301 GGTAATTTCTATTAGCTGTTTATGTTGACTAGAAATCCATTAAGTTGAATATTATTAAT 360

QY 361 GTCGAGAACTTTGGCACTATGATCTTCTCCGGTGCTACCGATCTAGAACTGTGAG 420
DB 361 GTTGAATAATTTGGTAATCTATGATCCATCTTCTGGTGCTACTGATTAAGTACTGTTGAA 420

QY 421 TGGACGAGTAGAATCTATGACTCGCAAGCACTCGCGTCAACGCACTAGCATCGAC 480
DB 421 TGTGATGTTCTATTATAGATTAGTAATAACTACTAGAGTTAATGACCATCTATTGAT 480

QY 481 GGCACCCAACCTTGCACCAATACTGTGCGGTCCGCCAGAGACAAGCGCACCAAGCGGTACC 540
DB 481 GGTACTCAAACTTTGCATCAATATTGCTCTGTAGACAAAGATAAAGAACTTCTGTACT 540

QY 541 GTCCAGACGGGCTGCCACTTGCAGCGCCTGGGCTCGCGCTGTTGAATGTCAACGGTGAC 600
DB 541 GTTCAAACTGGTTGCAATTTGATGCTTGGGCTAGAGCTGTTGAATGTTAATGTGAT 600

QY 601 CACTACTACAGATCGTTGCAACGAGGGGCTACTGACGAGCGGCTATGCTGCATCACC 660
DB 601 CATTAATTATCAAAATGTTGCAACTGAAGGTTATTCTCTTCTGTTATGCTAGAATTAAT 660

QY 661 GTTCTGACGTGG 674
DB 661 GTTCTGATGTTGG 674

RESULT 5
AAQ74098
ID AAQ74098 standard; DNA; 1123 BP.
XX AC AAQ74098;
XX AC
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 14-NOV-1995 (first entry)
XX DE Humicola xylanase gene.
XX KW Xylanase; vector; PAXX40-1-1; Aspergillus foetidus; ss.
XX OS Humicola insolens.
XX FH Key location/Qualifiers
FH CDS 126..809
FT /*tag= a
XX FT
XX PN WO9515390-A1.
XX PD 08-JUN-1995.
XX PF 29-NOV-1994; 94WO-US013612.
XX PR 01-DEC-1993; 93US-00160591.
XX PA (NOVO) NOVO NORDISK BIOTECH INC.
XX PI Berka RM, Yoder W, Takagi S, Boominathan K;
XX DR WPI; 1995-215270/28.
XX DR P-PSDB; AAR75421.
XX PT Aspergillus foetidus cells expressing heterologous enzyme - partic.
PT fungal lipase or xylanase, provide high yields without significant prodn.
PT of protease or mycotoxin.
XX PS Disclosure; Page 35-36; 47pp; English.
XX XX A DNA fragment (AAQ74098) encoding H. insolens xylanase (AAR75421) was
XX isolated from pyres (DSM 6995) and inserted into pHD414 (contg. the TAKA
XX promoter and AMG terminator) to form PAXX40-1-1-1. This plasmid and
XX pial77 (impairing hygromycin B resistance) were used to transform
XX protoplasts of A. foetidus NO953. The xylanase yield was 0.12 g/l.
XX (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
XX correct OS field.)
XX SQ Sequence 1123 BP; 249 A; 342 C; 293 G; 239 T; 0 U; 0 Other;

Query Match 35.4%; Score 239; DB 2; Length 1123;
Best Local Similarity 64.4%; Pred. No. 4.7e-55;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

QY 57 CTTCCCGGCAAGGAATGCCAGGAGCTCGAAAAAGCAGACACAACCCCACTCGGAGGG 116

Db 197 CGTTCCTCGGACAACCTCGACGGCCCTTCAAGCTCGACAGGTGACCCCAACGGCCGAGGG 256
Qy 117 CTGGCAGCATGGTTATTACTATTCTCTGGTGAAGTGAACGGTGAAGCCGACAGGTACAC 176
Db 257 CTGGCAACAACGGCTACTTCTACTCTGGTGGTCCGACGGCCGAGGCCAGGTTCACTACAC 316
Qy 177 CAACCTGGAAGCGGGCACTTACGAGATCAGCTGGGAGATGGCGGTAACTCTGTCGGTGG 236
Db 317 CAACCTCGAGGGCAGCCGCTACAGGTCAAGTGGCGTAAACCCGCAACTTCTGTCGGTGG 376
Qy 237 AAAGGCTGGAACCCCGCCTGAACGCAAGACCATCCACTTTGAGGGTGTTCACGACC 296
Db 377 TAAGGTTGGAACCCGGG--AACCGCCGCAAGATCAACTACGGCGGCTACTTCAACCC 433
Qy 297 AAACGGCAACGCTACCTTGGGTCTACGGTTGGAACCCGCAACCCGCTGTCGAGTATTA 356
Db 434 CCAGGGCAACGGCTACCTGGCCGCTACGGCTGGAACCCGCAACCCGCTGTCGAGTACTA 493
Qy 357 CATCGTCGAGAACTTTGGCACCCTATGATCTTCTCCGGTGTACCGATCTAGGAATGT 416
Db 494 TGTCACTGAGTCTGTAACGGCAGCTCAATCCCGCAGCCAGGCTCAAGTCAAGGGCACTT 553
Qy 417 CGAGTCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACTAGCAT 476
Db 554 CTATACCGACGGCGATCAGTATGACATCTTTGTAGCAACCCGCTCAACCAAGCCCAAGCAT 613
Qy 477 CGACGGCAACCAACCTTGCACCAATCTGGTCCGTCGCGCAAGCAAGCGCAACGACGG 536
Db 614 CGACGGCAACCGGACGTTCCAGCAGTACTGTTATCCGCAAGAACAAAGCGTGTGGAAG 673
Qy 537 TACCGTCAGACGGGCTGCCACTTGCAGCGCTGGGCTCGCGCTGTTGAATGTCAACGG 596
Db 674 CTGGTCAACATGCAAGACCACTTCAACGGCGTGGCAGCAGCAGGAATGCCGCT---CGG 730
Qy 597 TGACCACTACTACAGATCGTTGCAACGGAGGGCTACTTCAAGCAGCGGCTATGCTGCAT 656
Db 731 CCAGCACTACTACAGGTCGTGCGCCACCGAGGGCTACCAAGCAGAGTGCGAGTCCGACAT 790
Qy 657 CACCGTT 663
Db 791 CTATGTT 797

RESULT 6
AAQ94952
ID AAQ94952 standard; DNA; 1123 BP.

XX AAQ94952;
AC
XX
DT 25-MAR-2003 (revised)
DT 02-DEC-1995 (first entry)
XX
DE Humicola insolens xylanase.
XX
KM Xylanase; DSM 6995; ss.
XX
OS Humicola insolens.
XX
FH Key Location/Qualifiers
FT CDS 126..806
FT /*tag= a
XX
PN WO9515391-A2.
XX
PD 08-JUN-1995.
XX
PF 29-NOV-1994; 94MO-US013613.
XX
PR 01-DEC-1993; 93US-00161675.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
XX

PI Berka RM, Yoder W, Takagi S, Boomnathan K;
XX
XX WPI; 1995-215271/28.
DR P-PSDB; AAR78231.
XX
PT Aspergillus japonicus-type cells expressing heterologous protein - esp.
PT fungal enzyme, provide high yields without significant prodn. of protease
PT or mycotoxin.
XX
PS Example; Page 39-40; 50pp; English.
XX
CC A strain of E. coli contg. the approx. 1,100 bp xylanase HindIII/ XbaI
CC cDNA fragment in pYES is deposited in DSM as DSM 6995. The xylanase cDNA
CC fragment is isolated from one of the clones. The sequence of the xylanase
CC gene and protein are given in AAQ94952 and AAR78231 and the gene is
CC deposited as DSM 6995. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1123 BP; 249 A; 342 C; 293 G; 239 T; 0 U; 0 Other;

Query Match 35.4%; Score 239; DB 2; Length 1123;
Best Local Similarity 64.4%; Pred.No. 4.7e-55;
Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;

Qy 57 CTTCCTCGGAGGGAATGCCACGAGCTCGAAAAGCGACAGCAACCCCACTCGGAGGG 116
Db 197 CGTTCCTCGGAGCAACTCGACGGCCCTTCAAGCTCGACAGGTGACCCCAACGGCGAGGG 256
Qy 117 CTGGCAGATGGTTATTACTATTCTCTGGTGAAGTGAACGGTGAAGCCGACAGGTACAC 176
Db 257 CTGGCAACAACGGCTACTTCTACTCTGGTGGTCCGACGGCCGAGGCCAGGTTCACTACAC 316
Qy 177 CAACCTGGAAGCGGGCACTTACGAGATCAGCTGGGAGATGGCGGTAACTCTGTCGGTGG 236
Db 317 CAACCTCGAGGGCAGCCGCTACAGGTCAAGTGGCGTAAACCCGCAACTTCTGTCGGTGG 376
Qy 237 AAAGGCTGGAACCCCGCCTGAACGCAAGACCATCCACTTTGAGGGTGTTCACGACC 296
Db 377 TAAGGTTGGAACCCGGG--AACCGCCGCAAGATCAACTACGGCGGCTACTTCAACCC 433
Qy 297 AAACGGCAACGCTACCTTGGGCTTACGGTTGACCCGCAACCCGCTGTCGAGTATTA 356
Db 434 CCAGGGCAACGGCTACCTGGCCGCTTACGGCTGGACCCGCAACCCGCTGTCGAGTACTA 493
Qy 357 CATCGTCGAGAACTTTGGCACCCTATGATCCTTCTCCGGTGTACCGATCTAGGAATGT 416
Db 494 TGTCACTGAGTCTGTAACGGCAGTCAATCCCGCAGCCAGCTCAAGTACAAAGGCACTT 553
Qy 417 CGAGTCGACGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACTAGCAT 476
Db 554 CTATACCGACGGCGATCAGTATGACATCTTTGTAGCAACCCGCTACAAACGCAAGCAT 613
Qy 477 CGACGGCAACCAACCTTGCACCAATCTGTCGCTCCGCCAGAGCAAGCCGCAAGCCG 536
Db 614 CGACGGCAACCGGACGTTCCAGCAGTACTGTTATCCGCAAGAACAAAGCGTGTGAGG 673
Qy 537 TACCGTCAGACGGGCTGCCACTTGCAGCGCTGGGCTCGCGCTGTTGAATGTCAACGG 596
Db 674 CTGGTCAACATGCAAGACCACTTCAACGGCGTGGCAGCAGCAGGAATGCCGCT---CGG 730
Qy 597 TGACCACTACTACAGATCGTTGCAACGGAGGGCTACTTCAAGCAGCGGCTATGCTGCAT 656
Db 731 CCAGCACTACTACAGGTCGTGCGCCACCGAGGGCTTACCAAGCAGAGTGCGAGTCCGACAT 790
Qy 657 CACCGTT 663
Db 791 CTATGTT 797

RESULT 7
ABQ80362
ID ABQ80362 standard; cDNA; 666 BP.
XX
XX ABQ80362;
AC

XX 11-AUG-2003 (first entry)
DT A. fumigatus AfXYL1 cDNA.
XX
KM Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
KM beta-galactosidase; invertase; lipase; alpha-amylase; lactase;
KM polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KM glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KM glyceride; starch; maltodextrin; oxidated phenolic compound;
KM polygalacturonic acid chain; xylan; xyloligomer; food; feed; beverage;
KM textile; tea liquor; cleaning ability; ss.
XX
OS Aspergillus fumigatus.
XX
FH Key Location/Qualifiers
FT CDS 1..666
FT /*tag= a
FT /product= "Xylanase 1"
XX
PN WO2003012071-A2.
XX
PD 13-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024842.
XX
PR 03-AUG-2001; 2001US-0309870P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Jiang B, Storms R, Roemer T, Bussey H;
XX
DR MPI; 2003-332729/31.
DR P-PSDB; ABB80185.
XX
PT Novel isolated Aspergillus fumigatus polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.
XX
PS Claim 2; Page 163-64; 169pp; English.
XX
CC The sequences given in ABQ80319-66 encode enzymatic proteins derived from
CC A. fumigatus. The resulting proteins display the catalytic activity of an
CC enzyme such as tannase, cellulase, glucose oxidase, glucoamylase,
CC phytase, beta-galactosidase, invertase, lipase, alpha-amylase, lactase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidase are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrose or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylases are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC lactase are useful for modulating the amount of oxidated phenolic
CC compounds in a composition. Compositions comprising polygalacturonases
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanases are useful for modulating the amount of xylan or xyloligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A.fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers

CC for attachment to a nucleic acid array for examination of expression
CC patterns, and to raise anti-protein antibodies. The polypeptide having
CC tannase activity increases the yield of tea liquor from tea leaves,
CC improves the colour, flavour and health benefits of tea products,
CC particularly an instant tea product. The polypeptide having cellulase
CC activity enhances cleaning ability of detergent compositions
XX
SQ Sequence 666 BP; 142 A; 199 C; 192 G; 133 T; 0 U; 0 Other;
Query Match 33.3%; Score 224.6; DB 10; Length 666;
Best Local Similarity 61.5%; Pred. No. 3.5e-51;
Matches 413; Conservative 0; Mismatches 249; Indels 9; Gaps 3;
QY 1 ATGTCGGCTTACCCCGCTTGCCCTTGCGGCTTAGCCGCACTGGGGCCCTGACCTTC 60
DB 1 ATGTCCTATTCTTCTCTCTGTTCTGCTGCTCCACCGTTGCTGGCTGCTAGCTACA 60
QY 61 CCGG---CAGGAATGCCAGGAGCTCGAAAAGCGACAGACAACCCCACTCGAGGGC 117
DB 61 CCGGCTCGAGCAATACGTTGAGCTAGCCAAAGCGGAGCTCACCAAGCTTCGAGACTGGC 120
QY 118 TGGCAGATGTTATTACTATTCTCTGAGTGAAGTGAAGCGCAGGCGCACTACACC 177
DB 121 ACGAATAACGGCTACTACTACTCTTCTTGACCGACGGCGGCGGCAAGTGAACACC 180
QY 178 AACCTGAAGCGCGGACCTACGAGATCAGCTGGGAGATGGCGGTAACTCGTGGTGA 237
DB 181 AACGGCAATGGCGGCGCAATCAAGTCACTGCACTGAACAACCTGGCACTTGTGCTGG 240
QY 238 AAGGGCTGGAACCCCGGCTGAAACGCAAGAGCCATCCACTTTGAGGCTTTACCAAGCCA 297
DB 241 AAGGGCTGGAACCCCGGCC--AGCGAAGAAAGCGGTCACTTACAGCGGCTCCTGCGAGACC 297
QY 298 AACGGCAAGCTTACCTTGGCTCTACGCTTGAAGCCGCAACCCGCTGCTGAGTATTAC 357
DB 298 AAGCAAGAGCTTACCTTGGCTCTGAGTGAAGCGGCTGAGCAAGTCCGCTGCTGAAATTCTAC 357
QY 358 ATGTCGAGAATTGGCACCTATGATCTTCTCCGCTGCTACCGATCTAGGAATGTTC 417
DB 358 ATGTCGAGAATTACGCTCTTATGACCCCTCCAGGAGACCAACCATCTCGGACCCGTC 417
QY 418 GAGTGCAGCGGTAGCATCTATGCACTCGCAAGACCACTCGCTCAACGCACTAGCATC 477
DB 418 GAGAGCGACGGGGCCACGTACAACCTTACAAGAAGAGCGGAGCAATGCGCGGTCCATC 477
QY 478 GACGGCAACCAAACTTCGACCAATATCTGTCGCTCCGCCAGAGACAAGCGCACGCGGT 537
DB 478 CAGGGCAGCGCTTACTTTGACCAATCTGTCGCTTCCGACTTCGCACCCGCGAGAGTGA 537
QY 538 ACCGTCAGACGGGCTGCCACTTTCAGCGCTGCGCTGCTGCTTGAATGTCAACGCT 597
DB 538 ACTGTGACGACGAAGAACCACTTTGATGCGTGAAGAAATGCGGGTCTGCAATT---GGGG 594
QY 598 GACCACTACTACAGATCGTTGCAACGAGGGCTACTTCAGCAGCGGCTATGCTGCATC 657
DB 595 AACTTTGACTATATGATTTGTGCGACGAGGGGTACCAAGCAGCAGCGGCTTGTACTATC 654
QY 658 ACCGTTGCTGA 668
DB 655 ACTGTTCTTA 665
RESULT 8
ABQ80364
ID ABQ80364 standard; cDNA; 705 BP.
XX
AC ABQ80364;
XX
DT 11-AUG-2003 (first entry)
XX
DE A. fumigatus AfXYL2 cDNA.
XX
KW Gene; enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;

KM beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KM polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KM glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KM glyceride; starch; maltodextrin; oxidated phenolic compound;
KM polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
KM textile; tea liquor; cleaning ability; ss.
XX
OS Aspergillus fumigatus.
XX
FH Key Location/Qualifiers
FT CDS 1..705 /*tag= a
PT /product= "Xylanase 2"
XX
PN WO2003012071-A2.
XX
PD 13-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024842.
XX
PR 03-AUG-2001; 2001US-0309870P.
XX
PA (BLIT-) ELITRA PHARM INC.
XX
PI Jiang B, Storms R, Roemer T, Bussey H;
XX
DR WPI; 2003-332729/31.
DR P-PSDB; ABB80186.
XX
PT Novel isolated Aspergillus fumigatus polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.
XX
PS Claim 2; Page 165-66; 169pp; English.

XX The sequences given in ABQ80319-66 encode enzymatic proteins derived from
CC A. fumigatus. The resulting proteins display the catalytic activity of an
CC enzyme such as tannase, cellulase, glucose oxidase, glucoamylase,
CC phytase, beta-galactosidase, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidase are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrase or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylases are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC laccase are useful for modulating the amount of oxidated phenolic
CC compounds in a composition. Compositions comprising polygalacturonases
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A.fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers
CC for attachment to a nucleic acid array for examination of expression
CC patterns, and to raise anti-protein antibodies. The polypeptide having
CC tannase activity increases the yield of tea liquor from tea leaves,
CC improves the colour, flavour and health benefits of tea products,
CC particularly an instant tea product. The polypeptide having cellulase
CC activity enhances cleaning ability of detergent compositions

XX	Sequence	705 BP; 151 A; 227 C; 183 G; 144 T; 0 U; 0 Other;
SQ	Query Match	32.8%; Score 221.6; DB 10; Length 705;
	Best Local Similarity	60.5%; Pred. No. 2.4e-50;
	Matches	409; Conservative 0; Mismatches 249; Indels 18; Gaps 2;
QY	2	TGCTCGCTTTACCCCGTTGCCCTTGCGGCTTAGCCGCACTGGGGCCCTGCGCTTCC 61
DB	26	TGGCGTCTCCGCCATTGAGCTCTGGCTGCCCGCTCGAACCCGAGACCACTCTGTTCA 85
QY	62	CGCAGGGAATGCCACGAGCTCGAAAAGCAGACAAACCCCACTCGAGGGCTGGC 121
DB	86	ATGAGACTGCTCTTCATGAGTTGCTGAGCGCGCCGACCCCAAGCTCCACCGGCTGGA 145
QY	122	ACGATGGTTATTACTATTCTGTTGAGTGAACGTTGAGCGGACGACGCACTACCAACC 181
DB	146	ACAACGCTACTACTACTCTCTTGACTGATGGCGGCGGACGTACCTACCAATG 205
QY	182	TGGAAGCGGCACCTACGAGATCAAGTGGGAGATGCGGTAACCTCGTGGGAAAGG 241
DB	206	GCGCCGCTGGCTCTGACTCCGTCACCTGAGGAACGTGGGCACTTGTGGTGAAGG 265
QY	242	GCTGGAACCC-----CGGCTGAAGCGCAAGACCATTCACCTTTGAGGGTG 286
DB	266	GCTGAACCTTGGAAGCGCTAGGTACCGAGCTTTAAGTAGAACCATCACTACGGAAGCA 325
QY	287	TTTACCAAGCCAAACGGCAACAGCTACCTTGCGGTCTACGGTTGACCCGCAACCGCTGG 346
DB	326	GCTTCAACCCACGCGCAATGGCTTACCTGCTGTCTACGGCTGACCAACCAACCCCTTGA 385
QY	347	TCGATATTATCATCGTCAAGAACTTGGACCACTATGATCCTTCCCGTGTACCGATC 406
DB	386	TTGAGTACTACGTGTGTGATGCTATGTATACATACAAACCCGCGAGCGGCTACCTTCA 445
QY	407	TAGAACTGTCGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACCACTCGGTCACG 466
DB	446	GGGGCACTGTCAACACCGACGCTGGCACTTACACATCTACACGCGCGTCTGCAATG 505
QY	467	CACCTAGCATCGACGGGCACCAAACTTGCACCAATACTGTGGTCCGCCAGACAAGC 526
DB	506	CTCCCTCATCGAAGGACCAAGACCTTCAACCACTGCTGTGTGCGCACTTCCAAGC 565
QY	527	GCACCAAGGTACCGTCCAGACGGGCTGCCACTTGACGCGCTGGCTGCTTGA 586
DB	566	GTACCGCGGCACTGTACCACTGCGCAACCACTTCAACGCTGAGACGACTGGGCATGA 625
QY	587	ATGTCAACGGTGACCACTACTACAGATGTTGCAACGAGGGCTACTTCAGACGGGCT 646
DB	626	A---CTGGGAACCTACAACCTACAGATTGTGCGCACTGAGGGTTACGAGAGCGGAT 682
QY	647	ATGCTCGCATCACCGT 662
DB	683	CTGCTTCATCACTGT 698
RESULT 9		
AAZ28864	standard; DNA; 1195 BP.	
ID	AAZ28864	
XX	AAZ28864;	
AC	AAZ28864;	
XX	27-AUG-2003 (revised)	
DT	01-FEB-2000 (first entry)	
XX	Streptomyces olivaceoviridis xylanase (XynG) gene.	
DE	Xylanase; plasmid; expression; E.coli; xylo-oligosaccharide; xylan;	
KW	pulp-bleaching; ds.	
XX	Streptomyces olivaceoviridis.	
OS	Location/Qualifiers	
XX	Key	

FT CDS 298..993
FT /*tag= a
FT /gene= "XynG"
FT /product= "xylanase"
FT sig_peptide 298..417
FT /*tag= b
FT mat_peptide 418..990
FT /*tag= c
FT /note= "mature peptide is claimed"

XX JPI1266873-A.
XX
XX 05-OCT-1999.
XX
XX 20-MAR-1998; 98JP-00090702.
XX
XX 20-MAR-1998; 98JP-00090702.
XX
XX (NORO) NORINSUISANSO SHOKUHN SOGO.
XX (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
XX
XX WPI; 1999-613780/53.
XX P-PSDB; AAY44183.
XX
XX A xylanase gene, contiguous with a vector and a transformant - used for
XX pulp-bleaching.
XX
XX Claim 1; Page 5-6; 10pp; Japanese.
XX
XX This sequence corresponds to a degenerate sequence encoding a xylanase
XX precursor from Streptomyces olivaceoviridis. The sequence can be inserted
XX into the plasmid pQE60 to generate plasmid FERM P-16713 for expression in
XX e.g. E.coli. The xylanase is useful for the preparation of xylol-
XX oligosaccharide from xylan and for pulp-bleaching. (Updated on 27-AUG-
XX 2003 to correct OS field.)
XX
XX Sequence 1195 BP; 230 A; 457 C; 333 G; 174 T; 0 U; 1 Other;

Query Match 30.4%; Score 205; DB 2; Length 1195;
Best Local Similarity 62.9%; Pred. No. 9.5e-46;
Matches 354; Conservative 0; Mismatches 200; Indels 9; Gaps 2;

QY 100 ACCCCCACTCGAGGGCTGGACGATGTTATTACTATCTCTGAGTGAAGTGA 159
DB 430 ACCACCAACGAGACCGGACCAACGAGGTTCTACTCTCTTGACCGGCGGC 489
QY 160 GCGAGGCGACGATACCAACCTGAGAGCGGACCTACGAGATCAGCTGGGAGATGCG 219
DB 490 GGTTCGCTCGATGACCTGAACTCCGGCGGCACTACGACACTCGTGACGAACTGC 549
QY 220 GGTAACTCGTCGGTGGAAAGGCTGAAACCCCGGCTGAACGCAAGACCATCTTT 279
DB 550 GGGAACTTCGTCGCCGCGCAAGGCTGAGCAACGCGGACGC---AGGAACGTGCACTAC 606
QY 280 GAGGCTGTTACGACCCAAACGCGCAACGCTACCTTCCGCTTACGCTTGACCCCGCAC 339
DB 607 TCGGGCAGCTTCTACCCGTCGGCAACGCGCTACCTGCGCTGACGGGTGACCTCGAAC 666
QY 340 CCGCTGTGAGTATACATCGTCGAGAACTTTGGACCTATGATCTTCTCCGCTGCT 399
DB 667 CCGCTGTGAGTATACATCGTCGAGAACTTTGGGCAACTACCGGCGCCACC-----GGA 720
QY 400 ACCGATTAGAAGTGTGAGTGCAGCGGTAGCATCTATGACTCGGCAAGACCATCTGC 459
DB 721 ACGTACAAGGCGACGCTACACGACGCGGCGACGTACGACGCTACACGACGACGCGG 780
QY 460 GTCAACGACCTAGCATGACGCGCAACCAACTTGCACCAATGCTGCTCGTCCGCGAG 519
DB 781 TACAACGCCCCCTCCGTGGAAGGCAACCAACCTTCAACCACTGAGAGCGTCCGCGAG 840
QY 520 GACAAGCGCAACGAGGTAACGCTCCAGACGCGGCTGCCACTTCCAGCGCTGGGCTCGCGCT 579
DB 841 TCCAAGCGGACCGGCGGCAACCATCAACCGGCAACCACTTCCAGCGCTGGGCGCGCTAC 900

QY 580 GGTGATGTCAACCGGTGACCACTACTACCATGCTTGCAACGAGGCTACTTCAGC 639
DB 901 GGCATGCAACTGGGACGCTTACGCTACTACATGATCATGCGCACCGGCTTACAGAGC 960
QY 640 AGCGGCTATGCTCGCATCACCGT 662
DB 961 AGCGGCTCTCCAACCTCACGGT 983

RESULT 10
AAZ28865
ID AAZ28865 standard; DNA; 1195 BP.
XX
XX AAZ28865;
XX AC
XX 27-AUG-2003 (revised)
DT 01-FEB-2000 (first entry)
XX
XX Streptomyces olivaceoviridis xylanase (XynG) gene.
XX DE
XX Xylanase; plasmid; expression; E.coli; xylol-oligosaccharide; xylan;
XX KM pulp-bleaching; ds.
XX OS Streptomyces olivaceoviridis.
XX
XX Key Location/Qualifiers
FH 298..993
FT CDS
FT /*tag= a
FT /gene= "XynG"
FT /product= "xylanase"
FT sig_peptide 298..417
FT /*tag= b
FT mat_peptide 418..990
FT /*tag= c
FT /note= "mature peptide is claimed"

XX JPI1266873-A.
XX
XX 05-OCT-1999.
XX
XX 20-MAR-1998; 98JP-00090702.
XX
XX 20-MAR-1998; 98JP-00090702.
XX
XX (NORO) NORINSUISANSO SHOKUHN SOGO.
XX (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
XX
XX WPI; 1999-613780/53.
XX P-PSDB; AAY44183.
XX
XX A xylanase gene, contiguous with a vector and a transformant - used for
XX pulp-bleaching.
XX
XX Claim 4; Page 6-7; 10pp; Japanese.
XX
XX This sequence corresponds to the complete sequence encoding a xylanase
XX precursor from Streptomyces olivaceoviridis. The sequence can be inserted
XX into the plasmid pQE60 to generate plasmid FERM P-16713 for expression in
XX e.g. E.coli. The xylanase is useful for the preparation of xylol-
XX oligosaccharide from xylan and for pulp-bleaching. (Updated on 27-AUG-
XX 2003 to correct OS field.)
XX
XX Sequence 1195 BP; 230 A; 457 C; 333 G; 175 T; 0 U; 0 Other;

Query Match 30.4%; Score 205; DB 2; Length 1195;
Best Local Similarity 62.9%; Pred. No. 9.5e-46;
Matches 354; Conservative 0; Mismatches 200; Indels 9; Gaps 2;

QY 100 ACCCCCACTCGAGGGCTGGACGATGTTATTACTATCTCTGAGTGAAGTGA 159
DB 430 ACCACCAACGAGACCGGACCAACGAGGTTCTACTCTCTTGACCGGCGGC 489

QY 160 GCGCAGGCCACGTACACCAACCTGGAAGCGGCACCTACGATCAGCTGGGAGATGGC 219
DB 490 GGTTCGGTCTCGATGATACCTTGAACTCCGCGGCMACTACGACCTCGTGAGCACTGC 549
QY 220 GGTAACTCGTCGCTGGAAGGGCTGGAACCCCGGCTGAACGCAAGAGCCATCCATTY 279
DB 550 GGAACTTCGTGCGCGGCAAGGGCTGGAACGCAAGCGGAGCGC--AGAACTGCACTAC 606
QY 280 GAGGTGTTTACAGCCAAACGGCAAGCTACCTTGCGGTCTACGGTTGACCGCAAC 339
DB 607 TCGGGCAGCTTCTACCGCTCCGGCAAGGCTACCTGGCGGTGACGGGTGACCTCGAAC 666
QY 340 CCGCTGTCGAGTATTACATCGTCGAGAATTGGCACTTATGATCCTTCCGCGTCT 399
DB 667 CCGCTCGTCGAGTACTACATCGTCGACAACTGGGGCACTACCGGCCACC-----GGA 720
QY 400 ACCGATCTAGGAAGTGTGAGTGGCAGCGGTAGCATCTGACTCGGCAAGACCACTCGC 459
DB 721 ACGTACAAAGGGCAGGTCAACGAGCAGCGGCGCACTGACGCTTACCAAGACGCGG 780
QY 460 GTCAACGCACTAGCATGACGCGCAACCAACCTTGAACCAATCTGTCGTCGCGCAG 519
DB 781 TACAACGCCCCCTCGTGAAAGGCAACAAGACTTCAACAGTACTGAGCGTCCGGCAG 840
QY 520 GACAAGCGCACGAGCGTACCGTCCAGACGGGCTGCACTGACGCGCTGGCTCGCGCT 579
DB 841 TCCAAGCGGACCGGCGGCAACCAACCGGCAACCACTTGAACGCTGGGCGCGCTAC 900
QY 580 GGTTGAATGTCAACGGTGACCACTACTACCAAGTCGTTGCAACGGAAGGCTACTTCAAC 639
DB 901 GGCATGCAACTGGGAGCTTCACTACTATGATGATGAGCCACCGAGGGCTACGAGAGC 960
QY 640 AGCGGCTATGCTCGCATCACCGT 662
DB 961 AGCGGCTCCTCCAACCTCACCGT 983

RESULT 11

ADK70798
ID ADK70798 standard; DNA; 576 BP.
XX
AC ADK70798;
XX
DT 06-MAY-2004 (first entry)
XX
DE Streptomyces olivaceoviridis xylan enzyme encoding DNA SEQ ID NO:1.
XX
KW Streptomyces olivaceoviridis; xylan enzyme; enzyme; feed additive;
KW animal feed; gene; ds.
XX
OS Streptomyces olivaceoviridis.
XX
FH Key Location/Qualifiers
FT CDS 1..576
FT /*tag= a
FT /product= "xylan enzyme"

PN CN1405304-A.
XX
PD 26-MAR-2003.
XX
PF 14-SEP-2001; 2001CN-00142163.
XX
PR 14-SEP-2001; 2001CN-00142163.
XX
PA (FODD-) FODDER INST CHINBSE ACAD AGRIC SCI.
XX
PI Yao B, Fan Y, Zhang H;
XX
DR WPI; 2003-514374/49.
DR P-PSDB; ADK70799.
XX
PT Heat-resisting, antiprotease acidic-neutral xylanase and its gene.

XX
PS Claim 3; SEQ ID NO 1; 21pp; Chinese.
XX
CC The present sequence encodes the Streptomyces olivaceoviridis xylan
CC enzyme. The xylan enzyme has good heat stability, high activity under
CC acidic and neutral pH. The xylan enzyme can be used as a feed additive
CC and can be widely used in animal feed.
XX

XX Sequence 576 BP; 125 A; 207 C; 165 G; 79 T; 0 U; 0 Other;

Query Match 30.1%; Score 203.4; DB 10; Length 576;
Best Local Similarity 62.7%; Pred. No. 2.1e-45;
Matches 353; Conservative 0; Mismatches 201; Indels 9; Gaps 2;

QY 100 ACCCCCACTCGAGGGCTGGCAGATGTTATTACTATTCTTGTGAGTGAACGCTGA 159
DB 13 ACCACCAACGAGACCGGCAACCAACAGGTTCTACTCTTCTGACCGAGCGGCG 72
QY 160 GCGCAGGCCACGTACACCAACCTGGAAGCGGCACTACGAGATCAGCTGGGAGATGGC 219
DB 73 GGTTCGGTCTCGATGACCTGAACTCCGGCGGCACTACAGACACCTCGTGAGAACTGC 132
QY 220 GGTAACTCGTCGCTGGAAGGGCTGGAACCCCGGCTGAACGCAAGAGCCATCCATTY 279
DB 133 GGAACTTCGCGCGCGGCAAGGGCTGAGCAACGCGGAGACG--AGAACTGCACTAC 189
QY 280 GAGGTGTTTACAGCCAAACGGCAACAGTACTTGGCTTACGGTTGACCCGCAAC 339
DB 190 TCGGGCAGCTTCTACCGCTCCGGCAACGAGCTTACCTGCGGTGACCTCGAAC 249
QY 340 CCGCTGTCGAGTATTACATCGTCGAGAATTGGCACTTATGATCCTTCCGCGTCT 399
DB 250 CCGCTCGTCGAGTACTACTATCGTCGACCAACTGGGCAACTACCGGCCACC-----GGA 303
QY 400 ACCGATCTAGGAAGTGTGAGTGGCAGCGGTAGCATCTATGACTCGGCAAGACCACTCGC 459
DB 304 ACGTACAAAGGGCAGGTCAACGAGCGGCGGCAAGTACGAGCTTACCAAGACGCGG 363
QY 460 GTCAACGCACTAGCATGACGCGCACCCAAACCTTGAACCAATCTGTCGTCGCGCAG 519
DB 364 TACAACGCCCCCTCGTGAAAGGCAACCAAGACTTCAACAGTACTGAGCGTCCGGCAG 423
QY 520 GACAAGCGCACGAGCGTACCGTCCAGACGGGCTGCCACTTCGACGCGCTGGCTCGCGCT 579
DB 424 TCCAAGCGGACCGGCGGCAACCAACCGGCAACCACTTGAACGCTGGGCGCGCTAC 483
QY 580 GGTTGAATGTCAACGGTGACCACTACTACCAAGTCGTTGCAACGGAAGGCTACTTCAAC 639
DB 484 GGCATGCAACTGGGAGCTTCACTACTATGATGATGAGCCACCGAGGGCTACGAGAGC 543
QY 640 AGCGGCTATGCTCGCATCACCGT 662
DB 544 AGCGGCTCCTCCAACATCACCGT 566

RESULT 12

ADL23221
ID ADL23221 standard; cDNA; 696 BP.
XX
AC ADL23221;
XX
DT 20-MAY-2004 (first entry)
XX
DE A. niger (hemi)cellulase NMB021 coding sequence.
XX
KW ss; gene; A. niger; (hemi)cellulase; filamentous fungus; dough; bread;
KW biscuit; elasticity; stability; stickiness; extensibility; machinability;
KW crumb structure; softness; flavour.
XX
OS Aspergillus niger.

XX
FH Key Location/Qualifiers
FT CDS 1..696

FT FT /*tag= a
FT /product= "(Hemi) cellulase NBE021."
PN WO2004018662-A2.
XX 04-MAR-2004.
PD
XX
PF 15-AUG-2003; 2003WO-EP009147.
XX
PR 19-AUG-2002; 2002EP-00102152.
PR 19-AUG-2002; 2002EP-00102160.
PR 19-AUG-2002; 2002EP-00102161.
PR 30-AUG-2002; 2002EP-00102245.
PR 03-SEP-2002; 2002EP-00102279.
PR 03-SEP-2002; 2002EP-00102298.
XX
PA (STAM) DSM IP ASSETS BV.
XX
PI Folkers U, Fritz A, Gerhard B, Klugbauer S, Spreafico F,
PI Wagner C, Boer DL, Meima RB;
XX
DR WPI; 2004-226842/21.
DR P-PSDB; ADL23222.
XX
PT Novel hemicellulase NBE012, NBE021, NBE022, NBE064, NBE075 or NBE092
PT derived from Aspergillus niger, useful for preparing dough and/or baked
PT product.
XX
XX Disclosure; SEQ ID NO 5; 92pp; English.
PS
XX
XX This sequence encodes an A. niger (hemi)cellulase NBE021. The
CC (hemi)cellulase coding sequences of the invention are derived from a
CC filamentous fungus, preferably Aspergillus niger. The (hemi)cellulase is
CC useful in producing dough, which is useful for preparing a baked product
CC such as bread, biscuits from the dough. Fragments of the (hemi)cellulase
CC DNA are useful as probes and primers for detecting the expression of
CC (hemi)cellulose mRNA in a biological sample such as a tissue. They are
CC also useful as query sequences to identified other family members or
CC related sequences. Anti-(hemi)cellulase antibodies are useful for
CC qualitative or quantitative determination of a polypeptide in a
CC biological sample. These antibodies are also useful in diagnosing
CC organism is infected with Aspergillus. The dough prepared by using the
CC inventive (hemi)cellulase has increased strength, elasticity, stability,
CC reduced stickiness, improved extensibility and machinability. The
CC prepared baked product has improved crumb structure, softness and
CC flavour. The (hemi)cellulase has higher specificity towards the
CC substrate, is less antigenic and produces less undesirable side
CC activities.
CC
SQ Sequence 696 BP; 143 A; 221 C; 192 G; 140 T; 0 U; 0 Other;

Query Match 30.1%; Score 203; DB 12; Length 696;
Best Local Similarity 59.7%; Pred. No. 2.9e-45;
Matches 398; Conservative 0; Mismatches 260; Indels 9; Gaps 3;

QY 1 ATGATCGGCTTACCCCGTTGCCCTTGCGGCTTAGCCGCGACTGGGCGCTGCTTC 60
|||
DB 1 ATGATCGGCTTACCTCTCTCTCTCGCTCTTTCGCTGCTCGAGCGCGCTGCTTC 60
QY 61 CCGGCAAGGAATGCC--ACGGAAGTCGAAAAGCGACAGACAACCCCACTCGAGGGC 117
|||
DB 61 CCGAATGGCAAGGCCCTGCTGACATGCGCAAGCGAGTCTTAATTCTTCCGCGAAGGC 120
QY 118 TGGACGATGGTTATTACTATTCTGTGTGAGTGACGGTGAGCGGCGACGCTGAGCAACC 177
|||
DB 121 GAGAGCAACGGCTACTTCTACTCTTCTGACCAACGGTGAGGCGGACGTGACTTACACC 180
QY 178 AACCTGAAGCGCGCACCTACGATGACGTGGGAGATGGCGGTAACCTGTCGTGGA 237
|||
DB 181 AACGGCAGCGCTGTGATATACACCGTTGAGTGACCGACTGTGTGACTTTGTGCGCGC 240
QY 238 AAGGCTGAACCCCGGCTGAACGCAAGACCATTCATTGAGGGTGTATTACAGCCA 297
|||

DB 241 AAGGTTGGAACCCGGG--AGTCTCAGGCGGTTACCTACAGCGGATCATGGAAACC 297
QY 298 AACGGCAACAGCTACTTGGCGGTCTACCGGTTGGAACCCGCAACCCGCTGGTCAATATAC 357
|||
DB 298 GACGCCAAGCGCTACTGTCTCGTCTACCGTTGGAACCACTCCCGCTTGGTGAATTTAT 357
QY 358 ATCGTGAGAACTTTGGCACTATGATCTTCTCCGCTGCTACCGATCTAGGAATGTC 417
|||
DB 358 ATCGTGACAAAGTACGGTGAATTACGACCCCTCTCTGCGCTGACCGAGCTCGGCAACGTC 417
QY 418 GATGCGACGCTAGATCTATGACTCGGCAAGCACTCGGCTCAACGCACTAGCATC 477
|||
DB 418 GACAGCGACGACGGAACCTTCAAGATCTTACCAAGCAACCGTGAGAGCGCGACTCGATC 477
QY 478 GACGGCAACCAACCTTCGACCAATACTGGTCCGCGCAGACAAAGCGCAACGCGGT 537
|||
DB 478 GAAGGCACTGCCACCTTCAAGCACTACTGGTCCGTCGCACTGAGGGCGGCTATGGTGA 537
QY 538 ACCGTCCAGACGGGCTGCCACTTTCGACGCGCTCGGCTCGGCTTGAATGTCACGCT 597
|||
DB 538 ACCGTCAACACGACGAGAACCACTTCGATGCTGGGAGAACTTGCTGAGACT--GGGT 594
QY 598 GACCACTACTACAGATGTTGCCAACGAGGGCTACTTACGACAGCGGCTATGCTCGCATC 657
|||
DB 595 ACCTTCAACTACATGATGTTGCCACCGAGGATACGAGAGCAGCGGGTCTGCCACCATC 654
QY 658 ACCGTTG 664
|||
DB 655 ACCGTTG 661

RESULT 13
ADJ35015
ID ADJ35015 standard; DNA, 1008 BP.
XX
AC ADJ35015;
XX
DT 22-APR-2004 (first entry)
XX
DE DNA encoding xylanase from an environmental sample seq id 231.
XX
KW antibacterial; fungicide; thermostable xylanase activity;
KW dough conditioning; beverage production; nutritional supplement;
KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
KW fungal infection; coccidiosis; gene; ds.
XX
OS Unidentified.
XX
PN WO2003106654-A2.
XX
PD 24-DEC-2003.
XX
PF 16-JUN-2003; 2003WO-US019153.
XX
PR 14-JUN-2002; 2002US-0389299P.
XX
PA (DIVE-) DIVERSA CORP.
PI Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
PI Esteghlalian A;
XX
DR WPI; 2004-099016/10.
DR P-PSDB; ADJ35016.
XX
PT Novel xylanase recombinant polypeptide useful for improving textile
PT texture, treating paper, eliminating microorganisms.
XX
PS Claim 1; SEQ ID NO 231; 570pp; English.
XX
CC The invention describes an isolated or recombinant polypeptide (I),
CC having 50% or more identity to 190 300-1200 residue amino acid sequences
CC (S1), given in the specification, over a region of 100 or more residues
CC and the polypeptide as thermostable xylanase activity. (I) is useful for:

CC dough conditioning; beverage production; as a nutritional supplement in
CC animal feed; reducing lignin in a wood or a wood product; and for
CC eliminating and protecting animals from a microorganism comprising xylan.
CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
CC acid encoding a polypeptide having a xylanase activity which involves
CC amplification of a template nucleic acid with a primer pair capable of
CC amplifying (II) or its subsequence. (I) is useful for treating and
CC preventing bacterial infection and fungal infection e.g. candidiasis.
CC This sequence encodes xylanase protein isolated from an environmental
CC sample.

XX
SQ Sequence 1008 BP; 192 A; 362 C; 331 G; 123 T; 0 U; 0 Other;

Query Match 29.8%; Score 201.2; DB 12; Length 1008;
Best Local Similarity 59.9%; Pred. No. 9.9e-45;
Matches 376; Conservative 0; Mismatches 243; Indels 9; Gaps 2;

OY 37 GCCGCGACTGGGGCCCTGGCCCTCCCGGACAGGAATGCCACGAGCTCGAAAGCGACAG 96
DB 73 GTCGCGCTGGCGGGCGCTCGCCCGCTGATGCTGCGGGGACCGCCACGCGACCGGTC 132
OY 97 ACAACCCCACTCGGAGGCGTCGACGATGTTATTACTATTCTCTGTGAGTGAACGGT 156
DB 133 GTCACGACCAACCAAGAGGGGACCAACAACGCGCTACTACTACTCTGTTGAGCGACAGC 192
OY 157 GGAGCGGAGGCCACGTACACCAACTGGAAAGCGGCGACCTACGAGATCAGTGGGGAGAT 216
DB 193 CAGGCAACCTCTCATGAAATGAGGCTCCGGGCTCAGTACAGACACCTCGTGGCGCAAC 252
OY 217 GCGGTAACTCTGTCGGTGAAGAGGCTGGAACCCCGGCTGAACGCAAGACCATCCAC 276
DB 253 ACCGGCACTTCGTGCGGGCAAGGGCTGGGCAACGGGGCGCGCGGA---CCGTGACAG 309
OY 277 TTGAGGGTGTTTACACGCAACGGCAACAGACTACTTGGCGTCTACGGTTGACCCGC 336
DB 310 TACTCGGCGAGCTTCAACCCCTCGGCAACGCGTACTGCGGCTCTACGGATGACGTCG 369
OY 337 AACCCGCTGTCGAGTATTACATCTGCGAAGACTTGGCACTTATGATCTTCTCCGGT 396
DB 370 AACCCGCTGTCGAGTACTATCTGTCGACAACTGGGGCACTTACCGGCCACGCGGCG-- 427
OY 397 GCTACCGATCTAGGAATGTCGAGTCGACGGTAGCATCTATGACTCGGCAAGACCACT 456
DB 428 ---AGTCAAGGGCACCGTCAACGACGACGGGCACTTACGACATCTACAGACAGACC 483
OY 457 CGGTCACAGCACCTAGCATCGACGGCAACCAACCTTGCACCAATACTGTCGGTCCGC 516
DB 484 CGGTCACAAGCCCTCCGTGAGGGGCAACCGCACTTGCACCACTGAGCGTCCGC 543
OY 517 CAGGACAAGCGCACCGGTAACCGTCCAGACGGGCTGCCACTTGACGCGCTGGGCTCGC 576
DB 544 CAGGCGAAGCGGACCGGCGGACCATCAGACCGGCAACCACTTGACGCGCTGGGCGCG 603
OY 577 GCTGTTTGAATGTCAACGGTGAACCACTACTACCAATCTGTTGCAACGGAGGCTACTTC 636
DB 604 GCGGGGATGCGGCTCGGCAACTTACGCTACTACATGATGCGCACCGAGGCTACCAAG 663
OY 637 AGCAGCGGCTATGCTCGCATCACCGTTG 664
DB 664 AGCAGCGGCGAGCTCCAGCATCAACGTG 691

RESULT 14

AAT63044
ID AAT63044 standard; cDNA; 851 BP.
XX
AC AAT63044;
XX
DT 17-OCT-2003 (revised)
DT 22-JUL-1997 (first entry)
XX
DE Aspergillus niger xylanase cDNA.
XX

KW Endoxylanase; xylanase; protein detection; enzyme detection;
KW library screening; ds.
XX
OS Aspergillus niger; strain N400 (CBS120.49).

FH Key Location/Qualifiers
FT CDS 30..707
FT /*tag= a

PN WO9713853-A2.

PD 17-APR-1997.

PF 14-OCT-1996; 96WO-EP004510.

PR 13-OCT-1995; 95EP-00202777.

PA (KONN) GIST-BROCADES BV.

PI Van Den Broeck HC, De Graaff LH, Visser J, Van Ooyen AJJ;

DR WPI; 1997-235889/21.
DR P-PSDB; AAW14597.

PT Identifying DNA fragments encoding proteins, e.g. for new enzyme
PT discovery - by direct screening of a cDNA library in bacteria transformed
PT with DNA from eukaryotic organism producing the protein.

PS Claim 6; Page 19-20; 30pp; English.

XX
CC A cDNA clone (AAT63044), deposited as CBS 590.95, codes for a xylanase
CC (AAW14597) of Aspergillus niger N400 (CBS120.49). It was isolated using a
CC method for identifying a DNA fragment encoding a protein of interest. The
CC method involves the direct screening of a cDNA library prepd. in bacteria
CC (e.g. E. coli) transformed with DNA from a eukaryotic organism (e.g. A.
CC niger) that produces the protein. Screening for xylanase-producing clones
CC can be performed on agar plates containing oat spelt xylan and RBB-xylan.
CC The method was utilised in the identification of cDNA clones (AAT63042-
CC 46) coding for A. niger cellulase, xylanase and arabinoxylan degrading
CC enzymes (AAW14595-99). (Updated on 17-OCT-2003 to standardise OS field)

XX
SQ Sequence 851 BP; 201 A; 244 C; 224 G; 182 T; 0 U; 0 Other;

Query Match 29.4%; Score 198.4; DB 2; Length 851;
Best Local Similarity 61.5%; Pred. No. 5.5e-44;
Matches 354; Conservative 0; Mismatches 216; Indels 6; Gaps 2;

OY 98 CAACCCCACTCGAGGGCTGGACAGATGTTATTACTATTCTGTGGAGTGACGGTG 157
DB 142 CGACCCCGAGCTCGACCGCGGAGAACACCGGCTTCTACTACTCTTCTGACCGACGGCG 201
OY 158 GAGCGCAAGGCCACGTACACCAACCTGGAAGCGGCACTACGAGATCAGTGGGAGATG 217
DB 202 GTGAGAGCGTGACCTTACCAACGAGATGCTGTGCTTACACTGTGAGTGTCACACG 261
OY 218 GCGGTAACTCTGTCGGTGAAGAGGGCTGGAACCCCGGCTGAACGCAAGACCATCCACT 277
DB 262 TGGGCAACTTGTGCTGGAAGAGGGCTGGAACCCCGG--AAGTCCGAGGACATCACCT 318
OY 278 TTGAGGCTGTTTACCAAGCAACGCAACAGCTACCTTGCGGTCTACGCTTGACCCGCA 337
DB 319 ACAGCGGCACCTTCAACCCCTAGCGCAACGCGCTACCTCCGTCTATGGCTGACCACTG 378
OY 338 ACCGCTGTGAGTATTACATCGTGGAACCTTGGCACTATGATCCTTCTCCGCTG 397
DB 379 ACCCTGTGATGAGTACTACATCGTGAAGTCTTACGCGGCACTACACCCCGGAGTGAG 438
OY 398 CTACCGATCTAGGAATGTGAGTGGACGCGTACATCTATCGACTTCGCAAGACCACTC 457
DB 439 GCACGTACAAGGGCACCGTCACTCGGACGAGATCCGTTTACGATATCTACACGGCTACCC 498
OY 458 GCGTCAACGCACTTACATCGACGGCACCCAAACCTTGAACCAATACTGTCGGTCCGCC 517

Db 499 GTACCAATGCTGCTTCATTCAGGGAAACCGCTACTTCACTCAGTACTGCTCCGTTCCGCC 558
Qy 518 AGGACAAGCGCACCAGCGGTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCTGCGG 577
Db 559 AGACAAGAGAGTTGGCGGAACCGTTACCACTCCAAACCACTTCAATGCTTGGGCTAAGC 618
Qy 578 CTGCTTGAATGTCAACGGTGACCACTACTACCAAGATCGTTGCAACGAGGCTACTTCA 637
Db 619 TGGGATGAA---CCTGGGTACTCACACTACCAAGATCGTGCTACCGAGGGTTACCAGA 675
Qy 638 GCAGCGCTATGCTCGCATCACCGTTGCTGACGTGG 673
Db 676 GCAGTGGATCTTCGTCCATCATCTGTTGGTAAGCGG 711

RESULT 15
AAK90405
ID AAK90405 standard; DNA; 1375 BP.
XX
AC AAK90405;
XX

DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 28-SEP-1999 (first entry)
XX
DE Actinomadura sp. DSM43186 35 kDa xylanase encoding DNA.
XX
KW Actinomadura sp. DSM43186; xylanase; Actinomadura flexuosa; lignin;
KW thermostable; biobleaching; wood pulp; bleaching; hemicellulase;
KW paper processing; hemicellulose; ss.
XX
OS Nonomuraea flexuosa.

XX
FH Key Location/Qualifiers
FT CDS 303..1337
FT /*tag= a
FT /product= "xylanase"

XX US5935836-A.
XX PD 10-AUG-1999.
XX
PF 06-JUN-1995; 95US-00468812.
XX
PR 29-JUL-1994; 94US-00282001.
PR 31-OCT-1994; 94US-00332412.
XX
PA (ROHG) ROEHM ENZYME FINLAND OY.
XX
PI Fagerstrom R, Lantto R, Paloheimo M, Suominen P, Vehmaaperae J;
PI Maentylae A;
XX
XX
DR WPI; 1996-141347/38.
DR P-PSDB; AAY24480.
XX
PT Actinomadura xylan sequences and method of use.
XX
PS Disclosure; Fig 13; 54pp; English.
XX

CC The present invention describes a culture medium obtained from the
CC culture of a recombinant host cell that is not Actinomadura flexuosa and
CC has been transformed with a vector encoding a protein having xylanase
CC activity, where the protein comprises an amino acid sequence from a
CC xylanolytic fragment of the amino acid sequence in AAY24480 or AAY24481.
CC Also described is an enzyme preparation derived from the culture medium.
CC The enzyme composition can be used in a method for biobleaching,
CC modifying plant biomass properties, especially the reduction of lignin
CC content in pulp and paper processing. The xylanases are hemicellulases
CC which partially degrade the hemicellulose and enhance the extractability
CC of lignins by conventional chemical bleaching of wood pulp. It can be
CC used alone or as a supplement to other treatments that reduce lignin
CC retention. The culture medium can be used directly without the need to

CC purify the enzymes. Actinomadura flexuosa xylanases have a pH optimum and
CC thermostability desirable for the biobleaching of wood pulp reducing the
CC need to acidify the pulp prior to xylanase treatment. The xylanases
CC partially degrade the hemicellulose in wood pulp which enhances the
CC extractability of lignins by conventional bleaching chemicals and results
CC in a lower consumption of bleaching chemicals reducing the formation of
CC environmentally undesired organic compounds. The present sequence encodes
CC Actinomadura sp. DSM43186 35 kDa xylanase. N.B. This sequence is indexed
CC from US5935836 which is a treat as basic specification for F19503639.
CC (Updated on 25-MAR-2003 to correct DR field.) (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 1375 BP; 265 A; 517 C; 400 G; 193 T; 0 U; 0 Other;

Query Match 29.1%; Score 196.2; DB 2; Length 1375;
Best Local Similarity 59.0%; Pred. No. 2.5e-43;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;

Qy 5 TCGGCTTACCCCGTTGCCCTTGCGGCTTACCGCGACTGGGGCCCTTCCCGG 64
Db 349 TCGGCTTCCGGCGCATGTGACCAAGTGCCTTCCCTTGCACTCGCCATCGCGGTGCGC 408
Qy 65 CAGGGAATGCCACGAGCTCGAAAAGCGACAGCAACCCCACTCGGAGGCTGACAG 124
Db 409 TCGTCCCGGACGCGCCACGCGACACCATCAACCAGAACGAGGGGTACGACA 468
Qy 125 ATGCTATTACTATTCTGTGTGAGTGAAGCGTGAGCGCAGGCCACGTACCAACCTGG 184
Db 469 ACGGCTACTTCTACTCGTTCTGAGACGAGCGCGCGGAGCCGTCTTCATGACCTCCACT 528
Qy 185 AAGCGGCACTACGAGATCAGCTGGGAGATGCGGTAACTCGTGGTGAAGGGCT 244
Db 529 CGGGCGGCACTACAGCACTCGTGCGGAACACGGGAACCTCGTGGCGGCAAGGGCT 588
Qy 245 GGAACCCCGGCTGAACGCAAGACCATCCACTTTGAGGGTGTATACAGCAACGCA 304
Db 589 GGTCAACCGG---GGAGCGCGGAGCCGTGACCTTCAACGCTCTTCAACCGCTCGGGTA 645
Qy 305 ACAGCTACTTGGCGGTCTACGGTTGAGCCCGCAACCCGCTGTGAGTATTACATCGTCG 364
Db 646 ACGGCTTACCTCAGCGCTTACGGCTGAGCAGGAACCCGCTCGTCAAGTACTATCGTCG 705
Qy 365 AGAATTGGCACCTATGATCTTCTCTCCGGTGTACCGATCTAGGAATGTGAGTGGC 424
Db 706 AGAGCTGGGGCACCTACCGGCCACCGGC-----ACCTCAAGGGCACCGTCAACCGC 759
Qy 425 ACGGTAGCATCTATGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATCGACGGCA 484
Db 760 ACGGGGAACGTACGACATCTAAGAACCTGGCGGTACAACGCGCGTCAATCGAGGGCA 819
Qy 485 CCGAACCCTTGCACCAATACTGTGCTCGCTCCGCGCAAGCAAGCGCACCGGTACCGTCC 544
Db 820 CCGGACCTTCCAGCAGTCTGAGCGCTCCGCGCAAGCAAGCGCACCGGACCATCA 879
Qy 545 AGACGGCTGCCACTTGCAGCGCTGGGCTCGCGCTGTTGATGTCAACGCTGACCACT 604
Db 880 CCATCGCAACCACTTGCAGCGCTGGGCCCGCGCGGCATGAA---CCTGGGCAAGCCACG 936
Qy 605 ACTACGATGCTGTGCAACGAGGGCTACTTACAGCAGCGGCTATGCTCGCATCACCGTTG 664
Db 937 ACTACGATGCTGTGCAACGAGGGCTACTACAGAGCAGCGGTAGCTCCACCGTCTCATCA 996
Qy 665 CTGACGTGGGC 675
Db 997 GCGAGGTGGC 1007

Search completed: February 11, 2006, 18:30:53
Job time : 423.587 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:13:54 ; Search time 3418.97 Seconds
(without alignments)
9237.078 Million cell updates/sec

Title: US-09-467-368-1_COPY_31_705

Perfect score: 675
Sequence: 1 ATGGTCGGCTTACCCCGT.....TCACCGTTGCTGACGTGGC 675

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291.2	43.1	860	8 DR637934	DR637934 EST102855
2	291.2	43.1	883	8 DR643290	DR643290 EST103391
3	240.2	35.6	882	8 DR037502	DR037502 49478.2 L
4	233.4	34.6	675	8 DN588726	DN588726 49478.1 L
5	229	33.9	744	7 CF867983	CF867983 trico13xe
6	229	33.9	799	6 CB898036	CB898036 trico13xe
7	222.6	33.0	772	7 CN133022	CN133022 OX1_9 D10
8	220.4	32.7	639	8 DR624928	DR624928 EST101505
9	220.4	32.7	749	8 DR623097	DR623097 EST101322
10	219.4	32.5	686	8 DR624738	DR624738 EST101486
11	219.4	32.5	719	8 DR631520	DR631520 EST102164
12	219.4	32.5	733	8 DR630899	DR630899 EST102102
13	219.4	32.5	739	8 DR624376	DR624376 EST101450
14	219.4	32.5	741	8 DR625790	DR625790 EST101591
15	219.4	32.5	763	8 DR624330	DR624330 EST101445
16	219.4	32.5	784	8 DR628641	DR628641 EST101876
17	219.4	32.5	801	8 DR631291	DR631291 EST102141
18	219.4	32.5	807	8 DR621776	DR621776 EST101190
19	219.4	32.5	809	8 DR627394	DR627394 EST101752
20	219.4	32.5	842	8 DR630275	DR630275 EST102040
21	219.4	32.5	886	8 DR621753	DR621753 EST101188
22	219.4	32.5	891	8 DR632055	DR632055 EST102218

23	219.4	32.5	916	8 DR622008	DR622008 EST101213
24	219.2	32.5	729	8 DR629975	DR629975 EST102010
25	219.2	32.5	763	8 DR623625	DR623625 EST101375
26	219	32.4	734	8 DR622879	DR622879 EST101300
27	219	32.4	768	7 CF881056	CF881056 trico83xj
28	219	32.4	822	6 CB907827	CB907827 trico83xj
29	215.8	32.0	711	8 DR622988	DR622988 EST101311
30	215.8	32.0	770	8 DR622508	DR622508 EST101263
31	214.6	31.8	708	8 DR631672	DR631672 EST102180
32	211.4	31.3	921	6 CD458837	CD458837 Fg08_04b1
33	207.2	30.7	714	8 DR631518	DR631518 EST102164
34	202.8	30.0	671	8 DR632323	DR632323 EST102245
35	202	29.9	697	8 DR625721	DR625721 EST101584
36	201.8	29.9	673	8 DR625705	DR625705 EST101583
37	199.4	29.5	655	8 DR625642	DR625642 EST101577
38	199.4	29.5	677	8 DR629147	DR629147 EST101927
C	39	198.6	871	8 DR037503	DR037503 49478.3 L
	40	198.4	738	6 CD464145	CD464145 ETH1_48_B
	41	198.4	746	8 DR701170	DR701170 Asn_00615
	42	196.4	746	6 CB901964	CB901964 trico28xi
	43	196.4	746	7 CF871731	CF871731 trico28xi
	44	195	680	8 DR707969	DR707969 Asn_08783
	45	191.4	682	8 DR702584	DR702584 Asn_02201

ALIGNMENTS

RESULT 1
LOCUS DR637934 860 bp mRNA linear EST 11-JUL-2005
DEFINITION EST1028559 FvM Gibberella moniliformis cDNA clone FvMB275, mRNA
sequence.
ACCESSION DR637934 GI:70712768
VERSION DR637934.1
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 860)
Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
Utterback,T., Smith,S., Feldblum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR

JOURNAL
COMMENT
USDA
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FvMB275TH
Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES

source
1..860
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FvMB275"
/issue_type="mycelia"
/clone_lib="FvM"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FvM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was


```

QY          618 TGCAACGGAGGGCTACTTACGACAGCGGGCTATGCTCCGATCACCGTTTGCTGACGTGG 673
              ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db          636 CGCTACTGAGGGTTACTTCAGCAGCGGATCTTCTCACATGACC GTTTCTGAGGGGG 691
              ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
LOCUS      DR037502
DEFINITION DR037502                882 bp    mRNA       linear   EST 31-MAY-2005
            49478..2 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
            49478 5', mRNA sequence.
ACCESSION  DR037502
VERSION     DR037502.1 GI:66839397
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM    Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE   1 (bases 1 to 882)
AUTHORS     Flind,B., Rothwell,C., Sardana,R., Griffiths,R., Laque,M., De
            Koeyer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S.
TITLE       Generation of ESTs from late blight-challenged potato tubers
JOURNAL     Unpublished (2005)
COMMENT     Contact: Barry Flinn
            The Canadian Potato Genome Project - BioAtlantech
            921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
            Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

```

FEATURES
source

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Location/Qualifiers
1. .882
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="49478"
/tissue_type="Tubers"
/lab_host="XLI0-Gold"
/clone_1lb="Late Blight-Challenged Tubers"
/notes="Vector: pBluescript II SK(+), XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."
```

ORIGIN

Query Match	35.6%	Score 240.2;	DB 8;	Length 882;
Best Local Similarity	60.9%	Pred. No. 1.6e-55;		
Matches 411; Conservative	0;	Mismatches 258;	Indels 6;	Gaps 1;

[illegible]

DNA sequence:

```
OY      241 GCGCTGGAACCCCCGGCCTGAAACGCAAGAGCCATCCAATTGTAGGGTGTTTACCAGCCAAAC   300
        ||| ||||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     259 GGATGGAACCCCAAGAAAGTGCCCCAGACAATCACCTACTCTGGGACCTTCAACCCCAATGCT   318

OY      301 GGCACAACAGCTACCTTGGCGGTCTACCGGTTGSAACCCCGCAACCCGCTGGTCGAGTATTACATC   360
        ||| ||||| ||||| ||| | | | | | | | | | | | | | | | | | | | | |
Db     319 GGCACAACGCTACCTGTTCATCTATGTGCTGSAACCCGAAAACCCGCTGATTGAGTACTTACATC   378

OY      361 GTCGAAGACTTTGGCACTATGATCCTTCCTCCGGTGCTAACCGATCTAGGAACCTGTGAG   420
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     379 GTTGAAGCTTCGGTTCATATGACCCCTCCTCCGCTGCGTGAAGCAAGGCGACGGTCACC   438

OY      421 TCGCAGCGTAGCATCTATCGACTCGGCAAGAACCACTCGCGTCAAACGCACTTAGCATCGAC   480
        ||| ||| ||||| ||| | | | | | | | | | | | | | | | | | | | | |
Db     439 GTTGATGGCAGCACCTTAACAATCCTCCAGACTACCGTAAACCAACGACCTTCCATCGAT   498

OY      481 GGCACCCAAACCTTGCACCAATACTGTGCGTCCGCCAGACAAGCGCACCAAGCGGTACC   540
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     499 GGCACCTCGACCTTTCAGCAGTACTGTCTGTTCGCCAGAACCACCGCACCGCATCC   558

OY      541 GTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGCTGGTTGAATGTCAACGCTGAC   600
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     559 GTTGATGTGCAAGCTCACTTGGCGGCTGGAAGTCCAAGGAATGAACCTGGGCATGAG   618

OY      601 CACTACTACCAAGATCGTTGCACAACGAGGGCTACTTCAGCAGCGGCTATGCTGCATCAC   660
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     619 CACAACCTACCAAGATGTGTGCTTCGAGGGTTACCAACAGCAGCGGTTCCGCCGATATCACT   678

OY      661 GTTGCTGACGTGGGC   675
        ||||| ||| |||||
Db     679 GTTGATCCGGTGGC   693
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RESULT 4
DN588726
LOCUS
DEFINITION
49478.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
49478 5', mRNA sequence.
ACCESSION
DN588726
VERSION
DN588726.1 GI:61239134
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 675)
Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Iagüe, M., De
Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.
TITLE
Generation of ESTs from late blight-challenged potato tubers
JOURNAL
Unpublished (2005)
COMMENT
Contact: Barry Flinn

COMMENT

921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

```

FEATURES
Source

Location/Qualifiers
1. .675
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="49478"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
/clone_lib="Late Blight-Challenged Tubers"
/note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future

```


Db 693 ATTACCAGATTGTTGCCGTGGAGGGTTACTTtagctctgctctgctc 741

RESULT 6
CB898036 799 bp mRNA linear EST 02-JUL-2003
LOCUS tric013xe09 T.reesei mycelial culture, Version 3 april Hypocrea
DEFINITION jecorina cDNA clone tric013xe09, mRNA sequence.
ACCESSION CB898036
VERSION CB898036
KEYWORDS GI:30112694
SOURCE EST.
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1 (bases 1 to 799)
Foreman,P.K., Brown,D.E., Dankmeyer,L., Dean,R., Diener,S.,
Dunn-Coleman,N.S., Goedegebuer,F., Houfek,T.D., England,G.J.,
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
JOURNAL 12788920
PUBMED
COMMENT Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
1..799
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric013xe09"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN

Query Match 33.9%; Score 229; DB 6; Length 799;
Best Local Similarity 61.6%; Pred. No. 2.1e-52;
Matches 400; Conservative 0; Mismatches 245; Indels 4; Gaps 2;

QY 5 TCGGCTTTACCCCGTTGCCCTTGCGGCTTAGCGCGAGCTGGGGCCCTGGCCCTTCCCG 64
DB 151 TCACCTCCCTCTCGCCGGCGTGGCCATCTCGGCGCTTGGCCGCTCCCGCCCG 210
QY 65 CAGGAATGCCAGAGCTCGAAAAGCAGACAACCCCACTCGAGGGCTGGCAG 124
DB 211 AGTGAATCCGTGGCTGTGAGAAAGCCAGACGATTGAGGCCGGCAGCGCTACAACA 270
QY 125 ATGTTATTACTATTCTCTGTGAGTGAAGTGGAGCGCAAGCTACACCAACTGG 184
DB 271 ACGGCTACTTACTCTGTAAGTGAACATGGCCACGCGCGCTGACGTACACCAATGTC 330
QY 185 AAGCGGCACCTACGAGATCAGCTGGGAGATGGCGTAACTCTCGGTGAAAGGGCT 244
DB 331 CCGCGGGGCAAGTTCTCCGTCAACTGTGCCAACTCGGGCACTTTGTGCGGGCAAGGAT 390
QY 245 GGAACCCCGGCTGAACGCAAGACCACTTGAAGGTGTTTACCAGCCAAAGGCA 304
DB 391 GGCAGCCCCGGACCAAGACCAAGGTCACTTCTCGGGCAGCTACAAACCCCAAGGCA 450
QY 305 ACAGCTACCTTGGGGTCTACAGGTGGAAGCCGCAACCCGCTGAGTATTACATCGTCG 364
DB 451 ACAGTACCTCTCGTGTACGGGTGTGCCGCAACCCCTGATCGAGTACTACATCGTCG 510

QY 365 AGAAGTTGGCACTATGATCCTTCCCTCCGGTGCTACCGATCTAGAACTGTGAGTCGG 424
DB 511 AGAAGTTGGCACTATGATCCTTCCCTCCGGTGCTACCGATCTAGAACTGTGAGTCGG 570
QY 425 ACGGTAGCATCTATGACTCGGCAAGACCACTCGCGCTCAACGCACCTAGCATGACGGCA 484
DB 571 ACGGCAAGGTCTTACGACATTTACCGCAGCAGCGCGCTCAACGCACCTAGCATGACGGCA 630
QY 485 CCCAACTTGCACCAATATGCTGCTCGCTCCGCCAGCAAGCCGACCGGTACCGTCC 544
DB 631 CCGCACTTTTACCACTGCTGCTCGCTCCGCCAGCAAGCCGCTCGAGCGGCTCGTCA 690
QY 545 AGACGGCTGCCACTTGCAGCGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACT 604
DB 691 ACACGGGCAACCACTTCAACGGGTGGGCTCAGCAAGGCTGACGCT--CGGACGATGG 747
QY 605 ACTACGATCGTTG-CAACGAGGGCTACTTCAGCAGCGGCTATGCTC 652
DB 748 ATTACCAGATTGTTGCCGTGGAGGGTTACTTtagctctgctc 796

RESULT 7
CN133022 772 bp mRNA linear EST 01-APR-2004
LOCUS OX1_9_D10_A002 Oxidatively-stressed leaves and roots Sorghum
DEFINITION bicolor cDNA clone OX1_9_D10_A002 5', mRNA sequence.
ACCESSION CN133022
VERSION CN133022
KEYWORDS GI:45963542
SOURCE EST.
ORGANISM Sorghum bicolor (Sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 772)
Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C.,
Sun,F., Sullivan,R., Lim,S., Eastman,A. and Pratt,L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots
Unpublished (2003)
Other ESTs: OX1_9_D10_b1_A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).
Location/Qualifiers
1..772
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="OX1_9_D10_A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Oxidatively-stressed leaves and roots"
/note="Organ: Leaf and Root; Vector: pMB18S-FL3; Site 1:
XhoI; Site 2: XhoI; The library was prepared from polyA+
RNA from oxidatively stressed, hydroponically grown
sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.003% and leaves
were misted with 10 uM methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all

tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 33.0%; Score 222.6; DB 7; Length 772;
Best Local Similarity 63.5%; Pred. No. 1.2e-50;
Matches 374; Conservative 0; Mismatches 209; Indels 6; Gaps 2;

OY 74 CCACGGAGCTCGAAAAAGCGACAGACAACCCCACTCGGAGGGCTGGCAGATGTTATT 133
DB 132 CCTCGGTCTTGAGGGCCCGCCAGGTCACTGTGAAGGTTACCATATGAGATACT 191
OY 134 ACTATTCTGTGTGAGTGAAGTGAAGCGCAGGCCACGTACACCACTTGAAGCGGCA 193
DB 192 TCTACTCTTGTGTGTCTGTATGGCGGTGCTATGCCAATATCAAGATGGTGAGGAAATC 251
OY 194 CCTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAGGAGGCTGAACCCCG 253
DB 252 ACTACACGGTGAATTGGCGCAACACTGTGAACCTTGTGTGGAAAAGGTTGAACCCCG 311
OY 254 GCCTGAACGCAAGACCATCCACTTTGAGGGTGTATACCAAGCCAAACGCAACAGCTACC 313
DB 312 G---TACTGGCCGAACCATCACTATGGCGGTCTTTCAGCCCTCAGGGTAACGGCTACC 368
OY 314 TTGCGGTCTAAGGTGGAGCCCGCAACCCGCTGTGAGTATTAATCATCTGCGAATTTG 373
DB 369 TCTGCGTCTACGGCTGGACTCGCAGCCCTCTCGTTGAGTACTACGTATCGAAGAACTACG 428
OY 374 GCACCTATGATCTCTTCCCTCGGTCTACTCCGATCTAGGAAGTGTGAGTGGCAGCGTAGCA 433
DB 429 GCACCTTACAACCTTGCTGCTGTGCGCAGACAAAGGCGACCGTCTTACAACGACGGGACA 488
OY 434 TCTATGACTCGGCAAGACCACTCGGCTCAACGCACTGACCTGACGGCACCACCACTT 493
DB 489 CCTACGATCTTACACAGACCACCGCTTACAACAGCCCTTATTCAGCGGCCAACAGACT 548
OY 494 TCGACCAATATCTGTCGTCGCGCCAGCAAGCGCAGCAGCGGTACCGTCCAGACGGGCT 553
DB 549 TCAACCACTACTGGGCGCATCCGCGCAACAAGCGCAGCAGCGCGCGCTCAACATGACAGA 608
OY 554 GCCACTTCGACGCTGGGCTCGCGGTGTTGATGTCAACGGTGAACCACTACTACACAGA 613
DB 609 CTATCTTCAATGCTTGGGCTAACGCTGTATGAGACT--TGGAACAACACTACTACACAGA 665
OY 614 TCGTTGCAACGAGGGCTACTTACGACGCGGCTATGCTCGCATCACCGT 662
DB 666 TCCTGGCTACCGAGGGATACAGAGCAGTGATCTTCTTCTATCTATGT 714

RESULT 8
DR624928 639 bp mRNA linear EST 11-JUL-2005
LOCUS EST1015056 Fv1 Gibberella moniliformis cDNA clone FVIB05, mRNA
DEFINITION sequence.
ACCESSION DR624928
VERSION DR624928.1 GI:70699610
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
REFERENCE 1 (bases 1 to 639)
AUTHORS Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
JOURNAL spliced introns in multiple genes of the funomisin gene cluster
COMMENT Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR

USDA
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVIB05TH
Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES

source

Location/Qualifiers
1..639
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVIB05"
/tissue_type="mycelia"
/clone_id="Fv1"
/note="Vector: pBluescript II SK(+); Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.7%; Score 220.4; DB 8; Length 639;
Best Local Similarity 63.2%; Pred. No. 4.9e-50;
Matches 373; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

OY 74 CCACGGAGCTCGAAAAAGCGACAGACAACCCCACTCGGAGGGCTGGCAGATGTTATT 133
DB 24 CCTGTCTCTTGAAGGCCCGCAGGTACCGGTACTGTGAGGGTTACCAACAAGGATACT 83
OY 134 ACTATTCCTGTGTGAGTGAAGTGAAGCGCAGGCCACGTACACCACTGGAAGCGGCA 193
DB 84 TCTACTCTTGTGTGTCTGTATGGTGTGCTATGCCAATACCGTATGGTGAGGAAATC 143
OY 194 CCTACGAGATCAGCTGGGAGATGGCGGTAACTCTGCTGGTGAAGGCTGAACCCCG 253
DB 144 ACTACCAAGTGAATTGGCGCAACTGTGAATCTTGTGTGGAAAAGGTTGAACCCTG 203
OY 254 GCCTGAACGCAAGACCATCCATTGAGGGTGTTAACAGCCAAACGGCAACAGTACC 313
DB 204 G---TACTGGCCGAACATATCACTATGGCGGTCTTTCAGCCCTCAGGGTAAACGGCTATC 260
OY 314 TTGCGGTCTACGGTTGAGCCCGCAACCCGCTGTGCGATATTACATCTGTGAGAACTTTG 373
DB 261 TCTGCGTCTACGGCTGAGCCCGCAGCCCTCTGTCGAGTACTACGTATCGAAGAACTACG 320
OY 374 GCACCTATGATCTCTTCCGCTGTCTAACCGATCTAGGAATGTGAGTGCAGCGGTAGCA 433
DB 321 GCACTTACAATCCCGGCTCTGCTGGCCAGCAGCAAGGGGACCGCTTACAACGACGGGACA 380
OY 434 TCTATGACTCGGCAAGACCACTGCGGTCAACGCACTTAGCATTCGACGGCAACCAACT 493
DB 381 CCTATGATCTGTACAGACCAACCGCTTACAACCAAGCCCTCTTATTCAGCGGCCAACAGACT 440
OY 494 TCGACCAATATCTGTGTCGTCGCGCAGGACAAAGCGCAGCAGCGGTACCGTCCAGACGGGCT 553
DB 441 TCAACCACTACTGGGCGCATCCGCGCAACAAGCGCAGCAGCGCGCTGTCAACATGACAGA 500
OY 554 GCCACTTCGACGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACTACTACACAGA 613
DB 501 CTATCTTCAATGCTTGGCTAATGCTGCGATGAGACT--TGGAACAACACTACTATACAGA 557
OY 614 TCGTTGCAACGAGGGCTACTTCAAGCAGCGGCTATGCTCGCATCACCGTT 663

Db 558 TTCTAGCTACCGAGGATACCAAGAGCGATGATCTTCTTCATCTATGTT 607

RESULT 9
DR623097 749 bp mRNA linear EST 11-JUL-2005
LOCUS EST1013225 FvI Gibberella moniliformis cDNA clone FVIAM22, mRNA
DEFINITION sequence.
ACCESSION DR623097
VERSION DR623097
KEYWORDS DR623097.1 GI:70697745
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 749)
AUTHORS Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
JOURNAL Unpublished (2005)
COMMENT Contact: Brown, D.W.
USDA/ARS/NCAUR
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVIAM22TH
Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES
source
1. 749
Location/Qualifiers

/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVIAM22"
/issue_type="mycelia"
/clone_lib="FvI"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN
Query Match 32.7%; Score 220.4; DB 8; Length 749;
Best Local Similarity 63.2%; Pred. No. 5e-50;
Matches 373; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

Qy 74 CCACGAGCTCGAAAAAGCAGACAGACACCCCACTCGAGGGCTGGACGATGGTATT 133
Db 114 CCTCTGTCTTGAGGCCCGCAGGTCAACCGTAACTGTAGGGTTACCAACGGAATACT 173
Qy 134 ACTATTCTGGTGAAGTGAAGCGGAGCGCAACGTACACCAACTGGAAGCGGCA 193
Db 174 TCTACTCTTGGTGTCTGATGTGTGCTATGCCAATACCGTATGGTGAAGGAATC 233
Qy 194 CTTACGAGATCACTGGGAGATGGCGGTAACTGTCGGTGAAGAAAGGCTGAACCCG 253
Db 234 ACTACCAAGTTGATTGGCGCAACACTGTAACTTGTGTTGGTGAAGGGTTGAACCTG 293

Qy 254 GCCTGAACGAAGAGCCATTCATTGAGGGTGTATTACCAAGCCAAACGGCAAGCTACC 313
Db 294 G---TACTGGCCGAACACTATCACTATGCGGTTCTTTCAACCCCTCAGGGTAAAGGCTATC 350
Qy 314 TTGCGGTCTACGGTTGACCCGCAACCCGCTGTGCGAGTATTACATGTCGAGAATTGG 373
Db 351 TCTGCGTCTACGGCTGAGACCGGAGCCCTCTGTCGAGTACTACGTACATCGAAGTACG 410
Qy 374 GCACCTATGATCCTCTCCGGTCTACCGATCTAGAACTGTGAGTGGACCGGTAGCA 433
Db 411 GCACCTTAAATCCCGGCTGTGCTGGCCAGCACAAGGGCAACCGTCTAACACGACGGCACA 470
Qy 434 TCTATCACTCGGCAAGACCACTCCGCTCAACGCACTTACATGACGGGCAACCAACT 493
Db 471 CCTATGATCTGTACCAAGACCACTCGCTTACCAACGACCTTATCGACGGCCAAAGACCT 530
Qy 494 TCGACCAATACTGTGTCGGTCCGCAAGACCAAGCGGATACCGTCCAGACGGGCT 553
Db 531 TCAACCAATACTGGGCGCATCCGCGCAACAAAGCGGACGGCGGTGTCAACATGACAGA 590
Qy 554 GCCACTTCAGCGCCTGGGCTGCGCGCTGTTGAATGTCAACGGTGACCACTATCAGCA 613
Db 591 CTATCTTCAATGCTTGGGCTATGCTGGCATGAGACT--TGAAACCACTATCAGCA 647
Qy 614 TCGTTCGAACGAGGGCTACTTCAGACAGCGGCTATGCTGCATCACCGTT 663
Db 648 TTCTAGTACCGAGGATACCAAGACAGAGTATCTTCCATCTATGTT 697

RESULT 10
DR624738 686 bp mRNA linear EST 11-JUL-2005
LOCUS EST1014866 FvI Gibberella moniliformis cDNA clone FVIB801, mRNA
DEFINITION sequence.
ACCESSION DR624738
VERSION DR624738.1 GI:70699420
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 686)
AUTHORS Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
JOURNAL Unpublished (2005)
COMMENT Contact: Brown, D.W.
USDA/ARS/NCAUR
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVIB801TH
Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES
source
1. 686
Location/Qualifiers

/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVIB801"
/issue_type="mycelia"
/clone_lib="FvI"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FvI was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman

#1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to TRIZOL Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIZOL. The cDNA was directionally ligated into the pBluescript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.5%; Score 219.4; DB 8; Length 686;
Best Local Similarity 63.2%; Pred. No. 9.4e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

QY 74 CCACGAGCTCGAAAAAGCAGACACACCCCACTCGAGGGCTGGCAGATGTTATT 133
DB 70 CCTGTGCTTGAAGCGCCCGCAGGTCAACGGTTACTTGAGGGTTACCAACGCGATACT 129
QY 134 ACTATTCCTGGTGGAGTGAAGGTGAGCGCAGGCCACGTACACCAACCTGGAAGCGGCA 193
DB 130 TCTACTCTTGGTGTCTGATGGTGGCTATGCCAACTACCGTATGGGTGAGGGAATC 189
QY 194 CCTACGAGATCAGCTGGGAGATGGCGTAACTCTGTCGGTGAAGGCGTGAACCCCG 253
DB 190 ACTACCAAGTTGATTGGCGCAACACTGTAACTTTGTTGGTGAAGGTTGAACCTTG 249
QY 254 GCCTGAACGACAGCCATCCACTTTGAGGTGTTTACCAGCCAAACGCAACAGCTACC 313
DB 250 G---TACTGGCCGAATATCAACTATGCGGTCTTTCAAGCCCTCAGGTAACGGCTATC 306
QY 314 TTGCGGTCTACGGTTGGACCCGCAACCGGCTGTGAGTATTAATCGTCGAGACTTTG 373
DB 307 TCTGCGTCTACGGCTGAGCCCGCAGCCCTCTCGTGAAGTACTACGTCATCGAAGTACG 366
QY 374 GCACCTATGATCTCTCCGGTCTACCGATCTAGGAATGTGAGTGGACGGTAGCA 433
DB 367 GCACTTACATCCCGGCTCTGCTGGCCAGCAAGGGCACCGTCTTCAACGACGGCGACA 426
QY 434 TCTATCGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATGACGGCACCCAACT 493
DB 427 CCTATGATCTGTACCAAGACCAACCGCTTCAACGACCGCTTATGACGGCAACGACT 486
QY 494 TCGACCAATATCTGTCCGTCGCGCAAGCAAGCGCACCGGTACCGTCCAGACGGGCT 553
DB 487 TCAACCAAGTACTGGGCATCCGCGCAACGAGCAGCGCGCTGTCAACATGACGA 546
QY 554 GCCACTTCGACGCTGGGCTCGCGTGTGATGTCAACGCTGACCACTACTACGAGA 613
DB 547 CTATCTTCAATGCTTGGGCTAATGCTGCAAGACT---TGAACCACTACTACTACGA 603
QY 614 TCGTTCGACGAGGGCTACTTACGACGGGCTATGCTCGCATCACCGT 662
DB 604 TTCTAGCTACCGAGGATACCAAGCAGTGGATCTTCTTCCATCTATGT 652

RESULT 11

DR631520 719 bp mRNA linear EST 11-JUL-2005
LOCUS EST1021648 Fv1 Gibberella moniliformis cDNA clone FVIEA21, mRNA
DEFINITION sequence.

ACCESSION DR631520
VERSION DR631520.1 GI:70706360
KEYWORDS EST,
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE

AUTHORS Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,
Uterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
JOURNAL Unpublished (2005)

COMMENT

Contact: Brown, D.W.
USDA/ARS/NCAUR
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVIEA21TH
Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES

source

1..719
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVIEA21"
/tissue_type="mycelia"
/clone_lib="Fv1"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIZOL Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIZOL. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.5%; Score 219.4; DB 8; Length 719;
Best Local Similarity 63.2%; Pred. No. 9.5e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

QY 74 CCACGAGCTCGAAAAAGCAGACACACCCCACTCGAGGGCTGGCAGATGTTATT 133
DB 108 CCTGTGCTTGAAGCGCCCGCAGGTCAACGGTTACTTGAGGGTTACCAACGCGATACT 167
QY 134 ACTATTCCTGGTGGAGTGAAGGTGAGCGCAGCGCACTACCAACCTGGAAGCGGCA 193
DB 168 TCTACTCTTGGTGTCTGATGGTGGCTATGCCAACTACCGTATGGGTGAGGGAATC 227
QY 194 CCTACGATCAGCTGGGAGATGGCGGTAACTCTGTCGGTGAAGGCGTGAACCCCG 253
DB 228 ACTACCAAGTTGATTGGCGCAACACTGTAACTTTGTTGGTGAAGGTTGAACCCCTG 287
QY 254 GCCTGAACGCAAGACCATCACTTGAAGGTGTTTACAGCCAAACGGCAACAGTACC 313
DB 288 G---TACTGGCCGAATATCAACTATGCGGCTTCTTCAAGCCCTCAGGTAACGGCTATC 344
QY 314 TTGCGGTCTACGGTTGGACCCGCAACCGGCTGTGAGTATTACATCGTCGAGAACTTTG 373
DB 345 TCTGCGTCTACGGCTGAGCCCGCAGCCCTCTGTCGAGTACTACGTATCGAAGACTACG 404
QY 374 GCACCTATGATCTCTCCGGTCTACCGATCTAGGAATGTGAGTGCAGCGGTAGCA 433
DB 405 GCACTTACATCCCGGCTCTGCTGGCCAGCACAAGGGCAACCGTCTACAACGACGGGACA 464
QY 434 TCTATCGACTCGGCAAGACCACTGCGGTCAACGCACTTACATCGACGGCAACCAACT 493
DB 465 CCTATGATCTGTACCAAGACCAACCGCTTACCAACGACCCCTTATGACGGCCACAGACT 524
QY 494 TCGACCAATATCTGTCCGTCGCGCAAGCAAGCGCACCGGTACCGTCCAGACGGGCT 553
DB 525 TCAACCAAGTACTGGGCATCCGCGCAACGAGCGCAGCGCGCTGTCAACATGACGA 584
QY 554 GCCACTTCGACGCTGGGCTCGCGTGTGATGTCAACGCTGACCACTACTACGAGA 613
DB 585 CTATCTTCAATGCTTGGGCTAATGCTGCGATGAGACT---TGAACCACTACTACTACGA 641

Qy 614 TCGTGCACGAGGGCTACTTACAGCGGCTATGCTCGCATCACCGT 662
Db 642 TTCTAGCTACCGAGGATACACAGCAGTGATCTTCTTCATCTATGT 690

RESULT 12
LOCUS DR630899 733 bp mRNA linear EST 11-JUL-2005
DEFINITION EST1021027 Fv1 Gibberella moniliformis cDNA clone FVIDX40, mRNA
sequence.

ACCESSION DR630899
VERSION DR630899.1 GI:70705629
KEYWORDS EST.

SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 733)

AUTHORS Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.

TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)

JOURNAL Contact: Brown, D.W.
COMMENT USDA/ARS/NCAUR

USDA

1815 N. University St, Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncaur.usda.gov

TIGR sequence name: FVIDX40TH

Seq primer: AAT TAA CCC TCA AAG GG.

Location/Qualifiers

FEATURES

source

1. 733
/organism="Gibberella moniliformis"

/mol_type="mRNA"

/strain="m3125"

/db_xref="taxon:117187"

/clone="FVIDX40"

/tissue_type="mycelia"

/clone_lib="Fv1"

/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to Trizol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml Trizol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.5%; Score 219.4; DB 8; Length 733;
Best Local Similarity 63.2%; Pred. No. 9.5e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

Qy 74 CCACGAGCTCGAAAAAGCAGACAGACACCCCAACTCGAGGGCTGGACAGATGTTATT 133

Db 147 CCTGTCTCTTGAGGCCCGCAGGTCAACGGTAAGGTTACCAACGAGTACT 206

Qy 134 ACTATTCGTGTGAGTGAAGGTGAGCGCAGGCCACGTACCAACCACTGGAAGCGGCA 193

Db 207 TCTACTCTTGGTGTCTGATGTGTGGCTATGCCAACTACCGTATGGGTGAGGGAATC 266

Qy 194 CTTACGAGATCAGCTGGGAGATGGCGGTAACTCTGTCGGTGAAGGGCTGGAACCCCG 253

Db 267 ACTACGAGTTGATTGGCGCAACACTGTTACTTTGTTGGTGAAGGGTTGAACCCCTG 326
Qy 254 GCCTGAACGAAGAGCCATCCATTGAGGGTGTTCACGCAACGGCAAGACTACC 313
Db 327 G---TACTGGCCGAAGTATCACTATGCGGTTCTTTCAGCCCTCAGGGTAAAGGCTATC 383

Qy 314 TTGCGGTCTACGGTTGACCCGCAACCCGCTGTCGAGTATTACATCGTCGAGAATTGG 373

Db 384 TCTGCGTCTACGGCTGAGCCGCGAGCCCTCTCGTGAAGTACTACGTATCGAGAACTACG 443

Qy 374 GCACCTATGATCCTCTCCGGTGCTACCGATCTAGAACTGTGAGTCCGACGGTAGCA 433

Db 444 GCACCTTACAATCCCGGCTCTGCTGGCCAGCACAAGGGCAACCGTCTACAACGACGGCGACA 503

Qy 434 TCTATGACTCGGCAAGACCACTCGCTCAACGCACTAGCATCGACGGCAACCAACT 493

Db 504 CCTATGATCTGTACCAAGACCAACCCGCTTATCAACAGCCCTTATCGACGGCCAAAGACCT 563

Qy 494 TCGACCAATACTGTGTCGTCGCCAGGACCAAGCGCAGCAGCGGTACCGTCAGACGGGCT 553

Db 564 TCAACCACTACTGGGCCATCCGCCCAACAAGCGCAGCAGCGGCTGTCAACATGCAGA 623

Qy 554 GCCACTTCGACGCGCTGGCGCTGCGCTGTTGAATGTCAACGCTGACCACTATACAGA 613

Db 624 CTATCTCAATGCTTGCGCTATGCTGCGATGAGACT---TGGGAACCACTACTATCAGA 680

Qy 614 TCGTGCACGAGGGCTACTTACAGCAGCGGCTATGCTCGCATCACCGT 662
Db 681 TTCTAGCTACCGAGGATACCAAGCAGATGATCTTCTTCATCTATGT 729

RESULT 13

DR624376

LOCUS

DEFINITION EST1014504 Fv1 Gibberella moniliformis cDNA clone FVIB280, mRNA

sequence.

ACCESSION DR624376

VERSION DR624376.1 GI:70699058

KEYWORDS EST.

SOURCE Gibberella moniliformis

ORGANISM Gibberella moniliformis

REFERENCE 1 (bases 1 to 739)
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

AUTHORS Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.

TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)

JOURNAL Contact: Brown, D.W.

COMMENT USDA/ARS/NCAUR

USDA

1815 N. University St, Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncaur.usda.gov

TIGR sequence name: FVIB280TH

Seq primer: AAT TAA CCC TCA AAG GG.

Location/Qualifiers

FEATURES

source

1. 739

/organism="Gibberella moniliformis"

/mol_type="mRNA"

/strain="m3125"

/db_xref="taxon:117187"

/clone="FVIB280"

/tissue_type="mycelia"

/clone_lib="Fv1"

/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in

a suspension of 5 x 10⁶ conidia per ml. The inoculated roots and shoots were then incubated on moistened Whatman #1 filter paper at room temperature under sterile conditions for 4 days. Fungal mycelial was collected, frozen in liquid nitrogen, ground to a powder, and then added to TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIzol. The cDNA was directionally ligated into the pBluescript II SK(+) XR vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.5%; Score 219.4; DB 8; Length 739;
Best Local Similarity 63.2%; Pred. No. 9.5e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

Qy	74	CCACGGAGCTCGAAAAAGCGACAGACACCCCACTCGAGGGGCTGGCAGCATGTTATT	133
Db	119	CCTCTGTCTTGAAGGCCCGCCAGGTACCGGTAACTTGAGGGTTACCAACAGGATTA	178
Qy	134	ACTATTCCTGGTGAAGTGAAGCGAGCGCAGGCCACGTACCAACCTGGAAGCGGCA	193
Db	179	TCTACTCTTGTTGGTGTGATGTTGGTCTATGCCAATACCGTATGGTGAAGGAAGTC	238
Qy	194	CCTACGAAATCAGCTGGGAGATGGCGGTAACTCGTGGTGAAGGAGGCTGAACCCCG	253
Db	239	ACTACCAAGTTGATTGGCGCAACACTGTACTTGTGGTGAAGGAGGTTGAACCCCTG	298
Qy	254	GCCTGAACGCAAGACCATCCACTTTGAAGGTTTACCAAGCCAAACGGCAACACTAC	313
Db	299	G---TACTGGCCGAACACTATCAACTATGGCGGTTCTTTCAGCCCTCAGGGTAACGGCTATC	355
Qy	314	TTGCGGTCTACGGTTGGACCCGCAACCCGCTGTGAGTATTACATCGTCGAGAATTG	373
Db	356	TCTGCGTCAAGCGCTGAGCCCGCAGCCCTCTCGTGAAGTACTACGTCAAGAACTACG	415
Qy	374	GCACCTATGATCCTTCTCCGGTGTACCGATCTAGAACTGTGAGTCGACGGTAGCA	433
Db	416	GCACTTACAATCCCGGCTGTGTCGCGCAGACAAAGGCAACGCTCTACAACAGCGGAGCA	475
Qy	434	TCTATGACTCGGCAAGACCACTCGGTCACGCACTAGCATCGACGGCAACCAACT	493
Db	476	CCTATGATCTGTACCAAGACCAACCGCTATACAGCCCTATCGACGGCAACAGACT	535
Qy	494	TCGACCAATATGTCGTCGTCGCCCAAGCAAGCGCAACCGGTAACGTCACAGCGGCT	553
Db	536	TCAACCACTACTGGGCCATCCGCCGCAACAAGCGCAGCGCGCTGTCAACATGCA	595
Qy	554	GCCACTTCGACGCTGGGCTCGCGCTGTTGAATGTCAAGGTTGACCACTACTACAGA	613
Db	596	CTATCTTCAATGCTTGGGCTAATGTGGCATGAGACT--TGAACCACTACTACTACAGA	652
Qy	614	TGTTGCAAGAGGGCTACTTACGACGGGCTATGCTTCGATCAACCGT	662
Db	653	TTCTAGCTACGAGGATACCAAGAGCTGATCTTCTTCATCTATGT	701

RESULT 14
DR625790 741 bp mRNA linear EST 11-JUL-2005
LOCUS DR625790 Fv1 gibberella moniliformis cDNA clone FVIBR33, mRNA
DEFINITION sequence.
ACCESSION DR625790
VERSION DR625790.1 GI:70700504
KEYWORDS EST.
SOURCE Gibberella moniliformis
ORGANISM Gibberella moniliformis
REFERENCE 1 (bases 1 to 741)
AUTHORS Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
Utterback,T., Smith,S., Feldjlyum,T., Glenn,A.B., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively

JOURNAL
COMMENT
USDA
1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brown@ncaur.usda.gov
TIGR sequence name: FVIBR33TH
Seq primer: AAT TAA CCC TCA AAG GG.

FEATURES
source
1..741
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVIBR33"
/tissue_type="mycelia"
/clone_id="Fv1"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBluescript II SK(+) XR
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.5%; Score 219.4; DB 8; Length 741;
Best Local Similarity 63.2%; Pred. No. 9.5e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

Qy	74	CCACGGAGCTCGAAAAAGCGACAGACACCCCACTCGAGGGGCTGGCAGCATGTTATT	133
Db	125	CCTCTGTCTTGAAGGCCCGCCAGGTACCGGTAACTTGAGGGTTACCAACAGGATTA	184
Qy	134	ACTATTCCTGGTGAAGTGAAGCGTGAAGCGCAGCGCACTACCAACCTGGAAGCGGCA	193
Db	185	TCTACTTGGTGTGATGTTGGTGTGCTATGCCAATACCGTATGGTGAAGGAAGTC	244
Qy	194	CCTACGATCAGCTGGGAGATGGCGTAACTCGTGGTGAAGGGCTGGAACCCCG	253
Db	245	ACTACAGGTTGATTGGCGCAACTGTAACTTGTGTGGAAGGTTGAACCCCTG	304
Qy	254	GCCCTGAACGCAAGACCATCTTGAAGGTTTACCAAGCCAAACGGCAACACTAC	313
Db	305	G---TACTGGCCGAACACTATGAGCGGTTCTTCAAGCCCTCAGGGTAACGGCTATC	361
Qy	314	TTGCGGTCTACGGTTGACCCCGCAACCCGCTGTCAGATATTACATCGTCGAGAATTG	373
Db	362	TCTGCGTCTACGGCTGAGCCCGCAGCCCTCTCGTCGAGTACTACGTCATCGAAGTA	421
Qy	374	GCACCTATGATCCTTCTCCGGTCTACCGATCTAGGAATGTGAGTCCGACGGTAGCA	433
Db	422	GCACTTACAATCCCGCTCTGCTGCGCAGCACAAGGGCAACGCTTACAACGACGGGACA	481
Qy	434	TCTATGACTCGGCAAGACCACTGCGTCAACGCACTAGCATGACGGCAACCAACT	493
Db	482	CCTATGATCTGTACCAAGACCAACCGCTTATCGACGGCAACAGACT	541
Qy	494	TCGACCAATATGTCGTCGTCGCCCAAGCAAGCGCAACGGGTAACGTCACAGCGGCT	553
Db	542	TCAACCACTACTGGGCCATCCGCCGCAACAAGCGCAGCGGCTGTCAACATGCA	601
Qy	554	GCCACTTCGACGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACTACTACAGA	613

Db 602 CTATCTTCATGCTTGGGCTAATGCTGGCATGAGACT---TGGAACCACTACTATACAGA 658
Qy 614 TCGTTGCAACGAGGGGCTACTTCAAGACGGGCTATGCTCGCATCACCGT 662
Db 659 TTCTAGCTACCGAGGATACCAAGACAGTGATCTTCTTCACTCTATGT 707

RESULT 15

DR624330

LOCUS 763 bp mRNA linear EST 11-JUL-2005
DEFINITION EST1014458 Fv1 Gibberella moniliformis cDNA clone FVIB212, mRNA

ACCESSION

DR624330

VERSION

DR624330.1 GI:70699012

KEYWORDS

EST.

SOURCE

ORGANISM

Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 763)
Brown,D.W., Cheung,S., Proctor,R.H., Butenko,A.E., Zheng,L., Lee,Y.,
Utterback,T., Smith,S., Feldblum,T., Glenn,A.B., Platner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.

AUTHORS

Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster

TITLE

JOURNAL

COMMENT

USDA/ARS/NCAUR

USDA

1815 N. University St, Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncaur.usda.gov

TIGR sequence name: FVIB212TH

Seq primer: AAT TAA CCC TCA AAG GG.

Location/Qualifiers

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/organism="Gibberella moniliformis"

/mol_type="mRNA"

/strain="m3125"

/db_xref="taxon:117187"

/clone="FVIB212"

/issue_type="mycelia"

/clone_lib="Fv1"

/note="Vector: pBluescript II SK(+); Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
Fv1 was prepared from growth on excised maize seedling
roots and shoots. The roots and shoots were prepared as
described above and then inoculated by dipping briefly in
a suspension of 5 x 10⁶ conidia per ml. The inoculated
roots and shoots were then incubated on moistened Whatman
#1 filter paper at room temperature under sterile
conditions for 4 days. Fungal mycelial was collected,
frozen in liquid nitrogen, ground to a powder, and then
added to TRIzol Reagent (Invitrogen, Carlsbad CA) at
approximately 1 g mycelia per 10 ml TRIzol. The cDNA was
directionally ligated into the pBluescript II SK(+)
vector (cDNA Synthesis Kit; Stratagene)."

ORIGIN

Query Match 32.5%; Score 219.4; DB 8; Length 763;
Best Local Similarity 63.2%; Pred. No. 9.6e-50;
Matches 372; Conservative 0; Mismatches 211; Indels 6; Gaps 2;

Qy 74 CCACGAGCTCGAAAAGCAGACAGCAACCCCACTCGAGGGGCTGCACAGATGTTATT 133
Db 154 CCTCTGTCTTGAAGCCCGCAGGTCAACGTAATCTGAGGGTTACCAACAGGATACT 213

Qy 134 ACTATTCTCTGTGAGTGAAGTGAAGCGGACGACGTAACCAACCTGAAGCGGCA 193
Db 214 TCTACTCTTGTGCTGTGATGATGAGTGGCTATGCAACTACCGTATGGTGAGGAAGTC 273

Qy 194 CCTACGATCAGCTGGGAGATGGCGTAACCTCGTGGTGAAGGGCTGGAACCCG 253
Db 274 ACTACGAGTTGATTGGCGCAACCTGTAACTTTGTGTGGAAAGGTTGAACCTG 333
Qy 254 GCCTGAACGCAAGAGCCATTCATTGAGGGTGTTCACAGCCAAAGGCAAGCTACC 313
Db 334 G---TACTGGCCGAACCTATCACTATGCGGTTCTTCAACCCCTAGGGTAAAGGCTATC 390
Qy 314 TTGCGTCTACGTTGAGCCCGCAACCCGCTGTCAGTATTACATCGTCGAACTTTG 373
Db 391 TCTGCGCTACGCTGAGCCCGCAAGCCCTCTCGTCAGTACTACGTCATCGAAGTACG 450
Qy 374 GCACCTATGATCCTTCCGCTGCTACCGATCTAAGAACTGTCAGTGCACCGTAGCA 433
Db 451 GCACCTTAATCCCGGCTGTGCTGGCCAGCAAGGGCAACCGTCTAACAAGCAGCGACA 510
Qy 434 TCTATGACTCGGCAAGCACTCGGCTCAACGCACTAGCATCGACGGCAACCAACT 493
Db 511 CTTATGATCTGTACAGACCAACCGCTTATCAACAGCCCTCTATCGACGGCAACAGACT 570
Qy 494 TCGACCAATCTGTTGCTCGGTCGCGCAGAGCAAGCGCAACCGGTACCGTCAGACGGGCT 553
Db 571 TCAACGAGTACTGGGCAATCCGCGCAGCAACAGCGCAGCGGCTGTCAACATGACAGA 630
Qy 554 GCCACTTCAGACGCTGGGCTCGCGCTGTGTTGAATGTCAACGCTGACCACTACTACAGA 613
Db 631 CTATCTTCAATGCTTGGGCTTAATGCTGCGATGAGACT---TGGAACCACTACTATCAGA 687
Qy 614 TCGTTGCAACGAGGGCTACTTCAAGACGCGGTATGCTCGCATCACCGT 662
Db 688 TTCTAGCTACCGAGGATACAGAGAGAGTGTCTTCCATCTATGT 736

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Job time : 3419.97 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)
8096.696 Million cell updates/sec

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Perfect score: 675

Sequence: 1 ATGGTCGGCTTTACCCCGT.....TCACCGTTGCTGACGTGGC 675

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/lna/5_COMB.seq:*
- 3: /cgn2_6/ptodata/1/lna/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/lna/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/lna/H_COMB.seq:*
- 6: /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:*
- 7: /cgn2_6/ptodata/1/lna/PP_COMB.seq:*
- 8: /cgn2_6/ptodata/1/lna/RE_COMB.seq:*
- 9: /cgn2_6/ptodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	675	100.0	983	3	US-09-115-660-1 Sequence 1, Appli
3	239	35.4	1123	2	US-08-458-023B-3 Sequence 3, Appli
4	196.2	29.1	1375	2	US-08-468-812-1 Sequence 1, Appli
5	196.2	29.1	1375	3	US-08-590-563-1 Sequence 1, Appli
6	196.2	29.1	1375	3	US-09-770-621-1 Sequence 1, Appli
7	196.2	29.1	1375	3	US-09-235-832-1 Sequence 1, Appli
8	194.2	28.8	822	3	US-09-254-733-8 Sequence 8, Appli
9	190	28.1	1015	2	US-08-121-436A-1 Sequence 1, Appli
10	181.8	26.9	1281	3	US-08-768-373-1 Sequence 1, Appli
11	181.8	26.9	1281	3	US-09-849-242A-1 Sequence 1, Appli
12	168.4	24.9	675	2	US-07-744-570B-1 Sequence 1, Appli
13	164.6	24.4	927	2	US-08-507-431-5 Sequence 5, Appli
14	164.6	24.4	927	2	US-08-902-655A-5 Sequence 5, Appli
15	164.6	24.4	927	3	US-09-116-622-5 Sequence 5, Appli
16	164.6	24.4	927	3	US-09-219-277-5 Sequence 5, Appli
17	164.6	24.4	927	3	US-09-599-661-5 Sequence 5, Appli
18	162.4	24.1	489	2	US-08-119-169A-7 Sequence 7, Appli
19	159	23.6	2219	2	US-08-290-979A-7 Sequence 7, Appli
20	144.8	21.5	573	2	US-08-709-912-18 Sequence 18, Appli
21	144.8	21.5	573	2	US-09-047-370-18 Sequence 18, Appli
22	138	20.4	1174	3	US-08-768-373-3 Sequence 3, Appli
23	138	20.4	1174	3	US-09-849-242A-3 Sequence 3, Appli
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36	96.2	14.3	234	3	US-09-260-283-1 Sequence 46, Appli
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38	95.6	14.2	954	2	US-08-315-695-15 Sequence 15, Appli
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40	94	13.9	2055	2	US-07-842-349-1 Sequence 1, Appli
41	84.6	12.5	941	2	US-08-121-436A-3 Sequence 3, Appli
42	83	12.3	2364	3	US-09-390-234-23 Sequence 23, Appli
43	83	12.3	2364	3	US-09-603-311-23 Sequence 23, Appli
44	82.6	12.2	642	2	US-08-104-445-2 Sequence 2, Appli
45	82.6	12.2	1413	2	US-08-104-445-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-886-765-1
; Sequence 1, Application US/08886765
; Patent No. 5817500
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; APPLICANT: Wagner, Peter
; APPLICANT: Mullertz, Anette
; APPLICANT: Knap, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5817500 No. 5817500disk of No. 5817500th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Thermomyces lanuginosus
; STRAIN: DSM 4109
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..705

US-08-886-765-1

Query Match 100.0%; Score 675; DB 2; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.5e-179;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCTCGGCTTTACCCCGCTGCTTGGCGGCTTAGCCCGGACTGGGGCCCTGGCCTTC 60
    |||||||
Db 31 ATGCTCGGCTTTACCCCGCTGCTTGGCGGCTTAGCCCGGACTGGGGCCCTGGCCTTC 90

QY 61 CCGGCAAGGAATGCCACGAGCTCGAAAAGCAGACAACCCCACTCGGAGGGCTGG 120
    |||||||
Db 91 CCGGCAAGGAATGCCACGAGCTCGAAAAGCAGACAACCCCACTCGGAGGGCTGG 150

QY 121 CACGATGGTTATTACTATTCCTGGTGAGTGACCGGTGAGCGGACCGCATACCAAC 180
    |||||||
Db 151 CACGATGGTTATTACTATTCCTGGTGAGTGACCGGTGAGCGGACCGCATACCAAC 210

QY 181 CTGGAAGGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACTCGTGGTGAAG 240
    |||||||
Db 211 CTGGAAGGGCGGCACCTACGAGATCAGCTGGGGAGATGGCGGTAACTCGTGGTGAAG 270

QY 241 GGCTGGAACCCCGGCTGAACGCAAGACCATTCCACTTTGAGGGGTGTTACAGCCAAAC 300
    |||||||
Db 271 GGCTGGAACCCCGGCTGAACGCAAGACCATTCCACTTTGAGGGGTGTTACAGCCAAAC 330

QY 301 GGCAACAGCTACCTTGCGGTTCAGCTGGTGGACCCGCAACCCGCTGTCGAGTTATCATC 360
    |||||||
Db 331 GGCAACAGCTACCTTGCGGTTCAGCTGGTGGACCCGCAACCCGCTGTCGAGTTATCATC 390

QY 361 GTCGAGAACTTTGGCACCTATGATCCTTCCCGGTCTACCGATCTAGGAATGTGAG 420
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QY 481 GGCACCCAAACCTTGCACCAATACTGCTGGTCCGCCAGAGCAAGCGCACAGCGGTACC 540
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Db 511 GGCACCCAAACCTTGCACCAATACTGCTGGTCCGCCAGAGCAAGCGCACAGCGGTACC 570

QY 541 GTCCAGACGGGCTGCCACTTGCAGCGCTGGGCTCGCGTGGTTGATGTCACGCTGAC 600
    |||||||
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QY 601 CACTACTACAGATCGTTGCAACGAGGGCTACTTCAAGCAGCGGCTATGCTCGCATCAC 660
    |||||||
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QY 661 GTTGTGACGTGGGC 675
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Db 691 GTTGTGACGTGGGC 705
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RESULT 2

US-09-115-660-1

; Sequence 1, Application US/09115660

; Patent No. 6245546

; GENERAL INFORMATION:

; APPLICANT: Hansen, Peter Kamp

; APPLICANT: Wagner, Peter

; APPLICANT: Muller, Anette

; APPLICANT: Knap, Inge Helmer

; TITLE OF INVENTION: Animal Feed Additives

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 62455460 No. 6245546disk of No. 6245546th America, Inc.

; STREET: 405 Lexington Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10174

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/115,660

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/886,765

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J

; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 4324.204-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 983 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Thermomyces lanuginosus

; STRAIN: DSM 4109

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 31..705

; US-09-115-660-1

Query Match 100.0%; Score 675; DB 3; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.5e-179;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCTCGGCTTTACCCCGCTGCTTGGCGGCTTAGCCCGGACTGGGGCCCTGGCCTTC 60
    |||||||
Db 31 ATGCTCGGCTTTACCCCGCTGCTTGGCGGCTTAGCCCGGACTGGGGCCCTGGCCTTC 90

QY 61 CCGGCAAGGAATGCCACGAGCTCGAAAAGCAGACAACCCCACTCGGAGGGCTGG 120
    |||||||
Db 91 CCGGCAAGGAATGCCACGAGCTCGAAAAGCAGACAACCCCACTCGGAGGGCTGG 150

QY 121 CACGATGGTTATTACTATTCCTGGTGAGTGACCGGTGAGCGGACCGCATACCAAC 180
    |||||||
Db 151 CACGATGGTTATTACTATTCCTGGTGAGTGACCGGTGAGCGGACCGCATACCAAC 210

QY 181 CTGGAAGGGCGGCACCTACGAGATCAGCTGGGAGATGGCGGTAACTCGTGGTGAAG 240
    |||||||
Db 211 CTGGAAGGGCGGCACCTACGAGATCAGCTGGGAGATGGCGGTAACTCGTGGTGAAG 270

QY 241 GGCTGGAACCCCGGCTGAACGCAAGAGCCATCCACTTTGAGGGGTGTTACAGCCAAAC 300
    |||||||
Db 271 GGCTGGAACCCCGGCTGAACGCAAGAGCCATCCACTTTGAGGGGTGTTACAGCCAAAC 330

QY 301 GGCAACAGCTACCTTGCGGTTCAGCTGGTGGACCCGCAACCCGCTGTCGAGTTATCATC 360
    |||||||
Db 331 GGCAACAGCTACCTTGCGGTTCAGCTGGTGGACCCGCAACCCGCTGTCGAGTTATCATC 390

QY 361 GTCGAGAACTTTGGCACCTATGATCCTTCCCGGTCTACCGATCTAGGAATGTGAG 420
    |||||||
Db 391 GTCGAGAACTTTGGCACCTATGATCCTTCCCGGTCTACCGATCTAGGAATGTGAG 450

QY 421 TGGGACGGTAGCATCTATCGACTCGGCAAGACCACCTCGGTCACGCACTTAGCATCGAC 480
    |||||||
Db 451 TGGGACGGTAGCATCTATCGACTCGGCAAGACCACCTCGGTCACGCACTTAGCATCGAC 510

QY 481 GGCACCCAAACCTTGCACCAATACTGCTGGTCCGCCAGAGCAAGCGCACAGCGGTACC 540
    |||||||
Db 511 GGCACCCAAACCTTGCACCAATACTGCTGGTCCGCCAGAGCAAGCGCACAGCGGTACC 570
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QY      541 GTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTCGCGCTGGTTGAATGTCACGCGTGAC 600
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      |||||||

QY      601 CACTACTACCATGATCGTTGCACACGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACC 660
      |||||||
Db      631 CACTACTACCATGATCGTTGCACACGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACC 690
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QY      661 GTTGCTGACGTGGGC 675
      |||||||
Db      691 GTTGCTGACGTGGGC 705
      |||||||

RESULT 3
US-08-458-023B-3
; Sequence 3, Application US/08458023B
; Patent No. 5667990
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Yoder, Wendy
; APPLICANT: Takagi, Shinobu
; APPLICANT: Boominathan, Karuppan C.
; TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56679900 No. 5667990disk of No. 5667990th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,023B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowmey Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4086.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1123 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Humicola insolens
; INDIVIDUAL ISOLATE: DSM 6995
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126..806
US-08-458-023B-3

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	Query Match	35.4%	Score 239;	DB 2;	length 1123;	
	Best Local Similarity	64.4%;	Pred. No.	3.2e-57;		
	Matches	391;	Conservative	0;	Mismatches 210;	Indels 6;
	Gaps	2;				
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Db	197	CGTTCTTCGGACACTCGACGGCCCTTCAGGCTTCGACAGGTGAACCCCAACGGCGAGGG	256			

[illegible]

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1  RESULT 4
2  US-08-468-812-1
3  ; Sequence 1, Application US/08468812
4  ; Patent No. 5935836
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Vehmaamer, Jari
7  ; APPLICANT: M ntyl, Arja
8  ; APPLICANT: Fagerstr m, Richard
9  ; APPLICANT: Lantto, Raija
10 ; APPLICANT: Paloheimo, Marja
11 ; APPLICANT: Suominen, Pirkko
12 ; APPLICANT: Lahtinen, Tarja
13 ; APPLICANT: Kristo, Paula
14 ; TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
15 ; TITLE OF INVENTION: of Use
16 ; NUMBER OF SEQUENCES: 25
17 ; CORRESPONDENCE ADDRESS:
18 ; ADDRESSEE: STERNE, KESSLER, GOLSTEIN & FOX
19 ; STREET: 1100 New York Ave., N.W.
20 ; CITY: Washington
21 ; STATE: D.C.
22 ; COUNTRY: U.S.A.
23 ; ZIP: 20005
24 ; COMPUTER READABLE FORM:
25 ; MEDIUM TYPE: Floppy disk
26 ; COMPUTER: IBM PC compatible
27 ; OPERATING SYSTEM: PC-DOS/MS-DOS
28 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
29 ; CURRENT APPLICATION DATA:
30 ; APPLICATION NUMBER: US/08/468, 812
31 ; FILING DATE: 06-JUN-1995

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-08-468-812-1

Query Match 29.1%; Score 196.2; DB 2; Length 1375;
Best Local Similarity 59.0%; Pred. No. 3.5e-45;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;

QY 5 TCGGCTTACCCCGTTGCCCTTGGCGCTTAGCCCGGACTGGGGCCCTGGCCCTCCCG 64
DB 349 TCGGCTCCGGCGCATCGTACCAAGTGCCTTCCCTGGCACTGCCATCGCCGTCGCC 408
QY 65 CAGGAATGCCACGAGCTCGAAAAAGCAGACAAACCCCACTCGGAGGGCTGGCAGC 124
DB 409 TGCTGCCGGCAGCGCCGACGCGACCAACCATCACCAAGAACGAGCCGGTACGACA 468
QY 125 ATGTTATTACTATTCTGTGTGAGTGAAGGTGAGCGGAGCCGACGTAACCACTGG 184
DB 469 ACGGCTACTTACTCTGTTCTGACCGACGCGCCCGGACCGTCTCCATGACCTCCACT 528
QY 185 AAGCGGCACTACGAGATCAGTGGGAGATGCGGTAACCTCGTGGTGAAGGGCT 244
DB 529 CGGGCGGAGTACAGACACCTCGTGGGGAACACCGGAACTCGTCGCGGCAAGGGCT 588
QY 245 GGAACCCCGGCTGAACGAGACCATCACTTTGAGGGTGTTCACGACCAACGGCA 304
DB 589 GGTCCACCGG---GGAGCGGCGGACCGTGAACCTACAACGCTCTTCAACCCGTCGGTA 645
QY 305 ACAGCTACCTTGGGCTTACGCGTTGACCCGCAACCCGCTGGTCAAGTATTACATCGTCG 364
DB 646 ACGGCTACTCAAGCTCTACGCGTGAACGAGAACCCGCTCGTGAAGTACTACATCGTCG 705
QY 365 AGAATTGGCACTATGATCCTTCTCCGGTCTACCGATCTAGGAAGTGTGAGTGGC 424
DB 706 AGAGCTGGGCACTTACCGGCCACCGGCG-----ACCTAAGGGGACCGTCAACCG 759
QY 425 ACGTAGCATCTATCGACTCGCAAGCAACTCGCGTCAAGCAACTAGCATCGAGGCA 484
DB 760 ACGGGGAAAGTACGACATCTACGAGACCTGGCGGTACAAAGCGCGTCCATCGAGGCA 819
QY 485 CCCAAACCTTGCACCATATCTGTGGTCCCGCAGGACAGGCAACGCGGTACCGTCC 544
DB 820 CCGGACCTTCCAGCAGTCTTGAGCGCTCCGGCAGCAGAGCGGACGACCATCA 879
QY 545 AGACGGGCTGCCACTTCAGCGCGCTGGGCTCGCGCTGTTGAATGTCAACGCTGACCACT 604
DB 880 CCATCGGCAACCACTTCAGACGCTGGGCGCGCGCGGATGA---CCTGGGAGGCAAGC 936
QY 605 ACTACAGATCGTTGCAACGAGGGGCTACTTACGACGCGGCTATGCTCGCATCACCGTTG 664

DB 937 ACTACAGATCATGGCGACGAGGGCTACCAAGACGCGGTAGCTCCACCGTCTCCATCA 996
QY 665 CTGACGTGGC 675
DB 997 GCGAGGCTGC 1007

RESULT 5
US-08-590-563-1
Sequence 1, Application US/08590563
Patent No. 6300114

GENERAL INFORMATION:

APPLICANT: M ntyl , Arja
APPLICANT: Vehmaaper , Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 303..1334
US-08-590-563-1

Query Match 29.1%; Score 196.2; DB 3; Length 1375;
Best Local Similarity 59.0%; Pred. No. 3.5e-45;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;

QY 5 TCGGCTTACCCCGCTGCTCCCTTGGCGCTTAGCCGCGACTGGGGCCCTGCTTCCGG 64
 DB 349 TCGGCTTCCGGCGATGTCACAGTGGCTTCCCTTGGCGACTGGCCATCGCCGGTGGC 408
 QY 65 CAGGAATGCCAGGAGCTCGAAAGCGACAGAACCCCACTCGAGGGCTGGCG 124
 DB 409 TGCTGCGCGACGGCCCGACCGGACCAACCATCACCAGAACAGACGGGTACGACA 468
 QY 125 ATGTTATTACTATTCTCTGGTGAAGTGAAGCGGACGCAAGTACCAACTGG 184
 DB 469 ACGGCTACTTCTACTCTGTTGACCGACGCGCCCGGACCGTCTCATGACCTCCACT 528
 QY 185 AAGCGGCACTTACAGATCAGTGGGAGATGGCGGTAACTGCTGCTGGAAAGGCT 244
 DB 529 CGGGCGGACGCTACAGCACTCTGCGGGAACACCGGAACCTTCTGCGCGGCAAGGCT 588
 QY 245 GGAACCCCGGCTGAACGCAAGACCATCTTTGAGGGTGTAAACCAACGCGCA 304
 DB 589 GGTCCACCGG--GGAGCGCGGACCGTGAACCTTCAACGCTCTTCAACCGTGGGTA 645
 QY 305 ACAGCTACCTTGGCGTCTACGCTTGAACCGCAACCGCTGCTGAGTATTACATCGTC 364
 DB 646 ACGGCTACCTCAAGCTCTACGCTGAGCAAGAACCGCTGCTGAGTACTACATCGTCG 705
 QY 365 AGAATTGGCACTATGATCTTCTCCGGTGTACTACCATAGAGAACTGTGAGTGG 424
 DB 706 AGAGCTGGGGCACTACCGGCCACCGG--ACCTTCAAGGGCAACCGTACCAACCG 759
 QY 425 ACGGTAGCATCTATCGACTCGGCAAGCACTCGCGTCAACGCACTAGCATGAGCGCA 484
 DB 760 ACGGGGGAACGTACGACATCTACGAGACTGGCGGTACCAACGCGCTTCCATCGAGGCA 819
 QY 485 CCCAAACCTTGCACCAATATCTGCTGCTCGCCGAGAGCAAGCGCAACGCGGTACCGTCC 544
 DB 820 CCGGACCTTCAAGCACTTCTGAGCGCTCGGAGAGCAAGAGCGCAACGCGGACCATCA 879
 QY 545 AGACGGGCTGCACTTGCAGCGCTGGCTCGCGCTGTTGAATGTCAACGTTGACCACT 604
 DB 880 CCATCGGCAACCACTTGCAGCGCTGGCGCGCGCGCATGAA--CCTGGGAGCGCAAG 936
 QY 605 ACTACAGATGCTTGCAGCGAGGGCTTCTACGACGCGGTATGCTCGCATCACCGTGG 664
 DB 937 ACTACAGATGATGCGGAGCGGAGCGGCTTCAAGAGCAGCGGTAGCTCCACGCTTCA 996
 QY 665 CTGACGTGGG 675
 DB 997 GCGAGGGTGGC 1007

RESULT 6
 US-09-770-621-1
 ; Sequence 1, Application US/09770621
 ; Patent No. 6506593
 ; GENERAL INFORMATION:
 ; APPLICANT: M ntyl, Arja
 ; APPLICANT: Vehmaamp, Jari
 ; APPLICANT: Pajerstr m, Richard
 ; APPLICANT: Lantto, Raija
 ; APPLICANT: Paloheimo, Marja
 ; APPLICANT: Suominen, Pirkko
 ; APPLICANT: Lahtinen, Tarja
 ; TITLE OF INVENTION: Production and Secretion of Proteins of
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 ; STREET: 1100 New York Ave., N.W. Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/770,621
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/590,563
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/332,412
 FILING DATE: 31-OCT-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/282,001
 FILING DATE: 29-JUL-1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Bugalsky, Lawrence B.
 REGISTRATION NUMBER: 35,086
 REFERENCE/DOCKET NUMBER: 1050.0340003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1375 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: No. 6506593 Relevant
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 303..1334
 US-09-770-621-1

Query Match 29.1%; Score 196.2; DB 3; Length 1375;
 Best Local Similarity 59.0%; Pred. No. 3.5e-45;
 Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;
 QY 5 TCGGCTTACCCCGCTGCTCCCTTGGCGCTTAGCCGCGACTGGGGCCCTGCTTCCGG 64
 DB 349 TCGGCTTCCGGCGATGTCACAGTGGCTTCCCTTGGCGACTGGCCATCGCCGGTGGC 408
 QY 65 CAGGAATGCCAGGAGCTCGAAAGCGACAGAACCCCACTCGAGGGCTGGCG 124
 DB 409 TGCTGCGCGACGGCCCGACCGGACCAACCATCACCAGAACAGACGGGTACGACA 468
 QY 125 ATGTTATTACTATTCTCTGGTGAAGTGAAGCGGACGCAAGTACCAACTGG 184
 DB 469 ACGGCTACTTCTACTCTGTTGACCGACGCGCCCGGACCGTCTCATGACCTCCACT 528
 QY 185 AAGCGGCACTTACAGATCAGTGGGAGATGGCGGTAACTGCTGCTGGAAAGGCT 244
 DB 529 CGGGCGGACGCTACAGCACTCTGCGGGAACACCGGAACCTTCTGCGCGGCAAGGCT 588
 QY 245 GGAACCCCGGCTGAACGCAAGACCATCTTGAAGGTGTTTACAGCAACGCGCA 304
 DB 589 GGTCCACCGG--GGAGCGCGGACCGTGAACCTTCAACGCTCTTCAACCGTGGGTA 645
 QY 305 ACAGCTACCTTGGCGTCTACGCTTGAACCGCAACCGCTGCTGAGTATTACATCGTC 364
 DB 646 ACGGCTACTTCAAGCTCTACGCTGAGCAAGAACCGCTGCTGAGTACTACATCGTCG 705
 QY 365 AGAATTGGCACTATGATCTTCTCCGGTGTACTACCATAGAGAACTGTGAGTGG 424
 DB 706 AGAGCTGGGGCACTACCGGCCACCGG--ACCTTCAAGGGCAACCGTACCAACCG 759
 QY 425 ACGGTAGCATCTATCGACTCGGCAAGCACTCGCGTCAACGCACTAGCATGAGCGCA 484
 DB 760 ACGGGGGAACGTACGACATCTACGAGACTGGCGGTACCAACGCGCTTCCATCGAGGCA 819

; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 822
; TYPE: DNA
; ORGANISM: TRICHODERMA VIRIDE MC300-1
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (14)..(112)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)..(112)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (113)..(809)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)..(285)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (286)..(412)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (413)..(809)
; US-09-254-733-8

Query Match 28.8%; Score 194.2; DB 3; Length 822;
Best Local Similarity 69.0%; Pred. No. 1.1e-44;
Matches 281; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 256 CTGAACGCAAGGCATCCACTTTGAGGGTTTACCAGCCAAACGGCAACAGCTACTT 315
DB 402 CTGAAACCAAGGTCATCACTTCTCGGCACTACAAACCCCAACGGCAACAGCTACTT 461
QY 316 GCGGTCTACGGTTGACCCGCAACCCGCTGCTGAGTATTACATCGTCGAGAACTTGGC 375
DB 462 TCCGTGTACGGTGGTGGCGCAACCCCTGATGAGTACTACATCGTCGAGAACTTGGC 521
QY 376 ACCTATGATCCTTCTCCGGTGTACCGATCTAGAACTGTGAGTGGAGCGTAGCATC 435
DB 522 ACCTACAACCCGTCACCGGCGCAACGAGTGGGCGAGTGAAGTCGGACGGCAGCGTC 581
QY 436 TATCGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATCGACGGCAACCAACTTC 495
DB 582 TAGCATCTACCGCAACGAGCGCGTCAACCAAGCGTCCATCGAGGGCACTCCACTTT 641
QY 496 GACCAATACTGGTCGGTCCGGCAAGGACCAAGCGGACCGGTCACGAGCGGCTGC 555
DB 642 TACCACTACTGGTCGGTCCGGCAACCGCTCCAGCGGCTCGTCAACACGGCGAAC 701
QY 556 CACTTCGACGCTGGGCTCGCGTGTGATGTCACGCGTGAACCACTACTACGATC 615
DB 702 CACTTCACGCGTGGGCTCGCACGCGCTGACGCT--GGGCAACATGATTACCAGATT 758
QY 616 GTTGCAACGAGGCTACTTCAGCAGCGGCTATGCTGCATCAACGCT 662
DB 759 GTTGCGGTGAGGCTACTTAGCTCTGGCTCTGCTTCATCAACGCT 805

RESULT 9
US-08-121-436A-1
; Sequence 1, Application US/08121436A
; Patent No. 5837515
; GENERAL INFORMATION:
; APPLICANT: Suominen, Pirkko
; APPLICANT: Nevalainen, Helena
; APPLICANT: Saarelainen, Ritva
; APPLICANT: Paloheimo, Marja
; APPLICANT: Lahtinen, Tarja
; APPLICANT: Ragerstr m, Richard
; TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
; TITLE OF INVENTION: for Their Production
; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:
; ADDRESS: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,436A
; FILING DATE: 16-SEP-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,478
; FILING DATE: 18-JUN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI93/00221
; FILING DATE: 24-MAY-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,893
; FILING DATE: 29-MAY-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/524,308
; FILING DATE: 16-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbal, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.008000C
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(176..448, 557..952)
; US-08-121-436A-1

Query Match 28.1%; Score 190; DB 2; Length 1015;
Best Local Similarity 68.5%; Pred. No. 1.7e-43;
Matches 278; Conservative 0; Mismatches 125; Indels 3; Gaps 1;

QY 257 TGAACGCAAGGCATCCACTTTGAGGGTTTACCAGCCAAACGGCAACAGCTACTTG 316
DB 546 TAAAAAAGGTCATCACTTCTCGGGAAGCTACAAACCCCAACGGCAACAGCTACTTCT 605
QY 317 CGGTCTACGGTTGACCCGCAACCCGCTGCTGAGTATTACATCGTCGAGAACTTGGCA 376
DB 606 CCGTGTACGGCTGGTCCCGCAACCCCTGATGAGTACTACATCGTCGAGAACTTGGCA 665
QY 377 CCTATGATCCTTCTCCGGTGTACCGATCTAGGAAGTGTGAGTGGACGGTAGCATCT 436
DB 666 CCTACAACCGTCCACGCGGCGCAACAGCTGGGCGAGGTACCTCCGACGGCAGCGTCT 725
QY 437 ATGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATCGACGGCAACCAACTTCG 496
DB 726 ACGACATTTACCGCAGCAGCGGCTCAACAGCGCTCATCATCGGACCGCACTTTT 785
QY 497 ACCAATACTGGTGGTCCGCCAGGCAAGCGCACCGGCTAACCGTCCAGACGGGCTGCC 556
DB 786 ACCAGTACTGGTCCGTCGCGGCAACCAACCGCTCGAGCGGCTCCGTCAACACGGGAAC 845
QY 557 ACTTCAGCGCTGGGCTCGCGCTGTTGATGTCAACGGTGAACCACTACTACAGATCG 616
DB 846 ACTTCAACGCGTGGGCTCAGCAAGGCTGACGCT--CGGACGATGATTACAGATTG 902

QY 617 TTGCAACGAGGGCTACTTCAGCAGCGGCTATGCTCGCATCACCGT 662
Db 903 TTGCCGTGAGGGTACTTACGCTCTGGCTCTGCTTCATCACCGT 948

RESULT 10

US-08-768-373-1
; Sequence 1, Application US/08768373
; Patent No. 6228629
; GENERAL INFORMATION:
; APPLICANT: PALOHEIMO, MARJA
; APPLICANT: HAKOLA, SATU
; APPLICANT: M NTYL, ARJA
; APPLICANT: VEHMANPER, JARI
; APPLICANT: LANTTO, RAIJA
; APPLICANT: LAHTINEN, TARJA
; APPLICANT: PAGERSTR M, RICHARD
; APPLICANT: SUOMINEN, PIRKO
; TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/768,373
; FILING DATE: 17-DEC-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,746
; FILING DATE: 18-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,839
; FILING DATE: 28-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CIMBALA, MICHELE A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.054003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Chaetomium thermophilum
; STRAIN: CBS730.95
; FEATURE:
; NAME/KEY: exon
; LOCATION: 195..423
; OTHER INFORMATION: /product= "XLNA"
; NAME/KEY: exon
; LOCATION: 483..1039
; OTHER INFORMATION: /product= "XLNA"
; US-08-768-373-1

Query Match 26.9%; Score 181.8; DB 3; Length 1281;
Best Local Similarity 65.4%; Pred. No. 3,8e-41;
Matches 283; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

QY 237 AAAGGCTGGAACCCCGGCTGAACGGAAGCCATCCATTGAGGGTGTTCACAGCC 296
Db 478 AACAGGCTGAACCCCGGTAACCGATTAACCGTGTATCACTACACAGCCGACTACAGACC 537
QY 297 AAACGGCAACAGCTACCTTGGGCTCTACGGTTGACCCGCAACCCGCTGGTCAATTA 356
Db 538 CAACGGCAACTCTACCTCGCGCTCTACGGCTGACCCGCAACCCGCTGATGAGTACTA 597
QY 357 CATCGTCGAGAACTTTGGACCTATGATCCTTCGCGTCTACCGATCTAGAACTGT 416
Db 598 CGTGTGAGAGCTTCGGCACTACGACCGGTGACGGGGCGCACCCGATGGCAGCGT 657
QY 417 CGAGTGCACGGTAGCATCTATCGACTCGGCAAGACCACTGGCGTCAACGCACTAGCAT 476
Db 658 GACCACGACGGCGGCACTACATCTACCGCAGCAGCGGCTCAACGCGCCCTCCAT 717
QY 477 CGACGGCAACCAACCTTCGACCAATACTGTCGGTCCGCCAGGACAGCGCAACGCGG 536
Db 718 CGAGGGCAACCAACCTTCTACCAATACTGTCGTGTGCGCACTCCAAAGCGCACCGCGG 777
QY 537 TACGTCGACGAGCGGCTGCCACTTGCAGCGCTGGGCTGGCGCTGTTGAATGTCAACGG 596
Db 778 TACTGTACCATGCGCAACCACTTCAATGCTTGGAGCAGGCTGTCTGACGT--GGG 834
QY 597 TGACCACTACTACAGATCGTTGCAACGAGGGCTACTTCAGCAGCGGCTATGCTGCAT 656
Db 835 TTCCCATGATATCAGATGTGCTACTGAGGGTTACTCTGTCGCTCGGCGACTGT 894
QY 657 CACGTTGCTGAC 669
Db 895 CAATGTGCGCGC 907

RESULT 11

US-09-849-242A-1
; Sequence 1, Application US/09849242A
; Patent No. 6635464
; GENERAL INFORMATION:
; APPLICANT: PALOHEIMO, MARJA
; APPLICANT: HAKOLA, SATU
; APPLICANT: MONTYLO, ARJA
; APPLICANT: VEHMANPERO, JARI
; APPLICANT: LANTTO, RAIJA
; APPLICANT: LAHTINEN, TARJA
; APPLICANT: PAGERSTRM, RICHARD
; APPLICANT: SUOMINEN, PIRKO
; TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
; AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/849,242A
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/768,373
; FILING DATE: 17-DEC-1996
; APPLICATION NUMBER: US 60/008,746
; FILING DATE: 18-DEC-1995
; APPLICATION NUMBER: US 60/020,839
; FILING DATE: 28-JUN-1996

ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1716.0540004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: exon
LOCATION: 195..423
OTHER INFORMATION: /product= "XLNA"
FEATURE:
NAME/KEY: exon
LOCATION: 483..1039
OTHER INFORMATION: /product= "XLNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-849-242A-1

Query Match 26.9%; Score 181.8; DB 3; Length 1281;
Best Local Similarity 65.4%; Pred. No. 3.8e-41;
Matches 283; Conservative 0; Mismatches 147; Indels 3; Gaps 1;
QY 237 AAAGGCTGGAACCCCGCCTGAACGCAAGAGCCATCCACTTTGAGGGTTTACCAGCC 296
DB 478 AACAGGCTGGAACCCCGCTACCGATTAACCGTGTATCACTACACAGCCGACTACAGACC 537
QY 297 AAACGGCAACGCTACCTTGGCTCTACGGTTGACCGCAACCCGCTGTCAGTATTA 356
DB 538 CAACGGCACTCTACCTCGCCGCTTACGGCTGACCGCAACCCGCTGATGAGTACTA 597
QY 357 CATGCTGAGAACTTTGCACTATGATCCTTCCGCTGCTACCGATCTAGGAATGT 416
DB 598 CGTGTGAGAGCTTCGCACTTACGACCCGTCGACGGGGCCACCCGATGGCAGCGT 657
QY 417 CGAGTGCACGCTAGCATCTATGCACTCGGCAAGACCACTCGGCTCAACGCACTAGCAT 476
DB 658 GACCAACCAACGGCGGCACTTACATCATCTACCGACGCAAGCGGCTCAACGCGCTCCAT 717
QY 477 CGACGGCAACCAACCTTCGACCAATATGTCGGTCCGCCAGGACCAAGCGCAGCGG 536
DB 718 CGAGGGCAACCAACCTTCTACCAATATGTCGTGTGCGCACTCCAAAGCGCACCGGCGG 777
QY 537 TACCGTCCAGACGGGCTGCCACTTCGACGCGCTGGGCTGCGCTGTTGAATGTCAACGG 596
DB 778 TACTGTTACCATGGCCCAACCACTTCAATGCTTGAGGCAAGGCTGCTGCAAGT--GGG 834
QY 597 TGACCACTACTACAGATGTTGCAACGAGGGCTACTTCAAGACGCGTATGCTCGCAT 656
DB 835 TTCCCATGATATCAGATTGTGCTACTGAGGGTACTACTGCTGCTGCGCGCACTGT 894
QY 657 CACGTTGCTGAC 669
DB 895 CAATGTTGGCGGC 907

RESULT 12
US-07-744-570B-1
Sequence 1, Application US/07744570B
Patent No. 5202249
GENERAL INFORMATION:
APPLICANT: Kluempfel, D.
APPLICANT: Morosoff, R.
APPLICANT: Shareck, F.

TITLE OF INVENTION: Xylanase for Bioleaching
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael J. Bradley
STREET: 1200 South 47th Street
STREET: Box Number 4023
CITY: Richmond
STATE: California
COUNTRY: United States
ZIP: 94804-0023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44MB storage
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,570B
FILING DATE: 19910813
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single strand
TOPOLOGY: Circular
US-07-744-570B-1

Query Match 24.9%; Score 168.4; DB 2; Length 675;
Best Local Similarity 60.0%; Pred. No. 1.7e-37;
Matches 343; Conservative 0; Mismatches 211; Indels 18; Gaps 3;
QY 97 ACAACCCCACTCGAGGCTGGCAGATGTTACTATTCTGTTGAGTACGCT 156
DB 34 ACCATCACCAACCAACGAGCCGACCGAGCGCATGTACTACTGTTGAGCCGACGCG 93
QY 157 GAGCGCAGGCCACGTACCAACCTGGAAGGCGGCACTACAGATCAGCTGGGAGAT 216
DB 94 GCGGCTCCGCTCTCCATGACGCTCAACGGTGGCGGCACTATAGCACCCAGTGAACCAAC 153
QY 217 GCGGTAACCTCGTCCGTGGAAGGGCTGGAACCCCGGCTGAACGCAAGACCATCCAC 276
DB 154 TGCGCAACTTGTGCGCGGCAAGGGCTGAGCACCGG-----CGACGGCAACGTCCGC 207
QY 277 TTGAGGGTGTTCACCAAGCAACGCAACGCTTACCTGCGTCTACGGTTGACCCGCG 336
DB 208 TACAACGGCTACTTCAACCCGCTCGCAACGGCTACGGCTGCTACGGCTGACCTCG 267
QY 337 AACCGCTGTGAGTATATCATCGTGAAGACTTTGGCACCTATGATCCTTCCGCT 396
DB 268 AACCCGCTGTGAGTACTATCATCGTGCACACTGGGGCAGTTACCGGCCAAC----- 321
QY 397 GCTACCGATCTAGGAAGTGTGAGTGCAGCGGTAGCATCTATGATCGGCAAGACCACT 456
DB 322 GGTAGGTACAAAGGGCACCGTCTCCAGCGACGGAGGCACTTACGACATCTTACGACGACC 381
QY 457 CGGCTCAACGCACTAGCATGACGGCAACCAACCTTCGACCAATATGTTGGTCCGCG 516
DB 382 CGGTCAACGCCCCCTCGGTGGAAGGCAACCAAGACTTCCAGCAGTACTGAGTGTCCGG 441
QY 517 CAGACAAGCGCACAG-----CGTACCGTCCAGACGGGCTGCGCACTTGCAGCGCTGG 570
DB 442 CAGTCGAAGGTGACCAAGTGGCTCCGGCACCATCAACCGGCAACCACTTGCAGCGCTGG 501
QY 571 GCTCGGCTGTTGAATGTCAACGGTGACCACTACTACAGATGTTGCAACGAGGCGC 630
DB 502 GCGGCGCGGCGCATGACATGGGCCAGTTTCAAGTACTACATGATCATGGCCACCGAGGCGC 561
QY 631 TACTTACGACGCGGTATGCTCGATCACCGT 662
DB 562 TATCAGAGCAGTGAAGCTCGAATCATCACCGT 593

RESULT 13

US-08-507-431-5
Sequence 5, Application US/08507431
Patent No. 5693518
GENERAL INFORMATION:
APPLICANT: Kofod, Lene V.
APPLICANT: Kaupinen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: Si, Joan Q.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56935180 No. 5693518disk of No. 5693518th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,431
FILING DATE: 15-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,800
FILING DATE: 25-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3954.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-08-507-431-5

Query Match 24.4%; Score 164.6; DB 2; Length 927;
Best local similarity 58.3%; Pred. No. 2.3e-36;
Matches 346; Conservative 0; Mismatches 239; Indels 8; Gaps 3;

QY 77 CGAGCTCGAAGGCGAGACAGACACCCCACTCGAGGGGTGGCAGCATGTTATTACT 136
DB 134 CTGCCCTTGTCTGGGGCTGCTGAGCTGGAGCTCCACTGGCTACTGGAACGGCTATTACTATA 193
QY 137 ATTCCTGTGTGAGTACGCGTGAGCGGACCGACGTAACCACTGGAAGCGGACCT 196
DB 194 GCTTCTGACCGATGGCGCAAGCGGCGATGTTGATATACAGCAACGGCGCGGGGGGTCT 253
QY 197 ACAGATCACTGTGGGAGATGGCGGTAACTCTGCTGTGAAAGGGCTGGAACCCGCC 256
DB 254 ACAGCGTACCTGTGATCGGCTCGAATTCTGCTGTGAAAGGGCTGGAACCTGG-A 312
QY 257 TGAACGCAAGACCATCCACTTTGAGGGTGTATTACAGCC---AAACGCAACAGCTAC 312

DB 313 AGTCTCATGACATTAAGTACTCCGGCTCTCGAACACAGACAGAAATAGCAACAGTAC 372
QY 313 CTTCGGGTACCGGTTGACCCCGAACCCCGCTGTCGAGTATTACATCTCGAGAATT 372
DB 373 CTCTCCGTCTACCGGCTGAGACCAACCGGTCTCTGTCGAGTACTATATCTGAGAGTAC 432
QY 373 GGCACCTATGATCTTCTCCGCTCGGTCTACCGATCTAGAACTGTGAGTCCGACGTAAGC 432
DB 433 GGGAGTACAAACCCCGGCTCAGCTGGACATTAACAAGGCTCGGTCTACTCCGACGATCG 492
QY 433 ATCTATGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATCGACGCAACCCAAACC 492
DB 493 ACATACAATATCTACAGGCGACCCCGACCAACGCCCCCTCCATCCAGGCAAGGCACT 552
QY 493 TTGACCAATATCTGTGCTCGGTCGCCAGACAGCAAGCGGACCGGTACCGTCCAGACGGGC 552
DB 553 TTACAGCAGTACTGCTTCATTCGCCAGACAAAGCGCGTCCGGTACCGTGAAGAGTCC 612
QY 553 TGCCACTTCGACGCGCTCGGCTCGCGCTGCTTGAATGTCAACGCTGACCACTACTACAG 612
DB 613 AACCATTTCAATGCTTGGGCGAAGCTGGGAATGAATCT--GGGCAAGCAACTATCAG 669
QY 613 ATCGTTCAACGAGGCTACTTACAGACGCGCTATGCTCGCATCACCCTTGC 665
DB 670 ATCGTCTACTGAAGGCTACTACTCGTCTGGTCTGCGTCCATTACGGTTGC 722

RESULT 14
US-08-902-655A-5
Sequence 5, Application US/08902655A
Patent No. 5885819
GENERAL INFORMATION:
APPLICANT: Kofod, Lene V.
APPLICANT: Kaupinen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: Si, Joan Q.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
TITLE OF INVENTION: ASPERGILLUS ACULEATUS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58858190 No. 5885819disk of No. 5885819th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,655A
FILING DATE: 30-July-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl T.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-08-902-655A-5

Query Match 24.4%; Score 164.6; DB 2; Length 927;
Best Local Similarity 58.3%; Pred. No. 2.3e-36;
Matches 346; Conservative 0; Mismatches 239; Indels 8; Gaps 3;

QY 77 CGGAGCTGAAAAAGCAGACAAACCCCACTCGAGGCTGGCAGATGTTATTACT 136
DB 134 CTGCCCTTGCTGGCGCTCGACTGGAGCTCCACTGGCTACTCGAACGGCTATTACTATA 193
QY 137 ATTCCTGTGAGTGAAGCGGTGAGCGCAGGCAAGTACCACTGGAAGCGGCACCT 196
DB 194 GCTTCTGACCGATGGCGCAAGCGCGATGTTGAATACAGCAACGCGCGGGGGCTCT 253
QY 197 ACGAGATCAGCTGGGAGATGGCGGTAACCTCGCTGGAAGGGCTGGAACCCGGCC 256
DB 254 ACAGCGTACCTGCTCATCGCGCTCGAATTCTCGCTGGAAGGGCTGGAACCTGG-A 312
QY 257 TGAACGCAAGAGCCATCCACTTTGAGGGTTTACCAGCC---AAACGGCAACAGCTAC 312
DB 313 AGTCTCATGACATTACGTAATCCGGCTCTGAGCAGACAGGAATAGCAACAGCTAC 372
QY 313 CTTCGGCTCTACGGTGTGACCCCGCAACCGCTGTGCTGATTTACATGTCGAACTTT 372
DB 373 CTCTCCGCTTACGGCTGACCAACCGGCTCTCTCGTCACTATATCTCGAGGAGCTAC 432
QY 373 GGCACCTATGATCCTTCTCCGCTGCTACCGATCTAGGAATGTGAGTGCGAGGTAGC 432
DB 433 GGGAGTACAAACCCGGCTCAGCTGACACTTACAAAGGCTCGGTCTACTCCGACGATCG 492
QY 433 ATCTATGACTCGGCAAGACCACTCGGCTCAACGCACTAGCATCGACGGCAACCAACC 492
DB 493 ACATACATATCTACACGGCGACCCGCAACCAACGCCCCCTCCATCCAGGGCAGGCCACT 552
QY 493 TTGCACCAATACTGTCGCTCCGCCAGGACAAAGCGCACCGGTACCGTCCAGACGGGC 552
DB 553 TTCAACGCACTAGTGTTCATTGCGCCAGACAAAGCGCGTGGGTACCGTACGACTGCC 612
QY 553 TGCCACTTCGACGCGCTGGGCTCGCGCTGTTGAATGTCAACGCTGACCACTACTACAG 612
DB 613 AACCATTTCAATGCTGGCGGAAGCTGGGAATGAATCT---GGGACGCACACTATCAG 669
QY 613 ATGCTTGAACGAGGGCTACTTCAAGCAGCGGTATGCTGCATCACCCTTGC 665
DB 670 ATGCTGCTACTGAAGGCTACTACTGCTGCTGCTGCTGCATTAACGCTTGC 722

RESULT 15

US-09-116-622-5
Sequence 5, Application US/09116622
Patent No. 6080567
GENERAL INFORMATION:
APPLICANT: Kofod, Lene V.
APPLICANT: Kaupinen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heidt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: St, Joan O.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESS: No. 60805670 No. 6080567disk of No. 6080567th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor

CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,622
FILING DATE: 16-July-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Agrie, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(31..723, 727..849, 853..900, 904..927)
US-09-116-622-5

Query Match 24.4%; Score 164.6; DB 3; Length 927;
Best Local Similarity 58.3%; Pred. No. 2.3e-36;
Matches 346; Conservative 0; Mismatches 239; Indels 8; Gaps 3;

QY 77 CGGAGCTGAAAAAGCAGACAAACCCCACTCGAGGCTGGCAGATGTTATTACT 136
DB 134 CTGCCCTTGCTGGCGCTCGACTGGAGCTCCACTGGCTACTCGAACGGCTATTACTATA 193
QY 137 ATTCCTGTGAGTGAAGCGGTGAGCGCAGGCAAGTACCACTGGAAGCGGCACCT 196
DB 194 GCTTCTGACCGATGGCGCAAGCGCGATGTTGAATACAGCAACGCGCGGGGGCTCT 253
QY 197 ACGATCAGCTGGGGAATGGCGGTAACCTCGTCCGTGGAAGGGCTGGAACCCCGGCC 256
DB 254 ACAGCGTACCTGCTCATGCGCCCTCGAATCTCGTGGGTGGAAGGGCTGGAACCCCTGG-A 312
QY 257 TGAACGCAAGAGCCATCCATTGAGGGTGTTCACAGCC---AAACGGCAACAGCTAC 312
DB 313 AGTCTCATGACATTACGTAATCCGGCTCTCGTCAAGCAGACAGGAATAGCAACAGCTAC 372
QY 313 CTTCGGCTCTACGGTGTGACCCCGCAACCGCTGTGAGTATTACATCGTGAAGACTTT 372
DB 373 CTCTCCGCTTACGGCTGACCAACCGTCTCTCGTCACTATATCTCGAGGAGCTAC 432
QY 373 GGCACCTATGATCCTTCTCCGCTGCTACCGATCTAGGAATGTGAGTGCGACGGTAGC 432
DB 433 GGGAGTACAAACCCGGCTCAGCTGGCACTTACAAAGGCTCGGTCTACTCCGACGATCG 492
QY 433 ATCTATGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATCGACGCAACCAACC 492
DB 493 ACATACATATCTACACGGCGACCCGCAACCAACGCCCCCTCCATCCAGGGCAGGCCACT 552
QY 493 TTGCACCAATACTGTCGCTCCGCCAGGACAAAGCGCACCGGTACCGTCCAGACGGGC 552
DB 553 TTCAACGCACTAGTGTTCATTGCGCCAGACAAAGCGCGTGGCGGTACCGTGAAGACTGCC 612
QY 553 TGCCACTTCGACGCGCTGGGCTCGCGCTGTTGAATGTCAACGCTGACCACTACTACAG 612
DB 613 AACCATTTCAATGCTGGCGGAAGCTGGGAATGAATCT---GGGACGCACACTATCAG 669
QY 613 ATGCTTGAACGAGGGCTACTTCAAGCAGCGGTATGCTGCATCACCCTTGC 665

Db 670 ATCGTCCTACTGAAGGCTACTCGTCTGGGCTCTGCGCTCCATTACGGTTC 722

Search completed: February 11, 2006, 20:45:51
Job time : 149.191 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:35:33 ; Search time 702.684 Seconds
(without alignments)
7943.586 Million cell updates/sec

Title: US-09-467-368-1_COPY_31_705

Perfect score: 675

Sequence: 1 ATGGTCGGCTTACCCCGT.....TCACCGTGTGCTGACGTGGC 675

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	100.0	983	3	US-09-467-368-1 Sequence 1, Appli
2	582	86.2	588	6	US-10-237-386-9 Sequence 9, Appli
3	371.6	55.1	678	3	US-09-803-454-3 Sequence 3, Appli
4	257.2	38.1	850	8	US-10-425-115-177283 Sequence 177283,
5	246.6	36.5	749	8	US-10-425-115-82922 Sequence 82922, A
6	240.4	35.6	818	8	US-10-425-115-37173 Sequence 37173, A
7	224.6	33.3	666	5	US-10-213-990-65 Sequence 65, Appli
8	221.6	32.8	705	5	US-10-213-990-68 Sequence 68, Appli
9	196.2	29.1	1375	3	US-09-770-621-1 Sequence 1, Appli
10	196.2	29.1	1375	6	US-10-286-993-1 Sequence 1, Appli
11	189.2	28.0	739	5	US-10-213-990-67 Sequence 67, Appli
12	181.2	26.8	712	5	US-10-213-990-64 Sequence 64, Appli
13	165.4	24.5	942	5	US-10-213-990-71 Sequence 71, Appli
14	155.2	23.0	978	10	US-11-018-645-21 Sequence 21, Appli
15	147.2	21.8	1002	5	US-10-213-990-70 Sequence 70, Appli
16	146.4	21.7	596	6	US-10-307-441-39 Sequence 39, Appli
17	134.6	19.9	2225	3	US-09-790-070A-8 Sequence 8, Appli
18	124	18.4	2898	5	US-10-299-393-1 Sequence 1, Appli
19	124	18.4	2898	10	US-11-154-793-1 Sequence 1, Appli
20	119.2	17.7	557	3	US-09-970-616-1 Sequence 1, Appli
21	119.2	17.7	557	9	US-10-765-716-1 Sequence 1, Appli
22	119.2	17.7	642	3	US-09-149-310-31 Sequence 31, Appli
23	118	17.5	594	10	US-11-018-645-17 Sequence 17, Appli

24	103.6	15.3	2054	6	US-10-419-969-5	Sequence 5, Appli
25	101.8	15.1	643	6	US-10-340-860A-39	Sequence 39, Appli
26	94.2	14.0	561	10	US-11-018-645-13	Sequence 13, Appli
27	90.2	13.4	561	10	US-11-018-645-15	Sequence 15, Appli
28	89.4	13.2	972	10	US-11-018-645-19	Sequence 19, Appli
29	83.6	12.4	394	8	US-10-425-115-48309	Sequence 48309, A
30	82.6	12.2	642	9	US-10-626-583-4	Sequence 4, Appli
31	82.6	12.2	642	9	US-10-626-724-4	Sequence 4, Appli
32	80.8	12.0	539	7	US-10-437-963-15625	Sequence 15625, A
33	78.4	11.6	591	10	US-11-018-645-3	Sequence 3, Appli
34	78.4	11.6	628	10	US-11-018-645-10	Sequence 10, Appli
35	72.4	10.7	663	3	US-09-909-207-1	Sequence 1, Appli
36	72.4	10.7	663	3	US-09-909-207-2	Sequence 2, Appli
37	72.4	10.7	744	3	US-09-909-207-4	Sequence 4, Appli
38	72.4	10.7	744	3	US-09-909-207-5	Sequence 5, Appli
39	72.4	10.7	1513	3	US-09-909-207-10	Sequence 10, Appli
40	72.4	10.7	1513	3	US-09-909-207-11	Sequence 11, Appli
41	71.8	10.6	642	8	US-10-626-583-6	Sequence 6, Appli
42	71.8	10.6	642	8	US-10-626-583-12	Sequence 12, Appli
43	71.8	10.6	642	9	US-10-626-724-6	Sequence 6, Appli
44	71.8	10.6	642	9	US-10-626-724-12	Sequence 12, Appli
45	71.8	10.6	645	6	US-10-237-386-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-467-368-1
; Sequence 1, Application US/09467368
; Patent No. US20020160080A1
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; Wagner, Peter
; Mullertz, Anette
; Knap, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20020160080A1o No. US20020160080A1disk of No. US200201600
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,368
; FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Thermomyces lanuginosus

STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-467-368-1

Query Match 100.0%; Score 675; DB 3; Length 983;
Best Local Similarity 100.0%; Pred. No. 3.3e-203;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ATGCTGGCTTTACCCCGTGGCCCTTGCGGCTTAAGCCGCACTGGGGCCCTGGCTTC 60
DB 31 ATGCTGGCTTTACCCCGTGGCCCTTGCGGCTTAAGCCGCACTGGGGCCCTGGCTTC 90
OY 61 CCGGCAAGGAATGCCACGAGCTCGAAAAAGCAGACAGAACCCCACTCGAGGGGCTGG 120
DB 91 CCGGCAAGGAATGCCACGAGCTCGAAAAAGCAGACAGAACCCCACTCGAGGGGCTGG 150
OY 121 CACGATGGTTATTACTATTCTGTGGAGTGACGGGTGAGCGCAGGCCAGCTACCAAC 180
DB 151 CACGATGGTTATTACTATTCTGTGGAGTGACGGGTGAGCGCAGGCCAGCTACCAAC 210
OY 181 CTGGAAGCGGGCACTTACGAGATCACTGGGAGATGGCGGTAACTCTGTCGGTGAAAG 240
DB 211 CTGGAAGCGGGCACTTACGAGATCACTGGGAGATGGCGGTAACTCTGTCGGTGAAAG 270
OY 241 GGCTGGAACCCCGGCTGAACGCAAGAGCCATCCACTTTGAGGGGTGTTACAGCCAAAC 300
DB 271 GGCTGGAACCCCGGCTGAACGCAAGAGCCATCCACTTTGAGGGGTGTTACAGCCAAAC 330
OY 301 GGCAACGTAACCTTGCGGTCTACGAGTGAGACCCGCAACCCGCTGTCAGTAATACATC 360
DB 331 GGCAACGTAACCTTGCGGTCTACGAGTGAGACCCGCAACCCGCTGTCAGTAATACATC 390
OY 361 GTGGAACCTTGGCACCTATGATCCTTCTCGGTGCTACCGATCTAGGAATGTGAG 420
DB 391 GTGGAACCTTGGCACCTATGATCCTTCTCGGTGCTACCGATCTAGGAATGTGAG 450
OY 421 TGGACGGTATCATCTATGATCGCTGGCAAGACCACTCGGCTCAACGCACTAGCATGAC 480
DB 451 TGGACGGTATCATCTATGATCGCTGGCAAGACCACTCGGCTCAACGCACTAGCATGAC 510
OY 481 GGCACCCAAACCTTGCACCAATATCTGGTCCGTCGCCAGACAGCGCACCGGCTAAC 540
DB 511 GGCACCCAAACCTTGCACCAATATCTGGTCCGTCGCCAGACAGCGCACCGGCTAAC 570
OY 541 GTCCAGACGGGCTGCCACTTGCAGCGCTGGGCTGGCTGTTGAATGTCAACGGTGAC 600
DB 571 GTCCAGACGGGCTGCCACTTGCAGCGCTGGGCTGGCTGTTGAATGTCAACGGTGAC 630
OY 601 CACTACTACGAGATGTTGCAACGAGGGCTACTTACAGCAGCGGCTATGCTGCATCAC 660
DB 631 CACTACTACGAGATGTTGCAACGAGGGCTACTTACAGCAGCGGCTATGCTGCATCAC 690
OY 661 GTTGCTGACGTGGC 675
DB 691 GTTGCTGACGTGGC 705
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RESULT 2

US-10-237-386-9
Sequence 9, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 588
TYPE: DNA
ORGANISM: Thermomyces lanuginosus
US-10-237-386-9

Query Match 86.2%; Score 582; DB 6; Length 588;
Best Local Similarity 100.0%; Pred. No. 8.5e-174;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 94 CAGACAAACCCCAACTCGAGAGGGCTGGCACGATGTTATTACTATTCTGTGGAGTGAC 153
DB 4 CAGACAAACCCCAACTCGAGAGGGCTGGCACGATGTTATTACTATTCTGTGGAGTGAC 63
OY 154 GGTGAGCGCAGAGCGCACGTACCAACCTGGAAGCGGCACCTACGAGATCAGCTGGGA 213
DB 64 GGTGAGCGCAGAGCGCACGTACCAACCTGGAAGCGGCACCTACGAGATCAGCTGGGA 123
OY 214 GATGCGCGTAACCTCGTCGTGGGAAGAGGCTGGAACCCCGGCTGAACGCAAGCCATC 273
DB 124 GATGCGCGTAACCTCGTCGTGGGAAGAGGCTGGAACCCCGGCTGAACGCAAGCCATC 183
OY 274 CACTTTGAGGGGTGTTTACCAAGCCAAACGGCAACAGCTACTTGCGGTCTACGGTTGACC 333
DB 184 CACTTTGAGGGGTGTTTACCAAGCCAAACGGCAACAGCTACTTGCGGTCTACGGTTGACC 243
OY 334 CGCAACCCGCTGTCGAGTAATACATCGTCGAGAACTTTGGCACTATGATCTTCCTCC 393
DB 244 CGCAACCCGCTGTCGAGTAATACATCGTCGAGAACTTTGGCACTATGATCTTCCTCC 303
OY 394 GGTGTAACGATCTAGGAATGTGCGAGTGCAGCGGTAAGCATCTATGACTCGGCAAGACC 453
DB 304 GGTGTAACGATCTAGGAATGTGCGAGTGCAGCGGTAAGCATCTATGACTCGGCAAGACC 363
OY 454 ACTGCGTCAACGCACTAGCATCGACGCGCAACCACTTGCACCAATACTGTCGGTC 513
DB 364 ACTGCGTCAACGCACTAGCATCGACGCGCAACCACTTGCACCAATACTGTCGGTC 423
OY 514 CGCCAGACAAAGCGCACCGGCTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCT 573
DB 424 CGCCAGACAAAGCGCACCGGCTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCT 483
OY 574 CGGCTGGTTGAATGTCAACGGTGACCACTACTACAGATCGTTGCAACGAGGGCTAC 633
DB 484 CGGCTGGTTGAATGTCAACGGTGACCACTACTACAGATCGTTGCAACGAGGGCTAC 543
OY 634 TTCAAGACGGCTATGCTGCATCACCGTTGCTGACGTGGC 675
DB 544 TTCAAGACGGCTATGCTGCATCACCGTTGCTGACGTGGC 585
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RESULT 3

US-09-803-454-3
Sequence 3, Application US/09803454
Publication No. US20030022280A1
GENERAL INFORMATION:
APPLICANT: No. US20030022280A1ozymes A/S
APPLICANT: Takagi, Shinobu
APPLICANT: Terui, Yuri
TITLE OF INVENTION: High Expression of Industrial Enzymes
FILE REFERENCE: 6125-200-US
CURRENT APPLICATION NUMBER: US/09/803,454
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3

/ LENGTH: 678
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-09-803-454-3

Query Match 55.1%; Score 371.6; DB 3; Length 678;
Best Local Similarity 72.0%; Pred. No. 4.1e-107;
Matches 485; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

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QY 1 ATGTCGGCTTACCCCGTTGCCCTTGGCCCTTAGCCGCGACTGGGCGCTGCCCTTC 60
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Db 1 ATGTTGGTTTACTCCAGTTGCTTAGCTGCTTAGCTGCTAGCTGCTTACTGCTTTC 60

QY 61 CCGCAGGGAATGCCAGAGCTCGAAAAGCAGACAAACCCCACTCGAGGGCTGG 120
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Db 61 CCAGCAGGTAATGCTACTGAATTGAAAAAAGACAACAACCTCCAATTCTGAAGTTGG 120

QY 121 CACGATGGTTATTACTATTCTCTGCTGAGTGAAGGCTGAGCGGCAAGCCAGTACCAAC 180
    |||||
Db 121 CATGATGGTTATTATTATTCTTGGTGGTCTGATGGTGGTCTCAAGCTACTATTACTTAAT 180

QY 181 CTGGAAGGCGGCACTACGAGATCAGCTGGGAGATGGCGGTAACCTCGTCGGTGAAAG 240
    |||||
Db 181 TTAGAAAGGTGTAACCTATGAATTTCTGGGGTATGGTGAATTTAGTTGGTGTAAT 240

QY 241 GGCTGGAACCCCGGCTGAAACGCAAGACCATCCATTGAGGGTGTATACCAAGCAAC 300
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Db 241 GGTTGGAATCCAGGTTTAAATGCAAGACTATTCAATTTGAAGGTGTTATCAACCAAT 300

QY 301 GGCAACAGTACCTTGGCTCTACGGTTGGAACCCGCAACCCGCTGGTGGATATTACATC 360
    |||||
Db 301 GGTAATTCCTATTAGCTGTTATGGTTGAGACTAGAAATCCATTAGTGAATATTATAT 360

QY 361 GTCGAATCTTGGCACCTATGATCTTCTCCGCTGCTACCGATCTAGAACTGTCAG 420
    |||||
Db 361 GTTGAATTTTGGTACTTATGATTCATCTTCTGGTGTCTGATTTAGGTAAGTCTTGA 420

QY 421 TCGACCGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCCATGAC 480
    |||||
Db 421 TGTGATGGTTCTATTATAGATTAGTAAACTACTAGATTAAATGCAACCATCTATTGAT 480

QY 481 GGCACCCAAACCTTGCACCAATCTGCTGGTCCGCGCAGCAAGCGCACCGGTAAC 540
    |||||
Db 481 GGTAACCAACTTTCGATCAATATGCTCTGTAGACAAAGTAAAGAACTTCTGTAAT 540

QY 541 GTCCAGAGGGCTGCCACTTGCAGCGCTGGGCTCGCGTGTGAATGTCAACGGTGAC 600
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Db 541 GTTCAAACTGTTGTCATTTGATGCTTGGGCTAGAGCTGTTGAATGTTAATGAT 600

QY 601 CACTACTACAGATCGTTGCAACGAGGGCTACTTCAAGCAGCGCTATGCTCGCATCAC 660
    |||||
Db 601 CATTATTATCAAAATTTGTCGAACGGAAGTTATTCTTCTGCTTATGCTAGAAATTA 660

QY 661 GTTGTGAGCTGGG 674
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Db 661 GTTGTGATGTTGG 674
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RESULT 4

US-10-425-115-177283
/ Sequence 177283, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115

/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 177283
/ LENGTH: 850
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_93271C.1
US-10-425-115-177283

Query Match 38.1%; Score 257.2; DB 8; Length 850;
Best Local Similarity 64.2%; Pred. No. 7.6e-71;
Matches 420; Conservative 0; Mismatches 228; Indels 6; Gaps 2;

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QY 14 CCCCCGTTGCCCTTGGCCCTTAGCCGCACTGGGGCCCTTCCCGCAGGGAATG 73
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Db 139 CCACCGTCTCTGGCCGCCCGGTTGCTGACGCCAGCAGCACTTGTGAGCGCTCCC 198

QY 74 CCACGAGCTCGAAAAGCAGACAAACCCCACTCGAGGGCTGGCAGATGTTATT 133
    |||||
Db 199 TCAGTGTATTGACTGACAGTGGCGGTACCCCAAGCTCCAGGGCACCACCAAGGCTGCT 258

QY 134 ACTATCTGTGTGAGTGAAGTGAAGCGCAGGCAAGTACCAACCTGGAAGCGGCA 193
    |||||
Db 259 TCTACTCTGTGTGAGACCGACGCGCGCCCAAGGCTACTACCAACGAAGCGCGGCA 318

QY 194 CCTACGAGTACAGCTGGGGAATGGCGGTAACTCGTGGTGAAGGGCTGAACCCCG 253
    |||||
Db 319 AGTACAGGCTCAACTGGAAGACCGGTGTGAACATGTTGGTGAAGGGCTGAACCCCTG 378

QY 254 GCCTGAACGCAAGACCATCCATTGAGGGTGTACCAAGCCAAACGCAACAGCTACC 313
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Db 379 GTGCG---GCCGCAACATCACTACTCCGGTACTACAGCCCCAGGGTAATCTCTACC 435

QY 314 TTGCGGTCTACGGTTGACCCGCAACCCGCTGTGAGTATTACATCGTGAAGAACTTG 373
    |||||
Db 436 TTGCCATCTACGGCTGACCCGCAACCCCTTGTGAGTACTACGTTGTGAAGAACTTG 495

QY 374 GCACCTATGATCTTCTCCGCTGCTACCGATCTAGAACTGTGAGTGCAGCGGTAGCA 433
    |||||
Db 496 GTACCTAGAACCCGCTCTCGGGCCAGCGTCAAGGGCTCCGTCAACGCAAGGCTCGT 555

QY 434 TCTATGACTCGGCAAGCACTCGCGTCAACGCACTAGCATGACGCGCAACCAACT 493
    |||||
Db 556 CCTACAGATTTGCGCAGACTCAGCGTGTCAACCAAGCCCTCCATGACGCGCAACCAACT 615

QY 494 TCGACCAATACTGTCGCTCGGCGCAGGACCAAGCGCAAGCGGTACCGTCCAGCGGGCT 553
    |||||
Db 616 TCAACCACTACTGTCGCTCGGCGCAGAACCAAGCGCAAGCTCCGCTCCGTCAATGAAGA 675

QY 554 GCCACTTGCAGCGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACTACTACAGA 613
    |||||
Db 676 CCCACTTGCAGCGCTGGGCTCGGCTCAAGGGCATGACGCT---CGGTACAGCAACTACAGA 732

QY 614 TCGTGAACGGAAGGCTACTTCAAGCAGCGGCTATGCTGCATCACCGTTGCTG 667
    |||||
Db 733 TCGTGCACCGAAGGTTACTTCTCTCCGCGAGCTGTGATCACCGTTACTG 786
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RESULT 5

US-10-425-115-82922
/ Sequence 82922, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28

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; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 82922
; LENGTH: 749
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(749)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_175642C.1
US-10-425-115-82922
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Query Match          36.5%; Score 246.6; DB 8; Length 749;
Best Local Similarity 63.9%; Pred. No. 1.7e-67;
Matches 423; Conservative 0; Mismatches 230; Indels 9; Gaps 3;
```

```
QY 1 ATGTCGGCTTTACCCCGTTGCCCTTGCGCCTTAGCCGCACTGGAGCCCTGGCCTTC 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 ATGTTCTTTCACCTCCATCATCACCGCTGCTGTGGGCTACCGGCTCTTGCCGCC 139
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 CCGGCAAGGAATGCCACGAGCTCGAAAAGCAGACACACCCCACTCGAGGGCTGG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 140 CCGGC---CACTGATGTGTCTCTGTTGCCCGTCAAGAACCCCAACGGCGGTAAC 196
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CACGATGGTTATTACTATTCTGTGGAGTGAAGGTCAGCGGCAAGCCACGTACCAAC 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 197 CACAACGGCTGCTTCTGTGTGGTGTGTGATGCGGTGCCCGGCTACCTACCAAC 256
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 CTGAAAGCGGCACTTACAGAGATCAGCTGGGAGATGGCGTAACCTGTCGGTGAAG 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 257 GGTGCCGGTGTGTAAGCTACAGCGTAAGCTGGGAAAGCGTGGCAACCTGTCGGTGAAG 316
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 GGTGGAACCCCGCCTGAACGCAAGACCATCCACTTGAAGGTGTTTACCAGCCAAC 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 317 GGATGGAACCCAGG---AACTGCCGTAACATCACTACTCTGTACTTACAATACAAC 373
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 GGCAACAGTACCTTGCGGTCTACGGTTGGAACCCGCAACCCGCTGTGAGTAATACATC 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 374 GGCACTCTTACCTTGCCGTCTACGGCTGGAACCCGCAACCCCTTGTGAGTACTACGTC 433
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 GTCGAGACTTTGGCACTATGATCTTCTCCGGTGTGCTACCGATCTAGAACTGTGAG 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 434 GTTGAGAACTTCGGCACTACGACCCCTCTTCCAGTCCAGAAACAAGGTTACCGTCAAC 493
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 TGGACGGTAGCATCTATCGACTCGGCAAGACCACTCGGCTCAAGCAGCTAGCATGAC 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 494 TCTGATGATCTTCTTACAAGATCGCTCAGTGCAGCCCGTACCAACAGCCCTTCATGAT 553
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 GGCACCCAAACCTTGACCAATATGTCGTCCGCCAGCAAGCGCACAGCGGTAAC 540
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 554 GGCACCAAGACCTTTCAGCAGTATGTGTTGTCAGAACAAAGCGCTTTCGGCTCC 613
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 541 GTCCAGACGGGCTGCCACTTGACGCGCTGGGCTCGCGTGTGTTGAATGTCAACGGTGAC 600
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 614 GTCAATATGAAGACTCACTTTCAGCGCTGGGCCAGCAAGGGCATGAA---CCTGGCCAG 670
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 601 CACTACTACAGATCGTTGCAACGAGGGCTACTTCAGCAGCGGCTATGCTGCATCAC 660
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 671 CACTACTACAGATTTGGTGCCACCGANGTACTTCTCCACTGTGTAAAGGCCAGATCAC 730
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 661 GT 662
   ||
Db 731 GT 732
```

```
RESULT 6
US-10-425-115-37173
; Sequence 37173, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 37173
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133906C.1
US-10-425-115-37173
```

```
Query Match          35.6%; Score 240.4; DB 8; Length 818;
Best Local Similarity 62.5%; Pred. No. 1.6e-65;
Matches 411; Conservative 0; Mismatches 241; Indels 6; Gaps 2;
```

```
QY 5 TCGGCTTTACCCCGTTGCCCTTGCGCCTTAGCCGCACTGGGGCCCTGCGCTTCCCG 64
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 96 TCATCACTGCTGTGTGTGTCGCACTGTGTGCTTCTGCTCTCCCGCACTGATGTAAGT 155
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 65 CAGGAATGCCACGAGCTCGAAAAGCAGACACACCCCACTCGAGGGCTGGCACG 124
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 156 CTGTTCTCCGCGACCTGCTGCTCGCCAGAGACCCCAACCGCGAAGAACACACA 215
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 125 ATGTTATTACTATTCTGTGGAAGTGAAGGTGAGCGGCAAGCCAGTACACCAACTGG 184
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 216 ACGGCTCTTCTACTCTGTGGAGTGAAGTGTGCTCAAGTTACTTACACCAACGCTG 275
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 185 AAGCGCACTTACAGAGATCAGCTGGGAGATGGCGGTAACCTGTCGGTGAAGGCT 244
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 276 CAGGTGCACTACAGCGTCACTGGGGAAGCGCGCACTTGTGTGTGTAAGGCT 335
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 245 GGAACCCCGCCTGAACGCAAGACCATCCACTTTGAGGGTGTTCACGACCAACGCA 304
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 336 GGAACCTTGATCG--GCCGCAACGTTACCTACTTCGGGCTCTACAACCCCAACGCA 392
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 305 ACAGTACCTTGCGGTCTACGGTTGGAACCCGCAACCCGCTGTGAGTATTACATCGTC 364
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 393 ACTCTACCTTGCACTATGAGGTGACACGTAACCTCTGTCGAATACTATGTGTTG 452
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 365 AGAATTGGCACCTATGATCTTCTCCGGTGTACCGATCTAGAACTGTGAGTGG 424
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 453 AGAATTGGAACTATGACCGAGTTCAGAGGCTAGCAACAAGGTACCGTGAAGTGG 512
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 425 ACGTAGCATCTATGACTGGCAAGACCACTCGGCTCAAGCAGCACTAGCATCGAGCA 484
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 513 ACGGCTCTTCTACAAGATCGCTCAGTCGACCCGTAACCAAGCATTCATGATGAA 572
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 485 CCCAACTTTCGAACCAATATGTCGTCCGCCAGCAAGCGCACAGCGGTACCGTCC 544
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 573 CAAGGACCTTTCAGCAGTACTGTGTTGCGCAAGAACAGCGCTCAGCGGATCCGTA 632
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 545 AGACGGGCTGCCACTTGCAGCGCTGGGCTCGCGTGTGTTGAATGTCAACGGTGAAC 604
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 633 ACATGAAGACTCACTTGATGCTTGGGCGAGCAAGGGCATGACTCT--TGATAGCACT 689
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 605 ACTACAGATCGTTGCAACGAGGGCTACTTCAGCAGCGGCTATGCTGCATCACCGT 662
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 690 ACTACAGATTTGCTGCTACCGAGGGAATCTTCTCACCGGTTCTGCGTATCACTGT 747
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 7
US-10-213-990-65
; Sequence 65, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
```



```

1  APPLICANT: Roemer, Terry
2  TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
3  TITLE OF INVENTION: ENZYMES AND METHODS OF USE
4  FILE REFERENCE: 10182-019-999
5  CURRENT APPLICATION NUMBER: US/10/213,990
6  CURRENT FILING DATE: 2002-08-05
7  NUMBER OF SEQ ID NOS: 72
8  SOFTWARE: FastSeq for windows Version 4.0
9  SEQ ID NO 65
10 LENGTH: 666
11 TYPE: DNA
12 ORGANISM: Aspergillus
13 FEATURE:
14 NAME/KEY: CDS
15 LOCATION: (1)...(666)
16 US-10-213-990-65

```

Query Match	33.3%;	Score 224.6;	DB 5;	Length 666;
Best Local Similarity	61.5%;	Pred. No. 1.5e-60;		
Matches 413; Conservative	0;	Mismatches 249;	Indels 9;	Gaps 3;

QY	1	ATGTCGGCTTTACCCCCGTTGCCCCCTTGGCGCTTAAGCCCGCACTGGGGCCCTGGCCCTTC	60
Db	1	ATGCTCATTTCTTCTCTCGTTCTCGCTGECTCCACCGTTGCTGGCGTCTAGCTACA	60
QY	61	CCGG---CAGGGAATGCCACGAGCTCGAAAAGCGACAGACAACCCCCAACTCGAGGGC	117
Db	61	CCCGGCTCGAGCAATACGTTGAGCTAGCCAAAGCGGAGCTCACCAGACTCTCAGACTGGC	120
QY	118	TGGCAGATGGTTATTACTATTCCGTGGAGTGAAGCGTGGAGCGGACAGTACACC	177
Db	121	ACGAATAACGGCTACTACTACTCCTTCTTGACCCGACGGCGCGGCCAGGTGACCTACACC	180
QY	178	AACCTGGAAGCGGCACTACAGATCAGCTGGGGAGATGGCGGTAACTCTCGCTGGA	237
Db	181	AACGGCAATGGCGGCCAGATATCAGGTCGACTGGAACAACCTGCGGCACTTTGTTGCTGG	240
QY	238	AAGGGCTGGAACCCCGGCCCTGAAACGCAAGACCATTCCACTTTGAGGGTGTTCACAGCCA	297
Db	241	AAGGGCTGGAACCCGACC--AGCGAAGAAAGCGTCACTTACAGCGGCTCTCGGACAGCC	297
QY	298	AACGGCAACAGCTACTCTTGCGTCTACGGTTGGAACCCGCAACCGCTGTCGAGTATTAC	357
Db	298	AGCGGAAACGGCTACTCTCCGTGACGGCTGGAGACGACAGTCCGCTGGTGAATTCTAC	357
QY	358	ATCGTCGAGAACTTTGGCACCTATGATCCTTCCCGTGCTACCGATCTAGAACTGTC	417
Db	358	ATCGTGAGAGTTACGGCTCCTATGACCCCTCCACGGGAGCCACCATCTCGGCACCGTC	417
QY	418	GAGTCGACCGGTAGCATCTATCGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATC	477
Db	418	GAGAGCGACCGGGCCACGTACAACTCTACAAAGACGACGGGAGCAATGCGCCGTCCATC	477
QY	478	GACGGCACCCAAACTTCGACCCAATACTGTCGTCGCCACAGACAAGCGCACCGCGGT	537
Db	478	CAGGCGACGGCTACTTTTGACCAAGTACTGTCGTTTCGAACTTCGCACCGCAGAGTGA	537
QY	538	ACCGTCAGACCGGCTGCCACTTCGACGCGCTGGGCTCGCGTGTGTAATGTCAACGGT	597
Db	538	ACTGTGACGACGAGAACAACACTTTGATGCGTGGAGAAGAAATGCGGGTCTGCAATT--GGGG	594
QY	598	GACCACTACTACAGATCGTTGCAACGAGGGCTACTTCAGCAGCGGCTATGCTCGCATC	657
Db	595	AACTTGACTATATGATGTGTTCGACGGAAGGGGTACCAAGACAGCGGCTCTGCTACTATC	654
QY	658	ACCGTTGCTGA 668	
Db	655	ACTGTTTCTTA 665	

RESULT 8
US-10-213-990-68
; Sequence 68, Application US/10213990

```

; Publication NO. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(705)
US-10-213-990-68

```

Query Match	32.8%;	Score 221.6;	DB 5;	Length 705;
Best Local Similarity	60.5%;	Pred. No. 1.4e-59;		
Matches 409; Conservative	0;	Mismatches 249;	Indels 18;	Gaps 2;

OY		2	TGTCGGCTTTAACCCCGTTCCTTGCCGCTTAGCCCGCACTGGGGCCTGGCTTCC	61
Db		26	TGGCGTGTCCGCCATTGGAGCTCTGGCTGCCCGCTGAAACCGAGACCACCTCGTTCA	85
OY		62	CGGCAGGAATGCCACGGAGCTCGAAAAGCGACAGACAACCCCAACTCGGAGGCTGGC	121
Db		86	ATGAGACTGCTCTTCATGAGTTGCTGAGCGCGCCGCAACCCAAAGCTCCACCGGCTGGA	145
OY		122	ACGATGTTATTAATACTATTCCTGTGAGTGACGATGAGCGCAGGCCAGTACCAACC	181
Db		146	ACAACGGCTAATACTACTCTCTTGGACTGATGCGCGCGCAGCTGACTACCAATG	205
OY		182	TGGAAGCGGCACCTACGAGATCACCTGGGAGATGGCGGTAACCTCGTGGTGAAGG	241
Db		206	GCGCCGGTGGCTCGTACTCCGTCACATGAGGAAAGTGGCACTTGTCCGTGAAAGG	265
OY		242	GCTGGAACCC-----CGGCTGAACGCAAGACCATTCCACTTTGAGGGTG	286
Db		266	GCTGAACCTTGAAAGCGTAGGTACCGAGCTTTAAGTAGAAACCATCACTACGAGGCA	325
OY		287	TTTACCAAGCCAAACGGCAACAGTACTTTCGGTCTACGGTTGGAACCGCAACCGCTGG	346
Db		326	GCTTCAACCCACGCGCAATGGCTACTGGCTGTCTACGGCTGGAACCAACCCCTTGA	385
OY		347	TCGAGTATTACATCGTCGAGAATTGGCAACCTATGATCCTTCCTCCGGTCAACGATC	406
Db		386	TTGAGTACTACGTGTGTTGAGTCGTATGGTACATACAAACCCGCGAGCGGCTACTTCA	445
OY		407	TAGGAATGTTCGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGAACCACTCGCGTCAAAG	466
Db		446	GGGCACTGTCAACACCGACGGTGGCACTTACAACATCTAACACGGCCGTTCCGTACAATG	505
OY		467	CACCTAGCATCGACGGCAACCCAACTTCGACCAATACTGTGCTCGCCAGCAAGC	526
Db		506	CTCCCTCCATCGAAGGCAACCAAGACTTCAACCAATCTGTGTGCGCACTCCAAGC	565
OY		527	GCACCAAGGTAACCGTCCAGACGGGCTGCCACTTCGACGCTGGGCTCGCGTGTGTA	586
Db		566	GTACCGGGCGCACTGTCAACCATGGCAACCACTTCAAGCGCTGAGAGAGACTGGGCATGA	625
OY		587	ATGTCAACGTTGACCACTACTACAGATCGTTGCAACGAGGGCTACTTCAGCAGCGGCT	646
Db		626	A---CCTGGGAACCTACAACCTACAGATTGTGCGCACTGAGGGTTACCAAGACGCGGAT	682
OY		647	ATGCTCGCATCAACCGT 662	
Db		683	CTGCTTTCATCACTGT 698	

Qy 647 ATGCTGCATCACCCT 662
||| ||| ||| |||
Db 683 CTGCTTCATCACTGT 698

RESULT 9

US-09-770-621-1
; Sequence 1, Application US/09770621
; Patent No. US20010024815A1
; GENERAL INFORMATION:
; APPLICANT: M ncy1 , Arja
; APPLICANT: Vehmaaper , Jari
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Lahtinen, Tarja
; TITLE OF INVENTION: Production and Secretion of Proteins of
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W. Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,621
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/590,563
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332,412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/282,001
; FILING DATE: 29-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 1050.0340003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: No. US20010024815A1 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 303..1334
; US-09-770-621-1

Query Match 29.1%; Score 196.2; DB 3; Length 1375;
Best Local Similarity 59.0%; Pred. No. 1.8e-51;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;

OY 5 TCGGCTTTACCCCGCTGCGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGG 64
Db 349 TCGGCTTCGGCGCATGTCACACAGTGCCTTGGCGGCTGCGCATGCGCGGTGCGC 408
OY 65 CAGGAATGCCAGGAGCTCGAAAAGCGACAGACACCCCAACTCGGAGGCTGCGCAG 124

Db 409 TGCTGCCCGGCACGGCCGACGCCGACACCATCAACCAGAACGAGACCGGGTACGACA 468
OY 125 ATGTTATTACTATTCTGTGTGAGTGACGGGTGAGCGGCACGTAACCAACTGG 184
Db 469 ACGGCTACTTCTACTCGTTCTGGAACGACGCGCGGGGACCGTCTCCATGACCTCCACT 528
OY 185 AAGCGGCACCTACGAGATCAGCTGGGAGATGGCGGTAACTCTGTCGGTGAAGGGCT 244
Db 529 CGGGCGGCAGCTACAGACACTCTGTGGCGGAACCGGGAATTGTCGGCGGAGGGCT 588
OY 245 GGAACCCCGGCTGAACGCAAGACCATCTTGAAGGGTGTATACCAAGCAACGGCA 304
Db 589 GGTCCACCGG---GGAGCGCGGACCGGTGACCTAACAGCCTCTTCAACCGTCCGGTA 645
OY 305 ACAGCTACCTTGGCTGCTGCTGAGTGGACCCGCAACCGCTGTCGAGTATTAATCGTCG 364
Db 646 ACGGCTACCTCAGCTCAGGCTGAGCAGGAAACCGCTCGTGAATACATCGTCG 705
OY 365 AGAATTGGCACCTATGATCCTCTCCGGTGTACCGATCTAGGAACGTTCAGTGGC 424
Db 706 AGAGTGGGGCACCTACCGGCCCAACCGG-----ACCTACAAGGACACCGTCAACCA 759
OY 425 ACGGTACATCTATGACTGGGCAAGACCACTCGCGTCAACGCACTAGCATGACGGCA 484
Db 760 ACGGGGAACGTACGACATCTAAGAACCTGGCGGTACAACGCGCGCTCCATGAGGGCA 819
OY 485 CCCAACTTGCACCAATAGTGTGCTGCTGCGCCAGCAAGCGCACAGCGGTACCGTCC 544
Db 820 CCGGACCTTCCAGCAGTCTGGAAGCGTCCGGCAGCAAGCGGACGAGCCGACATCA 879
OY 545 AGACGGGCTGCCACTTGCAGCGCTGGGCTCGCGCTTGAATGTCAACGCTGACCACT 604
Db 880 CCATCGCAACCACTTGCAGCGCTGGGCGCGCGCATGAA---CCTGGCAGCCACG 936
OY 605 ACTACGATCGTTGCAACGAGGGCTACTTACAGACGGGCTATGCTCGCATCACCGTTG 664
Db 937 ACTACGATCATGCGGACGAGGGCTACCAAGACGCGGTAGCTCCACCGTCCATCA 996
OY 665 CTGACGTGGGC 675
Db 997 GCGAGGTGGC 1007

RESULT 10

US-10-286-993-1
; Sequence 1, Application US/10286993
; Publication No. US20030148453A1
; GENERAL INFORMATION:
; APPLICANT: Mantyla, Arja
; APPLICANT: Paloheimo, Marja
; APPLICANT: Lantto, Raija
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Lahtinen, Tarja
; APPLICANT: Suominen, Pirkko
; APPLICANT: Vehmaapera, Jari
; TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
; FILE REFERENCE: 1716.0340004
; CURRENT APPLICATION NUMBER: US/10/286,993
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/120,804
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/FI97/00037
; PRIOR FILING DATE: 1997-01-24
; PRIOR APPLICATION NUMBER: US 08/590,563
; PRIOR FILING DATE: 1996-01-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 1
; LENGTH: 1375
; TYPE: DNA
; ORGANISM: Actinomadura flexuosa (Strain: DSM43186)
; FEATURE:

```
; NAME/KEY: CDS
; LOCATION: (303)..(1337)
; OTHER INFORMATION: Product= AM35 xylanase
US-10-286-993-1
```

```
Query Match      29.1%; Score 196.2; DB 6; Length 1375;
Best Local Similarity 59.0%; Pred. No. 1.8e-51;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;
```

```
OY      5 TCGGCTTACCCCGCTGCTGCTTGGCGCTTACGCCGACTGGGGCCCTGGCCCTTCCCG 64
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     349 TCGGCTCCGGCGCATGTCACCAAGTGCCTTCCCTGCACTGCGCATCGCCGGTGGC 408
OY      65 CAGGAATGCCAGAGCTCGAAAAGCGACAGAACCCCACTCGAGGGCTGGCAG 124
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     409 TGCTGCCCGGCAAGGCCCAAGCCGACCAACATCACCAAGAACAGACGGGTACAGCA 468
OY     125 ATGTTATTACTATTCTGTGTGAGTGAAGGTGAGCGGCAAGCCACGTACACCAACTGG 184
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     469 ACGGCTACTTCTACTCGTTCTGTGACCGACCGCCCGGACCGCTCTCCATGACCTTCACT 528
OY     185 AAGCGGCACCTACAGATCAGTGGGAGATGGCGGTAACTTCGTGGTGAAGGAGCT 244
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     529 CGGGCGGCAAGCTACAGCACTCGTGGCGGAAACACCGGAACTTCTGTCGGCGCAAGGAGCT 588
OY     245 GGAACCCCGGCTGAACGCAAGACCATTCATTGAGGGTGTTTACCAAGCCAAAGGCA 304
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     589 GGTCCACCCGG---GGGACGGCGGACCGTGAACCTACAAAGCCTCTTCAACCCGTCGGGTA 645
OY     305 ACAGCTACCTTGGCGTCTACAGGTGACCCGCAACCCGCTGTGTGAGTATTACATCGTCG 364
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     646 ACGGCTACTCAAGCTCTACAGGTGACGAGAACCCGCTCGTGAAGTACTACATCGTCG 705
OY     365 AGAAGTTGGCACTATGATCTTCTCCGGGTGCTACCGATCTAGGAATGTGAGTGGC 424
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     706 AGAGCTGGGGCACTACCGGCCACCGGC-----ACCTACAAGGGCACCGTCAACCAACG 759
OY     425 ACGGTAGCATCTACGACTCGGCAAGCACTCGCGTCAACGCACTAGCATCGACGCA 484
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     760 ACGGGGGAACGATACGATCTACGAGACTTGGCGGTACAAAGCGCCGCTCATCGAGGCA 819
OY     485 CCCAAACCTTCGACCAATATCTGTGGTCCGCGCAGGACAAAGCGCAACGCGGTACCGTCC 544
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     820 CCGGACCTTCCAGAGTTCTGAGGCTCCGGCAGCAAGAGCGAACAGCGGCACATCA 879
OY     545 AGACGGGCTGCACTTCGACGCTGGGCTCGCGTGTGTAATGTCAACGGTGAACCACT 604
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     880 CCATCGGCAACCACTTCGACGCTGGGCGCGCGCGCATGAA---CTGGGCAAGCAAG 936
OY     605 ACTACCAAGATGTGCAACGAGGGGTACTTCAGCAGCGGCTATGCTGCATCACCGTTG 664
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     937 ACTACCAAGATGATGGCGACCGAGGGGTACCAAGAGCAGCGGTAGCTCCACCGTTCATCA 996
OY     665 CTGACGTGGC 675
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     997 GCGAGGGTGGC 1007
```

RESULT 11

```
US-10-213-990-67
; Sequence 67, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Busbey, Howard
; APPLICANT: Busbey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 739
; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-67
```

```
Query Match      28.0%; Score 189.2; DB 5; Length 739;
Best Local Similarity 57.7%; Pred. No. 2.6e-49;
Matches 410; Conservative 0; Mismatches 248; Indels 52; Gaps 2;
```

```
OY      2 TGGTGGCTTTACCCCGTTGCCCTTGGCGCTTACCGCGAAGTGGGCCCTGGCCTTCC 61
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     26 TGGCGTCTCCGCATTGAGCTCTGGCTGCCCGCTGAAACCGAGACCACTGTTCA 85
OY     62 CGGCAAGGATGCCACGAGCTGGAAGCAAGCAGACAGAACCCCACTCGAGGGCTGGC 121
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     86 ATGAGACTGCTCTTCATGAGTTGCTGAGCGCGCGGCAACCCCAAGCTCCACCGCTGGA 145
OY     122 ACGATGTTATTACTATTCTGTGTGAGTGAAGCGGTGAGCGGCAAGCCACGTACCAACC 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     146 ACAACGGCTACTACTACTCTTCTGAACTGATGGCGGCGGCAAGTGAACCTACCAATG 205
OY     182 TGGAAGCGGCACTTACGAGATCAGCTGGGAGATGGCGGTAACTCGTCGGTGAAGG 241
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     206 GCGCGGTGGCTCTGACTCCGTCAACTGAGAGAACTGGGCAACTTGTGGTGAAGG 265
OY     242 GCTGAACCCCGGCTG-----
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     266 GCTGAACCTTGAAGCGCTAGGTACCGAGCTTTGTCAAGTCGATGTGACAGCTGTG 325
OY     259 -----AAGCAAGAGCCATTCATTGAGGGTGTTAACAGCCAAAGGCAACAGCTAC 312
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     326 GCTGACAGAGTAGAACCATCACTACGAGGCGAGCTTCAACCCAGCGGCAATGGCTAC 385
OY     313 CTTCGGTCTACGGTTGAGACCCGCAACCCGCTGTGTGAGTATTACATCGTCAAGAACTTT 372
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     386 CTGGCTGTCTACGGCTGAGCAACCAACCCCTTGATGAGTACTACGTTGTGAGTCGTAT 445
OY     373 GGCACCTATGATCTTCTCCGGTGTCTACCGATCTAGAACTGTGAGTGGCAAGGTAGC 432
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     446 GTACATTAACAACCCCGCAGCGCGGTACCTTCAGGGGCACTGTCAACACGACGAGTGGC 505
OY     433 ATCTATGACTCGGCAAGCACTCGCGTCAACGCACTAGCATCGACGCGCAACCAACC 492
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     506 ACTTACAACATCTACAGCGCGGTTCGCTACAATGTCTCCATCGAAGGCAACCAAGACC 565
OY     493 TTGCAACAATACTGTGCGTCCGCCAGAGCAAGCGCAACGAGGTACCGTCCAGAGGGC 552
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     566 TTCACCAAGTACTGTGTGTGGCAACCTCCAAAGCTAACCGGCACTGTACCATGGCC 625
OY     553 TGCCACTTCGACGCGTGGGCTCGCGCTGTGTTGAATGTCAACGGTGACCACTACTACAG 612
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     626 AACCACTTCAACGCTGAGAGCAAGTGGCATGAA---CTGGAACTCAACAATAACAG 682
OY     613 ATGTTGCAACGAGGGTACTTCAGCAGCGGCTATGCTGCATCACCGT 662
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB     683 ATTGTGCCACTGAGGGTTACAGAGCAGCGGATCTGCTTCATCACTGT 732
```

RESULT 12

```
US-10-213-990-64
; Sequence 64, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Busbey, Howard
; APPLICANT: Busbey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
```

```
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 712
; TYPE: DNA
; ORGANISM: Aspergillus
; US-10-213-990-64
```

```
Query Match      26.8%; Score 181.2; DB 5; Length 712;
Best Local Similarity 57.7%; Pred. No. 8.7e-47;
Matches 412; Conservative 0; Mismatches 253; Indels 49; Gaps 3;
```

```
QY 1 ATGTCGGCTTTACCCCGTTGCCCTTGCGGCTTAGCCCGCACTGGGGCCCTGCGCTTC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGTCATCTCTTCTCTCTGTTCTGCTGCTCCACCGTTGCTGGCGTGAAGTACA 60
QY 61 CCGG---CAGGGAATGCCACGAGCTGAAAAAGCAGACAGAACCCCACTCGAGGGC 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CCGGCTCGGAGCAATACGTTGAGCTAGCCAAAGCGCAGCTCAACAGCTCTCAGCTGGC 120
QY 118 TGGCAGCATGTTATTACTATTCTGTTGAGTGACGGTGGAGCGCAGGCGCACTACACC 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ACGAATAACGGCTACTACTACTCTCTGAGCCGACGGCGGGCCAGTGACCTACACC 180
QY 178 AACCTGGAAGCGGCACCTACGAGATCAGCTGGGAGATGGCGGTAACTCTCGGTGA 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AACGGCAATGGCGGCCAGTATCAGGTGCACTGGAACAACCTGGGGCACTTGTGCTGGG 240
QY 238 AAGGCTGGAACCCCGGCTGAACGCA----- 264
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 AAGGCTGGAACCCCGGCGCAGGAGAAATATGCGTCTCTCCCTGCTTGTAGGTTCAAGC 300
QY 265 -----AGAGCCATCCACTTTGAGGGTGTTCACGCCAAACGGCAACAGCTACCT 314
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TAATGATTCAGACGGGTACCTACAGCGGCTCTGCGACAGCGGAAACGGCTACCT 360
QY 315 TGGGTCTACGGTTGACCCGCAACCGGCTGTGAGTATTACATCGTCGAGAACTTTGG 374
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 CTCGCTGACGGCTGAGCAGACCAAGTCGGCTGTGCAATTCTACATCGTGAGAGTTACGG 420
QY 375 CACCTATGATCCTTCTCCGCTGCTACCGATCTAGAACTGTGAGTGGACGGTAGCAT 434
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 CTCCTATGACCCCTCCACGGGAGCCACCATCTCGGCAACCTGAGAGCGAGCGGGCCAC 480
QY 435 CTATGACTCGGCAAGACCACTCGCGTCAACGCACTAGCATGCAAGCGCAACCCAACTT 494
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 GTACAACCTCTACAGAAGCAGCGCGGAGAAATGCGCCGTCCATCCAGGGCAGCGCTACTT 540
QY 495 CGACCAATACTGTCGGTCCGCCAGGACAGCAAGCGCAGCGGTACCGTCCAGACGGGCTG 554
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 TGACCAGTACTGTCGGTTCGACTTCGCAACCGGCAAGTGAAGTGTGACGACGAGAA 600
QY 555 CCACTTGACGCGCTGGGCTCGCGTGTGTAATGTCAACGGTGAACCACTACTACAGAT 614
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 CCACTTGTATGCGTGGAAGAAATGCGGCTGTGCAATT--GGGGAACCTTGAATAATGAT 657
QY 615 CGTTGCAACGAGGGCTACTTACGACGCGCTATGCTGCATCAACCGTTGCTGA 668
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 658 TGTTCGACGAGGGGTACCAAGACGAGCGGCTCTGCTACTATCACTGTTTCTTA 711
```

```
RESULT 13
US-10-213-990-71
; Sequence 71, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
; ENZYMES AND METHODS OF USE
```

```
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Aspergillus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(942)
; US-10-213-990-71
```

```
Query Match      24.5%; Score 165.4; DB 5; Length 942;
Best Local Similarity 59.3%; Pred. No. 9.4e-42;
Matches 340; Conservative 0; Mismatches 221; Indels 12; Gaps 3;
```

```
QY 96 GACACCCCACTCGAGGGCTGGCAGATGGTTATTACTATTCTGTGGTGAAGTACGG 155
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 99 GATCAGACCAAGCAGACAGGCAACAACATGGCTACTACTATTCTTCTGACCAACGG 158
QY 156 TGAAGCCGAGGCCACGTACCAACCACTGGAAGCGGCACCTACGAGATCAGCTGGG---- 211
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 159 TGCCGATCAGTCAATATACAAATGCTGCTGTGGCGAATATAGTGTACGTGGCGGAA 218
QY 212 --GAGATGGCGGTAACTCGTGGGTGAAAAGGGCTGGAACCCCGCTGAACGCAAGC 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 219 CCAGAACGGTGTGACTTACCTGTGGGAAGGCTGGAATCCAGG--GAGTGACCATGA 275
QY 270 CATCACTTTAGGGTGTTCACGCCAAACGGCAACAGCTACCTGCGGTCTACGGTTG 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 276 CATTACTTCTCTGCGAGCTTCAATCTTCCGAAATGCTTACCTGTCCGTATGATG 335
QY 330 GACCGCAACCCGCTGTGAGTATTACATGCTGAGAACTTTGGCACTATGATCCTTC 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 336 GACTACCAACCCCTAGTGAATACTACATCTCGAGAACTATGGCAGTTACAATCCTGG 395
QY 390 CTCGGTCTACCGATCTAGAACTGTGAGTGGACGGTAGCATCTATGACTCGGCAA 449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 396 CTCGGGATGACGCAAGGGCACCCTACCAAGCATGATCCACTACGACATCTATGA 455
QY 450 GACCACTGCGGTCAACGCACTAGCATGACGGGCAACCAACTTGCACCAATATGCTG 509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 456 GCACCAACAGGTCAACACGACCTTTCATGCTCGGCAAGGCACTTCAACCAATATGCTG 515
QY 510 GGTCCGCAAGCAAGCGCACGCGGTACCGTCCAGACGGGCTGCCACTTGCAGCGCTG 569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 516 CATCCGCCAAACAAAGCATCAGCGGACAGTACCAACCGGAATCACTTCAAGGCGCTG 575
QY 570 GGCTCGCGCTGTTGAATGTCAACGGTGAACCACTACTACAGATCGTTGCAACGAGGG 629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 576 GGCTAGTCTGGGGATGAA--CTGGGTATCCCATTAATCAAGATTGTTCCACTGAGGG 632
QY 630 CTACTCAGCAGCGGCTATGCTGCATCACCGT 662
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 633 ATATGAGCAGCGGTACTCTGACCATCACTGT 665
```

```
RESULT 14
US-11-018-645-21
```

```
; Sequence 21, Application US/11018645
; Publication No. US20050208178A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Bauer, Michael
; APPLICANT: Bedford, Michael
; APPLICANT: Pulliam, Derrick
; TITLE OF INVENTION: Microbially Expressed Xylanases and Their Use as Feed Additives a
; FILE REFERENCE: 70357WOPCT
; CURRENT APPLICATION NUMBER: US/11/018,645
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: 60/531,404
```

```
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xyl1A1E
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(978)
; US-11-018-645-21
```

```
Query Match      23.0%; Score 155.2; DB 10; Length 978;
Best Local Similarity 56.8%; Pred. No. 1.6e-38;
Matches 327; Conservative 0; Mismatches 243; Indels 6; Gaps 2;
```

```
QY 100 ACCCCCACTCGGAGGCTGGACGATGGTTATTACTATTCTGTGGAGTGAAGGTGA 159
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 19 ACGTCGAGCCAGACGGGCGACCAACAGGGCAATTACTTTTCGTTGMAAGACAGTCCG 78
QY 160 GCGGAGCCACGTACACCAACCTGGAAGCGGCACCTACGAGATCAGCTGGGAGATGGC 219
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 79 GGCACGGTGAATCTTGATGTAATGCGATGCGGCTATACCTCCAACTGGAGCGGCATC 138
QY 220 GGTAACTCGTGGTGGAAGGGCTGGAACCCCGGCTGAACGCAAGACCACTTCTT 279
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 139 AACAACTGGGTGGGGCGGCAAGGGCTGGGCTACCGGCTCCAGCCACAGATCAGTACTCC 198
QY 280 GAGGGTGTTCACAGCCAAACGGCAACAGCTACCTTGGGCTTAACGGTTGAGCCGCAAC 339
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 199 GGCACGTTCAATTGCGCG--GGCAACGGTTACCTGGCCCTGTATGGCTGACCAACAAT 255
QY 340 CCGCTGGTGAATATTACATCGTCGAGAACTTTGGCACCTATGATCCTTCCGCGTCT 399
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 256 CCATTGGTCGAGTACTACATCGTCGACAGCTGGGTACTACCTCGCCGCGGCGGCCAG 315
QY 400 ACCGATCTAGGAATGTGAGTCGACGGTAGCATCTATCGACTCGGCAAGCACTCGC 459
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 316 GGTTCATGGGCAACGTTAGTCGACGGGGCAGCTACGACGTCGTACCGGACCAACGC 375
QY 460 GTCAACGCACTAGCATGACGGCAACCAACCTTCGACCAATACTGTCGGTCCGCCAG 519
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 376 GTGAACCAAGCCATCATCATCGGCAACGCCACGTTCTACCACTACTGAGCGTGGCCAG 435
QY 520 GACAAGCCGACCAAGCGGTACCGTCCAGACGGGCTGCCACTTCGACCGCTGGCGCT 579
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 436 TCGAAGCGGCTGGGGCGGCAACCATTCGCAACCAATTTCAACGCTGGGCCACGCTG 495
QY 580 GGTTCGATGTCAACGGTGACCACTACTACAGATCGTTGCAACGGAGGGCTACTTCAGC 639
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 496 GGCATGAA---CCTGGCCAGCACACTACAGGTCAATGACCACGAGGTTTACCAAGAC 552
QY 640 AGCGGCTATGCTCGCATCACCGTGTGCTGACGTGGC 675
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 553 AGCGGCAAGCTCCGACATCACCGTGAACGGAAGTGGC 588
```

```
RESULT 15
US-10-213-990-70
; Sequence 70, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Bussey, Reg
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213, 990
; CURRENT FILING DATE: 2002-08-05
```

```
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Aspergillus
; US-10-213-990-70
```

```
Query Match      21.8%; Score 147.2; DB 5; Length 1002;
Best Local Similarity 62.2%; Pred. No. 5.6e-36;
Matches 249; Conservative 0; Mismatches 148; Indels 3; Gaps 1;
```

```
QY 263 CAAGACCATCCACTTTGAGGGTGTACCAAGCCAAACGGCAACAGCTACTTGGCTCT 322
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 329 CTATGACATTACTCTTCTGGCAGCTTCAATCCTTCCGGAATGCTTACTGTCCGTGT 388
QY 323 ACCGTTGACCCCGCAACCCGCTGGTCGAGTATTACATCGTCGAGAACTTGGCACTATG 382
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 389 ATGATGGAATACCAACCCCTAGTCGAATACTACATCTCTGAGAACTATGGCAGTTACA 448
QY 383 ATCTTCTCCGCTGCTACCGATCTAGAACTGTCAGTGCAGCGTAGCATCTATCGAC 442
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 449 ATCTGCGCTCGGCATGACGCAACAGGCAACCGTCAACGATGATCCACTACGACA 508
QY 443 TCGCAAGACCACTCGCGTCAACGCACTAGATCGACGGACCCAAACCTTCGACCAAT 502
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 509 TCTATGAGCACCAACAGGTCAACAGCTTCGATCGTCGGCAGCGCACCTTCAACCAAT 568
QY 503 ACTGTCGCTCCGCCAGGACAGCGCACCAAGCGGTACCGTCCAGACGGGCTGCCACTTCG 562
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 569 ACTGTCATTCGCCCAAAACAGCGATCCAGCGGCAAGTCAACCAACCGCAATCACTTCA 628
QY 563 ACGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACTACTACAGATCGTTGCAA 622
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 629 AGGCTGGGCTAGTCTGGGATGAA---CCTGGTAACCATATACTATCAGATTGTTCCA 685
QY 623 CGAGGCTACTTCAAGCAGCGGCTATGCTCGCATCACCGT 662
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 686 CTGAGGATATGAGAGCAGCGGTACCTCGAACCATCACTGT 725
```

Search completed: February 11, 2006, 23:51:28
Job time : 703.684 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 18:37:15 ; Search time 215.772 Seconds
(without alignments)
2812.856 Million cell updates/sec

Title: US-09-467-368-1_COPY_31_705

Perfect score: 675
Sequence: 1 ATGCTCGCCTTACCCCGT.....TCACCGTTGCTGACGTGGC 675

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New: *
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq: *
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq: *
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq: *
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq: *
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq: *
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10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3: *
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4: *
12: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582	86.2	588	11	US-11-170-653-9 Sequence 9, Appl1
2	201.2	29.8	1008	7	US-10-517-939-231 Sequence 231, App
3	196.2	29.1	1375	11	US-11-108-163B-1 Sequence 1, Appl1
4	189.2	28.0	663	11	US-11-108-163B-5 Sequence 5, Appl1
5	189.2	28.0	906	11	US-11-108-163B-4 Sequence 4, Appl1
6	186.2	27.6	1059	7	US-10-517-939-225 Sequence 225, App
7	186	27.6	663	11	US-11-108-163B-3 Sequence 3, Appl1
8	186	27.6	906	11	US-11-108-163B-2 Sequence 2, Appl1
9	185	27.4	1047	7	US-10-517-939-165 Sequence 165, App
10	170	25.2	1074	7	US-10-517-939-199 Sequence 199, App
11	170	25.2	1137	7	US-10-517-939-255 Sequence 255, App
12	165.8	24.6	1041	7	US-10-517-939-169 Sequence 169, App
13	165.6	24.5	1044	7	US-10-517-939-221 Sequence 221, App
14	165.4	24.5	1299	7	US-10-517-939-177 Sequence 177, App
15	160.8	23.8	1044	7	US-10-517-939-195 Sequence 195, App
16	160.8	23.8	1083	7	US-10-517-939-183 Sequence 183, App
17	159.8	23.7	1083	7	US-10-517-939-217 Sequence 217, App
18	156.2	23.1	1047	7	US-10-517-939-253 Sequence 253, App
19	150.8	22.3	1065	7	US-10-517-939-215 Sequence 215, App
20	150.6	22.3	1071	7	US-10-517-939-233 Sequence 233, App
21	150.2	22.3	1041	7	US-10-517-939-159 Sequence 159, App

22	146.4	21.7	1047	7	US-10-517-939-299	Sequence 299, App
23	141.8	21.0	1077	7	US-10-517-939-181	Sequence 181, App
24	131.2	19.4	1047	7	US-10-517-939-161	Sequence 161, App
25	128	19.0	1029	7	US-10-517-939-219	Sequence 219, App
26	127.8	18.9	747	7	US-10-517-939-227	Sequence 227, App
27	124	18.4	1695	7	US-10-517-939-317	Sequence 317, App
28	119.2	17.7	642	11	US-11-214-413-31	Sequence 31, Appl1
29	118	17.5	669	7	US-10-517-939-167	Sequence 167, App
30	116.4	17.2	1086	7	US-10-517-939-211	Sequence 211, App
31	114.8	17.0	1068	7	US-10-517-939-205	Sequence 205, App
32	109.2	16.2	1020	7	US-10-517-939-153	Sequence 153, App
33	108.4	16.1	633	7	US-10-517-939-207	Sequence 207, App
34	107.2	15.9	636	7	US-10-517-939-197	Sequence 197, App
35	106.8	15.8	555	7	US-10-517-939-251	Sequence 251, App
36	94.2	14.0	570	7	US-10-517-939-189	Sequence 189, App
37	93.4	13.8	1068	7	US-10-517-939-163	Sequence 163, App
38	91.8	13.6	570	7	US-10-517-939-377	Sequence 377, App
39	91.6	13.6	1338	7	US-10-517-939-367	Sequence 367, App
40	91.4	13.5	678	7	US-10-517-939-171	Sequence 171, App
41	91.4	13.5	1983	7	US-10-517-939-353	Sequence 353, App
42	91	13.5	645	7	US-10-517-939-157	Sequence 157, App
43	91	13.5	1053	7	US-10-517-939-191	Sequence 191, App
44	90.2	13.4	570	7	US-10-517-939-375	Sequence 375, App
45	89.8	13.3	1077	7	US-10-517-939-369	Sequence 369, App

ALIGNMENTS

RESULT 1
US-11-170-653-9
; Sequence 9, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
; FILE REFERENCE: 674509-2046
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Thermomyces lanuginosus
US-11-170-653-9

Query Match 86.2%; Score 582; DB 11; Length 588;
Best Local Similarity 100.0%; Pred. No. 4.7e-156;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	94	CAGACAAACCCCACTCGAGGCTGCACGATGTTATTACTATTCCTGCTGAGTGAC	153
DB	4	CAGACAAACCCCACTCGAGGCTGCACGATGTTATTACTATTCCTGCTGAGTGAC	63
QY	154	GGTGAAGCGCAGGCGCACTACCAACCACTGGAAGCGGCACCTACGAGATCAGCTGGGA	213
DB	64	GGTGAAGCGCAGGCGCACTACCAACCACTGGAAGCGGCACCTACGAGATCAGCTGGGA	123
QY	214	GATGGCGGTAACTCGTCGGTGGAAGGCGCTGGAACCCGGCGCTGAACGCAAGACCATC	273
DB	124	GATGGCGGTAACTCGTCGGTGGAAGGCGCTGGAACCCGGCGCTGAACGCAAGACCATC	183

```
QY 274 CACTTGAGGGGTGTTTACCAGCCAAACGGCAACAGCTTACCTTGGGTCTTACGGTTGGACC 333
    |||||||
Db 184 CACTTGAAGGGTGTATTACAGCCAAACGGCAACAGCTTACCTTGGGTCTTACGGTTGGACC 243
QY 334 CGCAACCGGCTGTGAGATATTATCATCTGTCGAGAACTTTGGCACTTATGATCTTCTCC 393
    |||||||
Db 244 CGCAACCGGCTGTGAGATATTATCATCTGTCGAGAACTTTGGCACTTATGATCTTCTCC 303
QY 394 GGTGCTACCGATCTAGGAACCTGTCGAGTCGACGGTAGCATCTATCGACTCGGCAAGACC 453
    |||||||
Db 304 GGTGCTACCGATCTAGGAACCTGTCGAGTCGACGGTAGCATCTATCGACTCGGCAAGACC 363
QY 454 ACTCGCTCAACCGCACCTAGCATCGACGGCAACCCAAACCTTCGACCAATATGTTGGTCC 513
    |||||||
Db 364 ACTCGCTCAACCGCACCTAGCATCGACGGCAACCCAAACCTTCGACCAATATGTTGGTCC 423
QY 514 CGCCAGAGCAAGCGCACCGCGGTACCGTCCAGACGGGCTGCCACTTCGACGGCTGGGCT 573
    |||||||
Db 424 CGCCAGAGCAAGCGCACCGCGGTACCGTCCAGACGGGCTGCCACTTCGACGGCTGGGCT 483
QY 574 CGCGCTGTTTGAATGTCAACGGTGAACCACTACTACAGATCGTTGCAACGGAGGGCTAC 633
    |||||||
Db 484 CGCGCTGTTTGAATGTCAACGGTGAACCACTACTACAGATCGTTGCAACGGAGGGCTAC 543
QY 634 TTCAGACGGGCTATGCTCGCATCAACGTTGCTGACGTGGGC 675
    |||||||
Db 544 TTCAGACGGGCTATGCTCGCATCAACGTTGCTGACGTGGGC 585
```

RESULT 2

```
US-10-517-939-231
; Sequence 231, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Bacteria
US-10-517-939-231
```

Query Match 29.8%; Score 201.2; DB 7; Length 1008;
Best Local Similarity 59.9%; Pred. No. 1.1e-47;
Matches 376; Conservative 0; Mismatches 243; Indels 9; Gaps 2;

```
QY 37 GCCGCGACTGGGCGCTTGCCCTTCCCGGAGGAATGCACGGAGCTCGAAAAGCGACAG 96
    |||||||
Db 73 GTCGGCTGGCGGCTCGCGCGCTGATGCTGCCGGGCAACGCCCAAGCCGACACGGTTC 132
QY 97 ACAACCCCACTCGAGAGGGCTGGCACGATGTTATTACTATTCTGTGTGAGTACGGT 156
    |||||||
Db 133 GTCACGACCAACGAGGAGGGGCAACCAACAGGCTACTACTACTGTTCTGACCGACAGC 192
QY 157 GGAGCGCAGGCGCACTACCAACCTGGAAGCGCGCACCTACGAGATCAGCTGGGGAGAT 216
    |||||||
Db 193 CAGGGCACCGTCTTCATGAACATGGGCTCCGGCGGTCAGTACAGCACTCGTGGCGCAAC 252
```

```
QY 217 GGGGTAACCTCGTCGGTGAAGAGGGCTGAAACCCCGGCTGAACGCAAGACCATCCAC 276
    |||||||
Db 253 ACCGGCAACTCTGTCGGGGCAAGGGCTGGGCCAACGGCGCCGGCA---CCGTGACAG 309
QY 277 TTGAGGGGTGTTTACAGCCAAACGGCAACAGCTTACCTTGCGTCTACGGTTGACCCGC 336
    |||||||
Db 310 TACTCGGGCAGCTTCAACCCCTCCGGCAACGGCTACCTGGCGTCTACGGATGAGCTCG 369
QY 337 AACCCGCTGTGAGATATTACATCGTCGAGAACTTTGGCACCTATGATCTTCTCCGGT 396
    |||||||
Db 370 AACCCGCTGTGAGATATTACATCGTCGACAACTGGGGCACTTACCCGGCCACGGCG-- 427
QY 397 GCTAACGATCTAGGAACCTGTCGAGTCGACGGGTAGCATCTATGACTCGGCAAGACCACT 456
    |||||||
Db 428 ---AGTACAAAGGACCGTCAACGACGGCGGCACTTACGACATCTTACAAAGACGACC 483
QY 457 CGCGTCAACGCACTAGCATCGACGGCAACCCAAACCTTCGACCAATATGTTGGTCCGC 516
    |||||||
Db 484 CGCGTCAACAAAGCCCTCCGTGAGGGCAACCCGCACTTCGACCAATATGAGCGTCCGC 543
QY 517 CAGACAAAGCGCACCGGTAACGTCAGACGGGCTGCAACGGGCTGCAACGGGCTGCGC 576
    |||||||
Db 544 CAGCGCAAGCGGACCGGCGGACCATCAGACCGGCAACCACTTCGACGGGTGGGCCCGG 603
QY 577 GCTGTTTGAATGTCAACGGTGAACCACTACTACAGATCGTTGCAACGGAGGGCTACTTC 636
    |||||||
Db 604 GCGGGAATGCCGCTCGGCAACTTACGCTACTACATGATGAGCCACCGAGGGCTACGAG 663
QY 637 AGCAGCGGCTATGCTCGCATCAACGGTTG 664
    |||||||
Db 664 AGCAGCGGCACTCTCAGCATCAACGTCG 691
```

RESULT 3

```
US-11-108-163B-1
; Sequence 1, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Raij
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
; FILE REFERENCE: 1716.03400B/MAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1375
; TYPE: DNA
; ORGANISM: Nonomuraea flexuosa
; FEATURE:
; OTHER INFORMATION: Nf xyn1A nucleotide sequence (A0508952), the coding region is
US-11-108-163B-1
```

Query Match 29.1%; Score 196.2; DB 11; Length 1375;
Best Local Similarity 59.0%; Pred. No. 3.1e-46;
Matches 396; Conservative 0; Mismatches 263; Indels 12; Gaps 3;

```
QY 5 TCGGCTTAAACCCCGTTGCCCTTGGCGGCTTAGCCGCGACTGGGCGCTTCCCGG 64
    |||||||
Db 349 TCGGCTCGGCGCATCGTACCAAGTGCCTTGGCCCTGCACTCGCCATCGCGGTGCGC 408
```

```
OY      65 CAGGAAATGCCACGGAGCTCGAAAAGCAGACAAACCCCACTCGGAGGCTGGCAGC 124
      409 TGCTGCCGGCAGCGCCCAAGCCGACACCAATCACCCAGAAACGACCGGGTACGACA 468
OY      125 ATGTTATTACTATTCTCTGTGAGTGAAGGTGAGCGGACGACATACCAACCTGG 184
      469 ACGGCTACTTCTACTCGTTCTGACCGACGCGCCCGGACCGTCTCCATGACCTCCACT 528
OY      185 AAGCGGCACCTACGAGATCAGCTGGGGAAGATGGCGGTAACTCGTGGTGAAGGGCT 244
      529 CGGGCGGACGTAACAGACCTCGTGGCGGAACACCGGGAATTGTCGCCGGCAAGGGCT 588
OY      245 GGAACCCCGGCTGAAACGCAAGCCATCCACTTTGAGGTGTTTACCAAGCCAAACGGCA 304
      589 GGTCCACCGGC--GACCGGCGACCTGACCTTCAACCGCTCTTCAACCCGTCGGGTA 645
OY      305 ACAGCTACTTGGCGGTCTACGGTTGACCCGCAACCCGCTGGTGAATATTACATCGTCG 364
      646 ACGCTTACTTCAAGCTTACGGCTGGAACAGAAACCGCTCGTGAATCTACATCGTCG 705
OY      365 AGAATTGACACCTATGATCTTCTCCGGTGTACCGATCTAGAACTGTGAGTGGC 424
      706 AGAGCTGGGACCTACCGGCCACCGGC-----ACCTACAAGGCAACGTCACCAACG 759
OY      425 ACGTAGCATCTATGACTCGGCAAGACCACTCGCGTCAACGCACCTAGCATGACGGCA 484
      760 ACGGCGGACGTACGACATCTACGAGACCTGGCGGTACAAACGCGCTCATGAGGGCA 819
OY      485 CCCAAACCTTGCACCAATATCTGTCGGTCCGCCAGAGCAAGCGCACAGCGGTACCGTCC 544
      820 CCGGACTTTCAGCAGATTCTGAGCGTCCGGCAGCAAGCGGACGACCAATCA 879
OY      545 AGACGGGCTGCCACTTGCAGCGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACT 604
      880 CCATCGGCAACCACTTGCAGCGCTGGGCGCGCGCGGCAAGAA---CCTGGCAGCCACG 936
OY      605 ACTACCATGATCGTTGCAACGAGGGCTTACTTACAGCAGCGGCTATGCTGCATCAACGGTTG 664
      937 ACTACCATGATCATGGCAGCCGAGGGCTAACAGAGCAGCGGTAGCTCCACCGTCTCATCA 996
OY      665 CTGACGTGGGC 675
Db      997 GCGAGGTGGC 1007

RESULT 4
US-11-108-163B-5
; Sequence 5, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Ralf
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
; FILE REFERENCE: 1716.034008/MAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Nonomuraea flexuosa
; FEATURE:
; OTHER INFORMATION: am24*, like am24 but 9 codons are changed in the sequence like in
```

```
; OTHER INFORMATION: am35* (See Example 10)
US-11-108-163B-5
Query Match      28.0%; Score 189.2; DB 11; Length 663;
Best Local Similarity 61.8%; Pred. No. 2.4e-44;
Matches 356; Conservative 0; Mismatches 208; Indels 12; Gaps 3;

OY      100 ACCCCCACTCGAGGGCTGGACGATGTTATTATTAATTCCTGTGAGTGAACGTGA 159
      13 ACCCAGAACGACCGGCTACGACAAAGGCTACTTCTACTCGTTCTGACCGACGCCCC 72
OY      160 GCGCAGGCACGTAACACCACTTGAAGGCGGCACTTACGAGATCAGCTGGGGAAGTGGC 219
      73 GGCACCTGCTCCATGACCTCCACTCGGCGGCAAGCTACAGACCTCGTGGCGCAACACC 132
OY      220 GGTAACTCGTGGTGAAGGGCTGGAACCCGCGCTGAACGCAAGACCATCCACTTT 279
      133 GGCACCTTCTGTCGCCGCAAGGGCTGTCCACCGC--GGCCGCGCAACGTCACCTAC 189
OY      280 GAGGTGTTTACCAAGCCAAACGCAACAGCTACCTTCCGGTCTACGGTTGACCCGCAAC 339
      190 AACGCTCTTCAACCCGTCGGGTAAAGCCTTACTTCAAGCTTACCGCTGAGACGAGAAC 249
OY      340 CCGCTGTGAGTATTATTCGTGAGAACTTTGGCACTTATGATCTTCTCCGGTCT 399
      250 CCGCTGTGAGTACTTCAATTCGTGAGAGCTGGGCACTTACCGGCCAAC-----GGC 303
OY      400 ACCGATCTAGGAACCTGTGAGTGCAGCGGTAGACATCTATCGACTCGGCAAGACCACTGCG 459
      304 ACCTACAAGGGCACCGTCAACCAACGCGGCAAGTACGACATCTACGAGACCTGGCGG 363
OY      460 GTCAACGCACCTAGCATCGACGGCACCCAAACCTTCAACCAATACTGTCGTCGCCAG 519
      364 TACAACGCGCGCTCATCGAGGGCACCCGACCTTCAAGCAATTTGAGCGTCCGGCAG 423
OY      520 GACAAGCGCACAGCGGTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCTCGGCT 579
      424 CAGAAGCGGACAGCGGCACTATCAACCATCGGCAACCACTTGCAGCGCTGGGCGCGCC 483
OY      580 GGTTTGAATGTCAACGGTGAACCACTACTACAGATCGTTGCAACGAGGGCTACTTACG 639
      484 GGCATGAA---CCTGGCAGCCACGACTACGATCATGGCAGCGGCTTACAGAGC 540
OY      640 AGCGCTATGCTCGCATCACCGTGTGACGTGGC 675
Db      541 AGCGGTAGCTCACCGCTCTCATCAGCAGGGTGGC 576

RESULT 5
US-11-108-163B-4
; Sequence 4, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Paloheimo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Fagerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Lantto, Ralf
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
; FILE REFERENCE: 1716.034008/MAC/DJN
; CURRENT APPLICATION NUMBER: US/11/108,163B
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/562,692
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 906
; TYPE: DNA
```

```
; ORGANISM: Nonomuraea flexuosa
; FEATURE:
; OTHER INFORMATION: am35*, like am35 but 9 codons are changed in the sequence. See
; OTHER INFORMATION: Example 10 (the changes do not alter the encoded amino acid
; OTHER INFORMATION: sequence)
US-11-108-163B-4
```

```
Query Match      28.0%; Score 189.2; DB 11; Length 906;
Best Local Similarity 61.8%; Pred. No. 2.7e-44;
Matches 356; Conservative 0; Mismatches 208; Indels 12; Gaps 3;
```

```
Oy 100 ACCCCCACTCGAGGGCTGGCAGATGTTATTAATTCCTGTGGAGTGACGGTGA 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 ACCCAGAACCAAGACCGCTACGACACGGCTACTTCTACTGTTCTGACGACGCCCC 72
Oy 160 GCGCAGCCACGTACACCAACCTGGAAGCGGCACCTACGATCAGTCACTGGGAGATGGC 219
    | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 73 GGCACCGTCTCCATGACCTCCACTCGGGCGCAGCTACAGCACTCGTGGCGCAACACC 132
Oy 220 GGTAACTCTGCTGGTGGAAAGGGCTGGAACCCCGGCTGAACGCAAGACCATTCCTTT 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 GGCACCTTCTGTCGGCGGCAAGGGCTGTCCACCGGC---GGCGCGCCACCGTCACTAC 189
Oy 280 GAGGGTGTTTACCAAGCCAAACGGCAACAGTACCTTGGGCTTACGGTTGACCCGCAAC 339
    | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 190 AACGCTCTCTTCAACCCGTCGGGTAAAGCCTACCTCAGGCTCTTACGGCTGACAGGAAC 249
Oy 340 CCGCTGCTGAGTATTACATCGTCGAGAACTTTGGCAGCTATGATCCTTCCCTCCGGTCT 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 CCGCTGCTGAGTACTACATCGTCGAGAGCTGGGGCAGCTTACCGGCCACC-----GGC 303
Oy 400 ACCGATCTAGGAACCTGTGAGTGGCAGCGGTAGCATCTATTCAGTCGGCAAGACCACTGC 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 ACCTACAAGGGCACCCTCACCACCGACGGCGCAGCTACGACATCTACGAGACTGGCGG 363
Oy 460 GTCAACGCACTAGCATGACGGGCAACCAACCTTGACCAATAGTGTGGTCCGCCAG 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 TACAACGGCCGCTCCATCGAGGGCACCAGGACCTTCCAGAGATTCTGAGCGTCCGGCAG 423
Oy 520 GACAAGCCGACCAAGCGGTACCGTCCAGACGGGCTGCCATTTCAGCGCTGGGCTCGCGCT 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 CAGAAGCGGACCAAGCGGCAACCATTCAGCAACCACTTCGACGCGCTGGGCCCGGCC 483
Oy 580 GGTGTAATGTCAACGGTGACCACTACTACAGATCGTTGCAACGGAGGCTACTTCAAC 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 GGCATGAA---CCTGGGCAAGCCACGACTACCAATCATGGCGGACCGAGGGCTTACAGAGC 540
Oy 640 AGCGGTATGCTCGCATCACCGTTGCTGACGTGGGC 675
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 AGCGGTAGTCCACCGTCTCCATCAGCAGGGGTGGC 576
```

RESULT 6

```
US-10-517-939-225
; Sequence 225, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
```

```
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-225
```

```
Query Match      27.6%; Score 186.2; DB 7; Length 1059;
Best Local Similarity 60.2%; Pred. No. 2e-43;
Matches 346; Conservative 0; Mismatches 223; Indels 6; Gaps 2;
```

```
Oy 100 ACCCCCACTCGAGGGCTGGCAGATGTTATTAATTCCTGTGGAGTGACGGTGA 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 ACCTCAGCGGACGGGACCAACAGCGGCACTACTATTCCTTCTGGAAGACAGTGGC 147
Oy 160 GCGCAGCCACGTACACCAACCTGGAAGCGGCACTACGATCAGCTGGGAGATGGC 219
    | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 148 GGCACCGTCACTTCTGTGATGTACGGAGACGGCCGCTACACCTCCACTGGAGCGGCATC 207
Oy 220 GGTAACTCTGCTGGTGGAAAGGGCTGGAACCCCGGCTGAACGCAAGACCATTCCTTT 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 AACAACTGGGTGGCGGCAAGGGCTGGCAGACCGGCTCAGCGCGGA---CGATCAGCTAC 264
Oy 280 GAGGGTGTTTACCAAGCCAAACGGCAACAGTACCTTGGGCTTACGGTTGGAACCCGCAAC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 265 TCGGGCTGTTCAACTCAGCCCGCAATGTTATCTCACTGTACGGTTGACCAACAAT 324
Oy 340 CCGCTGCTGAGTATTACATCGTCGAGAACTTTGGCACTTATGATCCTTCCCTCCGGTCT 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 325 CCATTGATCGAGTACTACATCGTCGACAACTGGGGCAGTACCGGCGCGGGAAGGCTCG 384
Oy 400 ACCGATCTAGGAACCTGTGAGTGGCAGCGGTAGCATCTATCGACTGGCAAGACCACTCGC 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 385 GGCTACATGGGACCGGTGACGAGCGAGCGGCACTACGAGCTTATCGACCCAGCGC 444
Oy 460 GTCAACGCACTAGCATCGACGGCACCACCACTTTCAGCAATAGTGTCCGCCAG 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 GTAAACCAAGCCTTCCATCATTCGGCACCGGACGCTTCTATCAATCTGAGCGTGGCCAG 504
Oy 520 GACAAGCCGACCAAGCGGTACCGTCCAGACGGGCTGCCACTTCAGCGCTGGGCTCGCGCT 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 505 CAGAAGCGGACCGGCGGACCATCACCACCGGCAATCACTTCGACGCGCTGGCGCATAC 564
Oy 580 GGTGTAATGTCAACGGTGACCACTACTACCAATCGTTGCAACGGAGGCTACTTCAAC 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 565 GGAATGAA---CCTCGGCAACCAACTACCAATCATAGGCGAGGCTTACCAAGAGC 621
Oy 640 AGCGGTATGCTCGCATCACCGTTGCTGACGTGGG 674
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 622 AGCGGAGTTCGACATCACGGTGAGCGAGGGCGG 656
```

RESULT 7

```
US-11-108-163B-3
; Sequence 3, Application US/11108163B
; Publication No. US20060014247A1
; GENERAL INFORMATION:
; APPLICANT: Palohelmo, Marja
; APPLICANT: Mantyla, Arja
; APPLICANT: Leskinen, Sanna
; APPLICANT: Pajerstrom, Richard
; APPLICANT: Kallio, Jarno
; APPLICANT: Puranen, Terhi
; APPLICANT: Iantco, Ralf
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
; FILE REFERENCE: 1716.034000B/MAC/DJN
; CURRENT FILING DATE: 2005-04-18
```


PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 663
TYPE: DNA
ORGANISM: Nonomurea flexuosa
FEATURE:
OTHER INFORMATION: am24, shortened form of am35, includes a STOP codon
US-11-108-163B-3

Query Match 27.6%; Score 186; DB 11; Length 663;
Best Local Similarity 61.5%; Pred. No. 2e-43;
Matches 354; Conservative 0; Mismatches 210; Indels 12; Gaps 3;

QY 100 ACCCCCACTCGGAGGGCTGGCAGATGTTATTACTATTCTGTGTGAGTGCAGTGA 159
DB 13 ACCCAGAACCAAGACGGGTACGACCAAGGCTACTTCTACTGTTCTGACCGCGCCC 72
QY 160 GCGCAGGCCACGTACCAACCTGGAAGCGGCACCTACGAGATCAGCTGGGAGATGGC 219
DB 73 GGGACCGTTCATGACCTCCACTCGGGCGGACGTAAGACCTCGTGGCGAACACC 132
QY 220 GGTAACTCTCGGTGGAAGGGCTGGAACCCCGCTGAACGCAAGACCATCACTTT 279
DB 133 GGGAACTTCGTGCGCGGCAAGGGCTGTCCACCGGC---GACGGCGGACCGTGACTTAC 189
QY 280 GAGGGTGTTCACAGCCAAACGGCAACAGCTACCTTGGCGTCTACGGTTGACCCGCAAC 339
DB 190 AAGCGCTCCTTCAACCCGTCGGGTACGCTTACCTCAACGCTCTACGGCTGACCGAAGC 249
QY 340 CCGCTGTGAGTATTACATCGTCGAGAACTTTGGCACTTATGATCCTTCCCTCGGTGCT 399
DB 250 CCGCTGTGAGTACTACATCGTCGAGAGCTGGGGCACTTACCGGCCACC-----GGC 303
QY 400 ACCGATCTAGGAAGTGTGAGTGCAGCGGTAGCATCTATGCACTCGGCAAGACCACTGCG 459
DB 304 ACCTTCAAGGGCAACGTCACCAACGCGGCGGACGTACGACATCTACGAGACCTTGGCGG 363
QY 460 GTCAACGCACTTAGCATCGACGGCAACCAACCTTGCACCAATACTGTCGTCGCGCCAG 519
DB 364 TACAACGCGCGCTCATCGAGGGCAACCGACCTTCCAGAGTCTTGAGCGTCCGGCAG 423
QY 520 GACAAGCGCACAGCGGTACCGTCCAGACGGGCTGCCATTTCAGCGCTGGGCTCGCGCT 579
DB 424 CAGAAGCGGACCAAGCGGACCATCAACCTGCGCAACCACTTGCAGCGCTGGGCGCGCC 483
QY 580 GGTGATGTCAACGGTGACCACTACTACAGATCGTTGCAACGGAAGGCTTACTTACG 639
DB 484 GGCATGAA---CTGGGCGAGCCAGCACTACAGATCATGCGGACCGAGGCTTACAGAGC 540
QY 640 AGCGGCTATGCTCGCATCACCGTGTGCTGACGTGGGC 675
DB 541 AGCGGTAGCTCCACCGTCTTCATCAGCAGGGGTGGC 576

RESULT 8

US-11-108-163B-2
Sequence 2, Application US/11108163B
Publication No. US20060014247A1
GENERAL INFORMATION:
APPLICANT: Palohelmo, Marja
APPLICANT: Mäntylä, Arja
APPLICANT: Leskinen, Sanna
APPLICANT: Fagerstrom, Richard
APPLICANT: Kallio, Jarno
APPLICANT: Puranen, Terhi
APPLICANT: Lantto, Ralf
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Method and DNA Constructs for Increasing the Production Level of
TITLE OF INVENTION: Carbohydrate Degrading Enzymes in Filamentous Fungi
FILE REFERENCE: 1716.03400B/MAC/DJN

CURRENT APPLICATION NUMBER: US/11/108,163B
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/562,692
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 906
TYPE: DNA
ORGANISM: Nonomurea flexuosa
FEATURE:
OTHER INFORMATION: am35, Nf xyn11A coding region for the mature Nf Xyn11A (AM35)
US-11-108-163B-2

Query Match 27.6%; Score 186; DB 11; Length 906;
Best Local Similarity 61.5%; Pred. No. 2.2e-43;
Matches 354; Conservative 0; Mismatches 210; Indels 12; Gaps 3;

QY 100 ACCCCCACTCGGAGGGCTGGCAGATGTTATTACTATTCTGTGTGAGTGCAGTGA 159
DB 13 ACCCAGAACCAAGACGGGTACGACCAAGGCTACTTCTACTGTTCTGACCGCGCCC 72
QY 160 GCGCAGGCCACGTACCAACCTGGAAGCGGCACCTACGAGATCAGCTGGGAGATGGC 219
DB 73 GGGACCGTTCATGACCTCCACTCGGGCGGACGTAAGACCTCGTGGCGAACACC 132
QY 220 GGTAACTCTCGGTGGAAGGGCTGGAACCCCGCTGAACGCAAGACCAATCCACTTT 279
DB 133 GGGAACTTCGTGCGCGGCAAGGGCTGTCCACCGGC---GACGGCGGACCGTGACTTAC 189
QY 280 GAGGGTGTTCACAGCCAAACGGCAACAGCTACCTTGGCGTCTACGGTTGACCCGCAAC 339
DB 190 AAGCGCTCCTTCAACCCGTCGGGTACGCTTACCTCAACGCTCTACGGCTGACCGAAGC 249
QY 340 CCGCTGTGAGTATTACATCGTCGAGAACTTTGGCACTTATGATCCTTCCCTCGGTGCT 399
DB 250 CCGCTGTGAGTACTACATCGTCGAGAGCTGGGGCACTTACCGGCCACC-----GGC 303
QY 400 ACCGATCTAGGAAGTGTGAGTGCAGCGGTAGCATCTATGCACTCGGCAAGACCACTGCG 459
DB 304 ACCTTCAAGGGCAACGTCACCAACGCGGCGGACGTACGACATCTACGAGACCTTGGCGG 363
QY 460 GTCAACGCACTTAGCATCGACGGCAACCAACCTTGCACCAATACTGTCGTCGCGCCAG 519
DB 364 TACAACGCGCGCTCATCGAGGGCAACCGGACCTTCCAGAGTCTTGAGCGTCCGGCAG 423
QY 520 GACAAGCGCACAGCGGTACCGTCCAGACGGGCTGCCATTTCAGCGCTGGGCTCGCGCT 579
DB 424 CAGAAGCGGACCAAGCGGACCATCAACCTGCGCAACCACTTGCAGCGCTGGGCGCGCC 483
QY 580 GGTGATGTCAACGGTGACCACTACTACAGATCGTTGCAACGGAAGGCTTACTTACG 639
DB 484 GGCATGAA---CTGGGCGAGCCAGCACTACAGATCATGCGGACCGAGGCTTACAGAGC 540
QY 640 AGCGGCTATGCTCGCATCACCGTGTGCTGACGTGGGC 675
DB 541 AGCGGTAGCTCCACCGTCTTCATCAGCAGGGGTGGC 576

RESULT 9

US-10-517-939-165
Sequence 165, Application US/10517939
Publication No. US20060003433A1
GENERAL INFORMATION:
APPLICANT: Steer, Brian
APPLICANT: Callen, Brian
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM

```
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 165
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; US-10-517-939-165
```

```
Query Match      27.4%; Score 185; DB 7; Length 1047;
Best Local Similarity 60.6%; Pred. No. 4.4e-43;
Matches 340; Conservative 0; Mismatches 215; Indels 6; Gaps 2;
```

```
QY 115 GGCTGGACGATGTTATTACTTCTGTGTGAGTGCAGTGGAGCGACGACGCTAC 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 97 GGACACCAACAGCGCTTCTACTATTCTGTCTGACCGACGCGGTGCTCCGTGCACTTC 156
    175 ACCAACCTGGAAGCGGACCTACGATCAGCTGGGAGATGGCGGTAACTCTGCTGGT 234
    157 TGCTGCAATCCGCCGGCGGTACACTCCAGCTGAGCAATGTGGAACCTGGGTCCGT 216
QY 235 GGAAGGGCTGGAACCCCGGCTGAACGCAAGAGCCATCCACTTTGAGGGTGTACCAG 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 217 GGCAAGGGCTGGCAGACCGGCGCGC--CGCAACATCAACTATTCGGGCACTTCAAT 273
QY 295 CCAACCGGCAACAGCTACCTTGGCGTCTACGGTTGACCCGCAACCCGCTGTCAGTAT 354
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 274 CCCTCGGGTACCGCTACCTGGCGCTCTATGGCTGACCAAGATCCCTGTGTGAGTAC 333
QY 355 TACATCGTGAAGAACTTTGGACCTATGATCCTTCCGTGCTACCGATCTAGAACT 414
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 334 TACATCGTGAACAACTGGGTACTATCTCCACCGGGTGGCAGGATTCATGGCAGC 393
QY 415 GTGAGTGCAGCGGTAGCATCTATGCACTCGGCAAGACCACTCGCTCAACGCACTAGC 474
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 394 GTGTGACGCAATGGCGGCACTACGATCTACCGCAGCAACGGGTCAACGGCCCTCC 453
QY 475 ATGACGGCAACCAACCTTCGACCAATACTGTCGCTCCGCCAGAGCAAGCGCACCAAC 534
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 454 ATTCAAGGGCAACGCACTTCTACCACTGAGCGTTCGCCAGTCCGAAGCGCACCGGT 513
QY 535 GGTAACGTCACAGCGGCTGCCACTTCGACCGCTGGGCTCGCGCTGTTGAATGTCAAC 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 514 GGAACCATCTCCACCGGCAACCAATTTGACGGCTGGGCGACGTTCCGCATGAA--CCTG 570
QY 595 GGTACCACTACTACCAAGATCGTTGCAAGGAGGCTACTTCAGCAGCGGCTATGCTGC 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 571 GGAACCTTCAATTAACAGATCGTGGCAGCAGAGGCTACCAAGACGCGCAATTCGAC 630
QY 655 ATCACCGTGTGACGTGGGC 675
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 631 ATCACGCTGAGCGATGGCGGC 651
```

```
RESULT 10
US-10-517-939-199
; Sequence 199, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
```

```
; APPLICANT: Blum, David
; APPLICANT: Begeghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 199
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; US-10-517-939-199
```

```
Query Match      25.2%; Score 170; DB 7; Length 1074;
Best Local Similarity 57.5%; Pred. No. 8.1e-39;
Matches 368; Conservative 0; Mismatches 260; Indels 12; Gaps 3;
```

```
QY 29 CGGCTTAAGCCGCGACTGGGGCCCTGGCCTTCCCGCAGGGAATGCCACGAGCTCGAAA 88
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 26 CGGGCAGCGCGCGCGCTGCGCGCTGGCTGCTTCCCGCCTTACATGGCCCGCGCA 85
QY 89 AGCGACAGAC-----AACCCTCACTCGAGGGCTGGCAGCATGTTATTACTATTCTCT 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86 ATGCGCAACCTGCATCAGCTGAGCGCAGCAGCGGGCAACCAACGCAACTACTTTTCGT 145
QY 143 GGTGAGTACCGGTGAGCGGCGCAGCCAGTACCAACCTTGAAAGCGGCGACCTACGAGA 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 146 TCTGAAAGACAGCCCGGCGCAGGTGAACCTTGTCAATGTACTCCGGCGCGCTACAGT 205
QY 203 TCAGCTGGGAGATGCGGTAACTCTGTGTGGAAGGGCTGGAACCCCGGCTGAACG 262
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 206 CCAACTGAGCGGCATCAACAACTGGGTGGCGGCAAGGGCTGGCAGAGGGCTGCTCC 265
QY 263 CAAGACCATCCACTTTGAGGGTGTTCACAGCCAAACGGCAACAGTACCTTGGGTCT 322
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 266 GCACCGTCTCCTACTCCGGCAGCTTCAATTCCCG--GTAACGGCTACCTGACGCTCT 322
QY 323 ACGGTGGAACCCGCAACCCGCTGCTGAGTATTACATCTTCGAACCTTTGGCACTATG 382
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 323 ACGGTGGAACCAACATCCGCTCATGACTACTACATCTGCAACACTGGGGCAGCTATC 382
QY 383 ATCTTCTCTCCGCTGCTACCGATCTAGGAACCTGTGAGTGGCAGGTAAGCATCTATCGAC 442
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 383 GTCCCGCGGTGGCAGGGCTTCATGGGCAAGGTGAACACGAGCGGCGCAGTACGACA 442
QY 443 TCGCAAGACCACTGCGCTCAACGCACTAGCATGACGCGCAACCAACCTTCGACCAAT 502
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 443 TCTATGCAAGCAACGAGGTCAACCAAGCTGATCATCGGCAACCGGCTTACCAAGT 502
QY 503 ACTGTGCGTCCGCCAGAGCAAGCGGCAACGCGTACCGGCTGCAAGCGGCTGCACTTCG 562
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 503 ACTGAGCGGTGGGCAAGTCAAGCGCACCGGCGCACCATCAACACGGCAACCACTTCA 562
QY 563 ACGCTGGGCTCGCGCTGTTGAATGTCAACGGTGAACCACTACTACAGATCGTTGCA 622
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 563 ATGCTGGGCGCAGCTCGGCATGAA--CCTGGGACAGCAACCACTACAGGTGATGGCCA 619
QY 623 CGGAGGGCTACTTACGAGCGGCTATGCTGCATCACCGT 662
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 620 CCGAGGGCTACAGAGCAGCGGCAAGCTCCGACATCACGGT 659
```

```
RESULT 11
US-10-517-939-255
; Sequence 255, Application US/10517939
```


Db 529 ACCGCCAACCACTTCAACGCGCTGGGCCACGCTGGGCATGAA--CCTGGGCCAGACACAAAC 585
QY 607 TACCAAGATCGTTGCCAACGGAGGCTACTTACAGACGGGCTATGCTCGCATCACCGTTGCT 666
Db 586 TACCAGGTGATGGCCACCGAGGGTTACAGAGCAGTGGCAGCTCCGACATCACCGTGACC 645
QY 667 GACGTGGGC 675
Db 646 GAGGCGGCGC 654

RESULT 13

US-10-517-939-221
; Sequence 221, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 221
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-221

Query Match 24.5%; Score 165.6; DB 7; Length 1044;
Best Local Similarity 58.0%; Pred. No. 1.4e-37;
Matches 332; Conservative 0; Mismatches 234; Indels 6; Gaps 2;
QY 104 CCAACTCGAGGCTGGCAGCATGTTATTACTATTCCTGGTGAAGTGAACGCTGAGCGGC 163
Db 89 CCAGCCAGACCGGCAACCAACAGCGCAATATTTTCATTCTGAAAGAACAAACCCGGGCA 148
QY 164 AGGCCACGTACACCAACCTGGAAGGCGGCACTACGAGATGAGCTGGGAGATGGCGGTA 223
Db 149 CGGTGACCTTCTGCATGTATGCCAACGGCGGCTACACCTCCAACTGGAGCGGCATCAACA 208
QY 224 ACCTCGTCGGTGAAGGGCTGGAACCCCGGCTGAACGCAAGAGCCATCCACTTTGAGG 283
Db 209 ACTGGGTGGTGGCAAGGGCTGGCAGACTGGCTCGAATCGCAACGCTGACTACTCCGGTT 268
QY 284 GTGTTTACCAAGCAACGGCAACAGCTAATTGCGGTCTACGGTTGACCCGCAACCGGC 343
Db 269 CGTTCAACTCGC--CGGCAACGGCTAACCCTCAACCTGTACGGGTGACCAAGAAATCCGC 325
QY 344 TGGTCGATATTACATCGTCGAGAACTTTGGCACTTATGATCTTCTCCGGTGTACCG 403
Db 326 TGATCGAGTACTACATCGTCGACAGTTGGGGCAGTTATCGACCGCCGGCGGCAAGGCT 385
QY 404 ATCTAGAACTGTGAGTGCAGCGGTAGCATCTATGACTCGGCAAGACCACTCGCGTCA 463
Db 386 TCATGGGACACCGTGAACGACCGGCGGCACTTACGACATCTATCGACGCAAGCGGCTGA 445
QY 464 ACGACCTAGCATCGACGGCAACCAACCTTGCACCAATATCTGCTCCGCGCAGGACA 523
Db 446 ACCAGCCTTCCATCATCGGCAACCGGCAAGCTTCTACCACTACTGAGAGCGGTGCGGCAATCGA 505

QY 524 AGGCCAACCGGTACCGTCCAGACGGGCTGGCACTTGACGCGCTGGGCTCGCGCTGTT 583
Db 506 AGCGCTGGGGGACACCATCACACCGCCAAACCACTTCAATGCTGGCGCAGCTGGGCA 565
QY 584 TGAATGTCAACGCTGACCACTACTACCAAGATCGTTGCAACGAGGGCTACTTACAGACG 643
Db 566 TGA--CCTGGGCAAGCAACTACAGGTGATGGCCACCGAGGGTTACAGAGACGCG 622
QY 644 GCTATGCTCGCATCACCGTTGCTGACGTGGC 675
Db 623 GCACTCCGACATCACCGGTGACCGAAGCGGC 654

RESULT 14

US-10-517-939-177
; Sequence 177, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 177
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-177

Query Match 24.5%; Score 165.4; DB 7; Length 1299;
Best Local Similarity 56.3%; Pred. No. 1.7e-37;
Matches 351; Conservative 0; Mismatches 266; Indels 6; Gaps 2;
QY 40 GCGACTGGGGCCCTTGCGCTTCCCGGCAAGGATGCCAGGAGCTCGAAGGCAAGACAGACA 99
Db 28 GCGATTGCTGCCGACGACTAGCGGTGGCGACTGTTCCAATCGCTCATGCGCAACGCTT 87
QY 100 ACCCCCACTCGAGAGGCTGGCAGATGTTATTACTATTCCTGTGAGTGAAGTGGTGA 159
Db 88 AGCTCAATGCCACTGGAACCCAGATGTTACTACTATTCGTTTGAAGATTCGGGT 147
QY 160 GCGCAGGCCAGTACACCAACTGGAAGGCGGCACTACAGATCAGCTGGGAGATGGC 219
Db 148 AAGCCACCATGACACTCGGTGCCGTGGAACACTATCTTCATCTCGAAGACAGCACT 207
QY 220 GGTAACTCGTCGGTGAAGGGCTGGAACCCCGGCTGAACGCAAGACCATCACTTT 279
Db 208 AACAACTGGGTGGCGGTAAAGGCTGATGCCGG--TACTCGGCGCACAGTACCTAT 264
QY 280 GAGGTGTTTACCAAGCAACGGCAACAGCTACCTTGCGGTCTACGGTTGACCCGCAAC 339
Db 265 TCGGGCAGTTATAGCGGAGTGAACCAAGCTACCTCGCACTTTACGGCTGAGCTGAAC 324
QY 340 CCGCTGTGAGTATTACATCGTCGAGAACTTTGGCACTTATGATCCTTCTCCGCTGCT 399
Db 325 CCGTGATGAAATATTACATTGTGAAAACTGGGTCAATTACAATCTGCGTCCGCGCA 384

QY 400 ACCGATCTAGGAAGTCTGAGTGCAGCGGTAGCATCTATCGACTCGGCAAGACCACTCGC 459
DB 385 ACGAATTATGGAGCTGTCAATATTTAGCGGACACCTACAGCTGGGCGGCAAGCGG 444
QY 460 GTCAACGCACTAGCATCGACGCGCAACCTTGCACCAATAGTGTGCTCGGCGAG 519
DB 445 GTTAATCAGCCATCTATTTGAAGGCAAGCGGCAAGTCTACCAATAGTGTGCGCAA 504
QY 520 GACAAGCGCAAGCGGTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCTCGGCT 579
DB 505 AACAGCGCACCGGACCGAATTAATTTGAGCGCATTTGCATGCGATGGGCTGCTGTG 564
QY 580 GGTGATGTCACGCTGACCACTACTACCAAGATCGTTGCAACGAGGGCTACTTCAAC 639
DB 565 GGCTTGAA--CCTGGGGACTCAGGATTAATGATGAGTGGCGAAGGCTTACCGAGAGC 621
QY 640 AGCGGCTATGCTCGCATCACCGT 662
DB 622 AGCGGCGAGTCCATATATCACGGT 644

RESULT 15

US-10-517-939-195
Sequence 195, Application US/10517939
Publication No. US20060003433A1
GENERAL INFORMATION:
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wu, Di
APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 564462007901
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 195
LENGTH: 1044
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-195

Query Match 23.8%; Score 160.8; DB 7; Length 1044;
Best Local Similarity 59.0%; Pred. No. 3.3e-36;
Matches 333; Conservative 0; Mismatches 222; Indels 9; Gaps 3;

QY 115 GGCTGGCAGATGTTATTACTATCTCGTGGAGTGAAGGCGGCAAGCGGCAAGCTAC 174
DB 97 GGCACCAACAAGGCTTCTATATCTCTTGGAAGACAGTCCGGGTTCAGTGAATTTC 156
QY 175 ACCAACCTGGAAGCGGCGACCTACGAGATCAGCTGGGAGATGGCGGTAACTCTCGCT 234
DB 157 TGCATGTACTCCGGCGGTGCTACAGCTGAGCTGAGCGGCGATCAACAATGGGTCGGC 216
QY 235 GGAAGGGCTGGGAACCCCGGCTGAAGCAAGAGCCATCACTTTGAGGGTGTTTACCAAG 294
DB 217 GGCAAGGGCTGGCAACCGGATCGGCGGAGCCATCAACTACTCCGGCAGCTTCAACTCG 276
QY 295 CCAACCGGCAAGCTACCTTGGGCTTACGTTGACCGGCAACCGCTGGTGAAGTAT 354
DB 277 CCG---GGCAATGGCTACCTCGCGCTCTACGAGTGAACCAATCCACTCGTGAAGTAC 333
QY 355 TACATCGTGAAGAACTTTGGACACTATGATCCTTCCGCTGCTACCGATCTAGGAAGT 414

DB 334 TACATCGTGAACAACCTGGGCGGAGTATCGTCCGCGCGGCGGCAAGGCTATGAGCAAG 393
QY 415 GTCAGTGGGACGGTAGCATCTATCGACTCGGCAAGACCACTGGCGTCAACGAC--CT 471
DB 394 GTACAGAGGAGCGGCGGCGGCAAGTGAAGTCTATCGAAAGCAAGAGTGTGATGCGCTCG 453
QY 472 AGCATGACGGGCAACCAACCTTGAACCAATATCTGTGCTCGGCGGCAAGAGCGGCAAC 531
DB 454 ATCATGTGATGATCAGCAGACCTTCTATCAATAGTGAAGCGTGCATGCAAGAGAGACC 513
QY 532 AGCGGTACCGTCCAGACGGGCTGCCACTTGCAGCGCTGGGCTCGGCTGTTGAATGTC 591
DB 514 GGCGAAGCATCAGCAGCGGCAACCACTTGCATGAGCTGGGCGAGCTACGGCATGAA--C 570
QY 592 AACGTGACCACTACTACCAAGATCGTTGCAACGAGGGCTACTTACGAGCGGCTATGCT 651
DB 571 CTGGGAAGTCAACAATACTACCAATCTTGGCGAGCGAGGGTTATCAAGAGAGCGGAGCTCG 630
QY 652 CGCATCACCGTGTGCTGACGTGGGC 675
DB 631 GACCTCACCGGTGAGCGGAAGGAGC 654

Search completed: February 11, 2006, 22:06:17
Job time : 217.772 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 14:49:18 ; Search time 151.432 Seconds
(without alignments)
652.836 Million cell updates/sec

Title: US-09-467-368-2
Perfect score: 1238
Sequence: 1 MVGFTPVALLAALATGALAF.....VATEGYFSSGYARITVADVG 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1238	100.0	225	2	AAW01112	Aaw01112 Xylanase.
2	1238	100.0	225	2	AAW05187	Aaw05187 Endo-1,4-
3	1238	100.0	225	7	ABR63119	Abt63119 Thermomyc
4	1238	100.0	225	9	AEBO0305	Aeb00305 Xylanase
5	1088	87.9	194	5	AAE18456	Aae18456 Thermomyc
6	1083	87.5	194	5	AAAB48543	Aab48543 Thermomyc
7	1083	87.5	194	5	AAO18649	Aao18649 T. lanugin
8	1083	87.5	194	8	ADI66751	Adi66751 T. lanugi
9	965	77.9	194	3	AAAB48542	Aab48542 Paecilomy
10	965	77.9	194	5	AAO18648	Aao18648 P. varioti
11	965	77.9	194	8	ADI66750	Adi66750 P. variot
12	806.5	65.1	221	3	AAAB48548	Aab48548 Cochliobo
13	806.5	65.1	221	5	AAO18654	Aao18654 C. carbonu
14	806.5	65.1	221	8	ADI66756	Adi66756 C. carbon
15	688.5	55.7	227	9	AEBO0301	Aeb00301 Xylanase
16	688.5	55.6	227	2	AAAR75421	Aar75421 Humicola
17	688.5	55.6	227	2	AAAR75421	Aar75421 Humicola
18	685.5	55.4	223	2	AAAR75422	Aar75422 Humicola
19	684.5	55.3	223	2	AAAR75422	Aar75422 Humicola
20	684.5	55.3	223	2	AAAR75422	Aar75422 Humicola
21	681.5	55.0	221	6	ABB80185	Abb80185 A. fumiga
22	678.5	54.8	261	2	AAW18115	Aaw18115 Chaetomiu
23	671	54.2	234	6	ABB80186	Abb80186 A. fumiga
24	663	53.6	197	2	AAW60736	Aaw60736 Xylanase

25	663	53.6	197	3	AAV98068	Aay98068 S. commun
26	663	53.6	197	3	AAAB48537	Aab48537 Schizophy
27	663	53.6	197	5	AAO18643	Aao18643 S. commune
28	663	53.6	197	5	AAE18445	Aae18445 Schizophy
29	663	53.6	197	8	ADI66745	Adi66745 S. commun
30	662.5	53.5	230	2	AAW18116	Aaw18116 Chaetomiu
31	647.5	52.3	190	7	AAO30298	Aao30298 Trichoder
32	647.5	52.3	190	7	AAO30297	Aao30297 Trichoder
33	646.5	52.2	190	5	AAE18492	Aae18492 Trichoder
34	646.5	52.2	190	5	ABE47005	Aeb47005 Thermophi
35	644.5	52.1	190	5	AAE18496	Aae18496 Trichoder
36	644.5	52.1	190	5	AAE18494	Aae18494 Trichoder
37	644.5	52.1	190	5	ABE47006	Aeb47006 Thermophi
38	643.5	52.0	190	7	AAO30285	Aao30285 Trichoder
39	643.5	52.0	190	7	AAO30284	Aao30284 Trichoder
40	643.5	52.0	190	7	AAO30286	Aao30286 Trichoder
41	643.5	52.0	190	7	AAO30283	Aao30283 Trichoder
42	643.5	52.0	190	7	AAO30293	Aao30293 Trichoder
43	643.5	52.0	190	7	AAO30294	Aao30294 Trichoder
44	640.5	51.7	190	5	ABE47004	Aeb47004 Thermophi
45	640.5	51.7	190	5	ABE47001	Aeb47001 Thermophi

ALIGNMENTS

RESULT 1	AAW01112	standard; protein; 225 AA.
ID	AAW01112	standard; protein; 225 AA.
XX		
AC	AAW01112;	
XX		
DT	21-MAY-1997	(first entry)
XX		
DE	Xylanase.	
XX		
KW	Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermoascus;	
KW	Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia;	
KW	Byssoschlamus; Paecilomyces; animal feed additive; in-vivo breakdown;	
KW	plant cell wall; growth rate; feed conversion.	
XX		
OS	Thermomyces lanuginosus.	
XX		
PN	WO9623062-A1.	
XX		
PD	01-AUG-1996.	
XX		
PF	26-JAN-1996;	96WO-DK000046.
XX		
PR	26-JAN-1995;	95DK-00000094.
XX		
PA	(NOVO) NOVO-NORDISK AS.	
XX		
PI	Hansen PK, Wagner P, Muellertz A, Knap IH;	
XX		
DR	WPI; 1996-454790/45.	
DR	N-PSDB; AAT40742.	
XX		
PT	Fungal xylanase preps. for use as animal feed additives - and DNA	
PT	construct for producing recombinant Thermomyces xylanase.	
XX		
PS	Claim 5; Page 45-46; 69pp; English.	
XX		
CC	This sequence represents the xylanase from Thermomyces lanuginosus strain DSM 4109. This xylanase, and xylanases derived from Humicola, Thermoascus, Chaetomium, Mucor, Talaromyces, Malbranchea, Myceliophthora, Thielavia, Byssoschlamus or Paecilomyces strains can be used in the monocomponent xylanase preparations of the invention. The xylanase preparations and the recombinant Thermomyces xylanase are useful as animal feed additives, which promote in-vivo breakdown of plant cell wall material and thus improve digestibility, growth rate and/or feed conversion	
CC		
XX		

SQL Sequence 225 AA;

Query Match 100.0%; Score 1238; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3e-108;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGFTPVLAALAAATGALAFAPGNATELEKROTPNSEGWHGYYYSWSDGGAQATYTN 60
1 MVGFTPVLAALAAATGALAFAPGNATELEKROTPNSEGWHGYYYSWSDGGAQATYTN 60
DB 1 MVGFTPVLAALAAATGALAFAPGNATELEKROTPNSEGWHGYYYSWSDGGAQATYTN 60
QY 61 LEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQVYQPNNGNSYLAVYGWTRNPLVEYYI 120
61 LEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQVYQPNNGNSYLAVYGWTRNPLVEYYI 120
DB 61 LEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQVYQPNNGNSYLAVYGWTRNPLVEYYI 120
QY 121 VENFGTYDPSSGATDLGTVCECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
121 VENFGTYDPSSGATDLGTVCECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
DB 121 VENFGTYDPSSGATDLGTVCECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADV 225
181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADV 225
DB 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADV 225

RESULT 2
AAW05187
ID AAW05187 standard; protein; 225 AA.

AC AAW05187;

DT 16-OCT-2003 (revised)
DT 22-FEB-1997 (first entry)

DE Endo-1,4-beta-D-xylanase.

KW Endo-1,4-beta-D-xylanase; xylanase; Thermomyces lanuginosus;
KW Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae; yeast;
KW flour; baking; dough.

OS Thermomyces lanuginosus; (strain DSM 4109).

PN WO9632472-A1.

PD 17-OCT-1996.

PF 11-APR-1996; 96WO-DK000171.

PR 11-APR-1995; 95DK-00000435.

PA (NOVO) NOVO-NORDISK AS.

PI Jorgensen OB, Si JQ, Jakobsen TS;

DR WPI; 1996-477123/47.
N-PSDB; AAT43010.

PT Bread improving additive contg. xylanase from Thermomyces - and opt.
PT alpha-amylase, increases volume, improves anti-staling properties etc.

PS Claim 4; Page 31-32; 41pp; English.

CC The sequence represents an endo-1,4-beta-D-xylanase from Thermomyces
CC lanuginosus (Humicola lanuginosa), which may be used as a bread-
CC improving additive. The enzyme may be expressed recombinantly from a
CC plasmid pYES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed),
CC and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour,
CC optionally along with other enzymes (amylase, maltogenase, lipase,
CC cellulase, hemicellulase, pentosanase, glucose-oxidase, laccase,
CC protease and/or peroxidase). The enzyme combines particularly well with
CC amylolytic enzymes, and may be used to improve baking properties of flour
CC and/or dough, by increasing volume and improving texture, flavour, crumb
CC softness, freshness and anti-staling properties, while improving dough
CC machinability and stability. (Updated on 16-OCT-2003 to standardise OS
CC field)

SQL Sequence 225 AA;

Query Match 100.0%; Score 1238; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3e-108;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGFTPVLAALAAATGALAFAPGNATELEKROTPNSEGWHGYYYSWSDGGAQATYTN 60
1 MVGFTPVLAALAAATGALAFAPGNATELEKROTPNSEGWHGYYYSWSDGGAQATYTN 60
DB 1 MVGFTPVLAALAAATGALAFAPGNATELEKROTPNSEGWHGYYYSWSDGGAQATYTN 60
QY 61 LEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQVYQPNNGNSYLAVYGWTRNPLVEYYI 120
61 LEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQVYQPNNGNSYLAVYGWTRNPLVEYYI 120
DB 61 LEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQVYQPNNGNSYLAVYGWTRNPLVEYYI 120
QY 121 VENFGTYDPSSGATDLGTVCECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
121 VENFGTYDPSSGATDLGTVCECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
DB 121 VENFGTYDPSSGATDLGTVCECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADV 225
181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADV 225
DB 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADV 225

RESULT 3
ABR63119
ID ABR63119 standard; protein; 225 AA.

AC ABR63119;

DT 18-DEC-2003 (first entry)

DE Thermomyces lanuginosus xylanase.

KW Xylanase; thermostable; enzyme; feed additive.

OS Thermomyces lanuginosus.

FH Key Location/Qualifiers

FT Peptide 1..30 /label= Signal_peptide

FT Protein 31..225 /label= Mature_protein

PN WO2003062409-A2.

PD 31-JUL-2003.

PF 23-JAN-2003; 2003WO-DK000039.

PR 25-JAN-2002; 2002DK-00000130.

PA (HOFF) ROCHE VITAMINS AG.

PI Wu W, Pettersson D, Fuglsang CC;

DR WPI; 2003-731382/69.

PT Composition useful as an animal feed additive comprises at least two
PT thermostable enzymes selected from endoglucanase, xylanase, phytase,
PT protease, galactanase, mannanase, dextranase and alpha-galactosidase.

PS Disclosure; Page 60-61; Opp; English.

CC The present sequence is the protein sequence of a thermostable xylanase
CC of Thermomyces lanuginosus. The xylanase has a melting temperature (Tm)
CC of 75.0 degrees C at pH 7.0. It is preferred for use in a claimed
CC composition of the invention, which comprises at least 2 thermostable
CC enzymes selected from an endoglucanase, xylanase, phytase, protease,
CC galactanase, mannanase, dextranase and alpha-galactosidase. The
CC composition is useful for improving the nutritional value of animal
CC feeds, especially those containing soya, wheat, barley, oats and/or rye
CC

Seq	Sequence	225 AA;
Query Match	100.0%;	Score 1238; DB 7; Length 225;
Best Local Similarity	100.0%;	Pred. No. 1.3e-108;
Matches	225; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MVGFTPVALAALATGALAFAPGNATELEKQQTTPNSEGMHDGYIYSWMSDGAQATYTN 60
DB	1	MVGFTPVALAALATGALAFAPGNATELEKQQTTPNSEGMHDGYIYSWMSDGAQATYTN 60
QY	61	LEGGTYEISWGDGGLVGGKGNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI 120
DB	61	LEGGTYEISWGDGGLVGGKGNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI 120
QY	121	VENFGTYDPSSGATDLGIVECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
DB	121	VENFGTYDPSSGATDLGIVECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
QY	181	VQTGCHFDAMARAGLNVNGDHYIQIVATEGYFSSGYARITVADVG 225
DB	181	VQTGCHFDAMARAGLNVNGDHYIQIVATEGYFSSGYARITVADVG 225

RESULT 4
 AEB00305
 ID AEB00305 standard; protein; 225 AA.
 XX
 AC AEB00305;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE xylanase SEQ ID NO:15.
 XX
 KW enzyme; xylanase; feedstuff; alcohol; fermentation; brewing; filtration..
 XX
 OS Thermomyces lanuginosus.
 XX
 PN WO2005059084-A1.
 XX
 PD 30-JUN-2005.
 XX
 PF 17-DEC-2004; 2004WO-DK000880.
 XX
 PR 19-DEC-2003; 2003DK-00001895.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Feesteren RM, Viksø-Nielsen A, Joergensen CT, Christensen LH;
 DR WPI; 2005-458778/46.
 XX
 PT Preparation of a mash (having enhanced filterability and/or improved
 PT extract yield after filtration) comprises preparing a mash in the
 PT presence of enzyme activities comprising xylanase of GH family 10 and
 PT filtering to obtain wort.
 XX
 PS Disclosure; SEQ ID NO 15; 68bp; English.
 XX
 CC The invention relates to a process for preparing a mash (A) (having
 CC enhanced filterability and/or improved extract yield after filtration)
 CC which comprises preparing a mash in the presence of enzyme activities
 CC (comprising a xylanase of GH family 10 at at least 15% w/w of the total
 CC xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a
 CC wort. Also described is a composition is useful for reducing the
 CC viscosity of an aqueous solution comprising a starch hydrolysate, which
 CC is a mash for beer making or a feed composition. The process is useful
 CC for the production of an alcoholic beverage, such as beer or whiskey and
 CC the composition is useful in the mashing and filtration step in brewing
 CC process. The present sequence represents a xylanase used in the mashing
 CC process of the invention.
 XX
 XX
 Sequence 225 AA;

	Query Match	100.0%;	Score 1238;	DB 9;	Length 225;
	Best Local Similarity	100.0%;	Pred. No. 1.3e-108;		
	Matches 225;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MVGFTPVALAALATGALA	FPAGNATELEKQTTPNSEGWHDGYYSWSWSDGAQATYTN	60	
Db	1	MVGFTPLAALAAATGALA	FPAGNATELEKQTTPNSEGWHDGYYSWSWSDGAQATYTN	60	
QY	61	LEGTTYEISWGDGNLVGGK	WNPGLNARAIHFEGVYQPNNGNSYLAVYGWTRNPVREYYI	120	
Db	61	LEGTTYEISWGDGNLVGGK	WNPGLNARAIHFEGVYQPNNGNSYLAVYGWTRNPVREYYI	120	
QY	121	VENFGTYDPSSGATDLGTVECDGS	IYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT	180	
Db	121	VENFGTYDPSSGATDLGTVECDGS	IYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT	180	
QY	181	VQTGCHPDAMARAGLNVNGDHYYQIV	ATEGYFSSSGARITTVADVG	225	
Db	181	VQTGCHPDAMARAGLNVNGDHYYQIV	ATEGYFSSSGARITTVADVG	225	

```

RESULT 5
AAE18456
ID AAE18456 standard; protein; 194 AA.
XX
XX AAE18456;
AC
XX 16-MAY-2002 (first entry)
DT
XX Thermomyces lanuginosus xylanase, Xyn.
DE
XX Modified xylanase; thermostability; alkalophilicity; industrial process;
KW pulp manufacture; poultry; swine feed; enzyme; Xyn.
XX Thermomyces lanuginosus.
OS
XX WO200192487-A2.
PN
XX 06-DEC-2001.
PD
XX 31-MAY-2001; 2001WO-CA000769.
PF
XX 31-MAY-2000; 2000US-0213803P.
PR
XX (CANADA ) NAT RES COUNCIL CANADA.
PA
XX
XX Sung WL;
PI
XX WPI; 2002-171435/22.
DR
XX
XX Modified xylanase exhibiting increased thermostability and
PT alkalophilicity useful for industrial processing e.g. for pulp
PT manufacturing.
XX
XX Disclosure; Page 83-84; 109pp; English.
PS
XX
XX The present invention relates to a modified xylanase exhibiting increased
CC thermostability and alkalophilicity. Modified xylanase is useful in
CC industrial process such as pulp manufacturing. Modified xylanase is also
CC useful for bleaching of pulp, processing of precision devices and
CC improved digestibility of poultry and swine feed. Modified xylanase has
CC improved performance at conditions of high temperature and pH and
CC exhibits improved thermophilicity and/or alkalophilicity in comparison to
CC corresponding native xylanase. The present sequence is Thermomyces
CC lanuginosus xylanase, Xyn
XX
XX
SQ Sequence 194 AA;

Query Match 87.9%; Score 1088; DB 5; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.7e-94;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0
32 QPTPNEGWHHDGYRYSWMSDGAQATYTNLEGGTYEISWGDGGLNVGGKGNPGLNARAI 91

```

Db 1 QTPNSEGWHGDIYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAI 60
OY 92 HFEGVYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVCECDGSIYRLGKT 151
Db 61 HFEGVYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVCECDGSIYRLGKT 120
OY 152 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAAGLNVNGDHYIQIVATEGY 211
Db 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAAGLNVNGDHYIQIVATEGY 180
OY 212 FSSGYARITVADVG 225
Db 181 FSSGYARITVADVG 194

RESULT 6
AAB48543
ID AAB48543 standard; protein; 194 AA.

XX AAB48543;
AC AAB48543;
XX 05-MAR-2001 (first entry)
DT 05-MAR-2001 (first entry)
XX Thermomyces lanuginosus xylanase.
DE Thermomyces lanuginosus xylanase.
XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
KM bleaching agent.
XX Thermomyces lanuginosus.
OS Thermomyces lanuginosus.
XX WO200068396-A2.
PN 16-NOV-2000.
XX 12-MAY-2000; 2000WO-US013172.
PF 12-MAY-2000; 2000WO-US013172.
XX 12-MAY-1999; 99US-0133714P.
PR 12-MAY-1999; 99US-0133714P.
XX (XENC-) XENCOR INC.
PA (XENC-) XENCOR INC.
XX Bentzien JM;
PI Bentzien JM;
XX WPI; 2000-679800/66.

XX Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX Disclosure; Fig 16L; 114pp; English.
XX
XX The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
XX Sequence 194 AA;

Query Match 87.5%; Score 1083; DB 3; Length 194;
Best Local Similarity 100.0%; Pred. No. 5.1e-94;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 TTPNSEGWHGDIYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAIH 92
Db 2 TTPNSEGWHGDIYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAIH 61
OY 93 FEGVYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVCECDGSIYRLGKT 152
Db 62 FEGVYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVCECDGSIYRLGKT 121

OY 153 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAAGLNVNGDHYIQIVATEGY 212
Db 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAAGLNVNGDHYIQIVATEGY 181
OY 213 SSGYARITVADVG 225
Db 182 SSGYARITVADVG 194

RESULT 7
AAO18649
ID AAO18649 standard; protein; 194 AA.

XX AAO18649;
AC AAO18649;
XX 24-OCT-2002 (first entry)
DT 24-OCT-2002 (first entry)
XX T lanuginosus xylanase.
DE T lanuginosus xylanase.
XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KM liquid clarification; coffee extraction; plant oil extraction;
KM starch extraction; food thickener; animal food additive; mutant; mutein.
XX Thermomyces lanuginosus.
OS Thermomyces lanuginosus.
XX WO200238746-A2.
PN 16-MAY-2002.
XX 09-NOV-2001; 2001WO-US048018.
PF 10-NOV-2000; 2000US-00710050.
XX 10-NOV-2000; 2000US-00710050.
PR (XENC-) XENCOR INC.
XX (XENC-) XENCOR INC.
PI Bentzien J, Dahiyat B;
XX Bentzien J, Dahiyat B;
XX WPI; 2002-608200/65.

XX Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX
XX Disclosure; Fig 16L; 121pp; English.
XX
XX The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
CC described in the exemplification of the invention
XX
XX Sequence 194 AA;

Query Match 87.5%; Score 1083; DB 5; Length 194;
Best Local Similarity 100.0%; Pred. No. 5.1e-94;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 TTPNSEGWHGDIYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAIH 92
Db 2 TTPNSEGWHGDIYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAIH 61
OY 93 FEGVYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVCECDGSIYRLGKT 152
Db 62 FEGVYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVCECDGSIYRLGKT 121

Db 62 FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 121

Qy 153 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGYF 212

Db 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGYF 181

Qy 213 SSGYARITVADVG 225

Db 182 SSGYARITVADVG 194

RESULT 8

ADI66751

ID ADI66751 standard; protein; 194 AA.

XX AC ADI66751;

XX DT 22-APR-2004 (first entry)

XX DE T. lanuginosus xylanase.

XX KM Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;

KW paper industry; food; animal feed; thermostability; alkaliphilic;

KW hot alkali treatment.

XX OS Thermomyces lanuginosus.

XX PN US6682923-B1.

XX PD 27-JAN-2004.

XX PF 12-MAY-2000; 2000US-00570856.

XX PR 12-MAY-1999; 99US-0133714P.

XX PR 07-JUN-1999; 99US-0138156P.

XX PA (XENC-) XENCOR.

XX PI Bentzien J, Dahiyat BI;

XX DR WPI; 2004-118575/12.

XX PT New mutant xylanase (XA) protein comprising at least four amino acid

PT substitutions as compared to Bacillus circulans xylanase, useful for

PT bleaching (paper) pulp, and in the food and animal feed industries..

XX PS Disclosure; SEQ ID NO 24; 84pp; English.

XX CC The invention relates to a mutant xylanase activity (XA, endo-1,4-beta

CC xylanase from Bacillus circulans) protein appearing as ADI66730. Also

CC included is a bleaching agent comprising the XA protein. The non-

CC naturally occurring XA protein comprises at least four amino acid

CC substitutions as compared to Bacillus circulans xylanase ADI66728. The

CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,

CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,

CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is

CC useful for bleaching pulp in the paper and related industries, but is

CC also useful in the food and animal feed industries. The new protein is

CC active at higher pH and temperature ranges than naturally occurring

CC xylanases, simplifying incorporation of the xylanase treatment step into

CC pulp processing, especially where the enzyme is added after hot alkali

CC treatment. The present sequence is a xylanase from another species

CC included for comparison.

XX SQ Sequence 194 AA;

Query Match 87.5%; Score 1083; DB 8; Length 194;

Best Local Similarity 100.0%; Pred. No. 5.1e-94;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 TTPNSEGWHDGYYSWSDGAQATYTNLEGGTYEISWGDGNTLVGKGWNPGLNARAIH 92

Db 2 TTPNSEGWHDGYYSWSDGAQATYTNLEGGTYEISWGDGNTLVGKGWNPGLNARAIH 61

Qy 93 FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 152

Db 62 FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 121

Qy 153 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGYF 212

Db 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGYF 181

Qy 213 SSGYARITVADVG 225

Db 182 SSGYARITVADVG 194

RESULT 9

AAB48542

ID AAB48542 standard; protein; 194 AA.

XX AC AAB48542;

XX DT 05-MAR-2001 (first entry)

XX DE Paecilomyces variotii xylanase.

XX KM Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;

KW bleaching agent.

XX OS Paecilomyces variotii.

XX PN WO200068396-A2.

XX PD 16-NOV-2000.

XX PF 12-MAY-2000; 2000WO-US013172.

XX PR 12-MAY-1999; 99US-0133714P.

XX PA (XENC-) XENCOR INC.

XX PI Bentzien JM;

XX DR WPI; 2000-679800/66.

XX PT Non naturally occurring XA protein with enhanced thermophilicity,

PT alkalophilicity or thermostability relative to the naturally occurring

PT Bacillus circulans xylanase is used in an agent for bleaching pulp.

XX PS Disclosure; Fig 16K; 114pp; English.

XX CC The present sequence is given in a specification relating to non

CC naturally occurring xylanase activity (XA) proteins. The XA proteins

CC comprise an amino acid sequence less than 97% identical to a naturally

CC occurring Bacillus circulans xylanase. They are modified to exhibit

CC enhanced thermophilicity, alkalophilicity or thermostability relative to

CC the naturally occurring B. circulans xylanase. They may be used as the

CC active compound in a bleaching agent which is used for bleaching pulp

XX SQ Sequence 194 AA;

Query Match 77.9%; Score 965; DB 3; Length 194;

Best Local Similarity 87.6%; Pred. No. 7.5e-83;

Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 33 TTPNSEGWHDGYYSWSDGAQATYTNLEGGTYEISWGDGNTLVGKGWNPGLNARAIH 92

Db 2 TTPNSEGWHDGYYSWSDGSDSTYTNNSGTYEITWNGGNTLVGKGWNPGLNARAIH 61

Qy 93 FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTT 152

Db 62 FEGVYQPNGNTSYLSVYGWTRNPLVEYYIVENFGSSNPSSGSTDLGTVSCDGSYYTLGOST 121

Qy 153 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGYF 212

Db 122 RYNAPSIDGTQTFNQYWSVRQDKRSSGTVGTGCHFDAMASAGLNTGDHYVQIVATEGYF 181
Qy 213 SSGYARITVADVG 225
Db 182 SSGYARITVADVG 194

RESULT 10
AAO18648
ID AAO18648 standard; protein; 194 AA.

XX AAO18648;

DT 24-OCT-2002 (first entry)

DE P variotli xylanase.

KW xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KW liquid clarification; coffee extraction; plant oil extraction;
KW starch extraction; food thickener; animal food additive; mutant; mutein.
OS Paecilomyces variotli.

PN WO200238746-A2.

PD 16-MAY-2002.

PF 09-NOV-2001; 2001WO-US048018.

PR 10-NOV-2000; 2000US-00710050.

PA (XENC-) XENCOR INC.

PI Bentzien J, Dahiyat B;

DR WPI; 2002-608200/65.

PT Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.

PS Disclosure; Fig 16K; 121pp; English.

CC The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermostability,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductor. The present sequence is a xylanase protein
CC described in the exemplification of the invention

XX Sequence 194 AA;

Query Match 77.9%; Score 965; DB 5; Length 194;
Best Local Similarity 87.6%; Pred. No. 7.5e-83;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 33 TTPNSEGWHDGYYSWSWSDGAQATYTNLEGTYEISWGDGNLVGKGWNPGLNARAIIH 92

Db 2 TTPNSEGWHDGYYSWSWSDGGGSTYTNNSGTYEITWGNGNLVGKGWNPGLNARAIIH 61

Qy 93 FEGVYQPNNGNSYLAIVYGWTRNPLVEYYIIVENFGTYDPSSGATDLGTVCDGSIVRLGKTT 152
Db 62 FTGVYQPNGTSYLSYVYGWTRNPLVEYYIIVENFGSSNPSSGSTDLGTVSCDGSITYLQGST 121

Qy 153 RYNAPSIDGTQTFPDQYWSVRQDKRTSGTVGTGCHFDAMARAGLNVNGDHYVQIVATEGYF 212
Db 122 RYNAPSIDGTQTFNQYWSVRQDKRSSGTVGTGCHFDAMASAGLNTGDHYVQIVATEGYF 181
Qy 213 SSGYARITVADVG 225
Db 182 SSGYARITVADVG 194

RESULT 11
AD166750
ID AD166750 standard; protein; 194 AA.

XX AD166750;

DT 22-APR-2004 (first entry)

DE P. variotli xylanase.

XX xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
KW paper industry; food; animal feed; thermostability; alkalophilic;
KW hot alkali treatment.

XX Paecilomyces variotli.

PN US6682923-B1.

PD 27-JAN-2004.

PF 12-MAY-2000; 2000US-00570856.

PR 12-MAY-1999; 99US-0133714P.

PR 07-JUN-1999; 99US-0138156P.

PA (XENC-) XENCOR.

PI Bentzien J, Dahiyat BI;

DR WPI; 2004-118575/12.

PT New mutant xylanase (XA) protein comprising at least four amino acid
PT substitutions as compared to Bacillus circulans xylanase, useful for
PT bleaching (paper) pulp, and in the food and animal feed industries.

PS Disclosure; SEQ ID NO 23; 84pp; English.

XX The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
CC xylanase from Bacillus circulans) protein appearing as AD166730. Also
CC included is a bleaching agent comprising the XA protein. The non-
CC naturally occurring XA protein comprises at least four amino acid
CC substitutions as compared to Bacillus circulans xylanase AD166728. The
CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
CC useful for bleaching pulp in the paper and related industries, but is
CC also useful in the food and animal feed industries. The new protein is
CC active at higher pH and temperature ranges than naturally occurring
CC xylanases, simplifying incorporation of the xylanase treatment step into
CC pulp processing, especially where the enzyme is added after hot alkali
CC treatment. The present sequence is a xylanase from another species

XX Sequence 194 AA;

Query Match 77.9%; Score 965; DB 8; Length 194;
Best Local Similarity 87.6%; Pred. No. 7.5e-83;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 33 TTPNSEGWHDGYYSWSWSDGAQATYTNLEGTYEISWGDGNLVGKGWNPGLNARAIIH 92

Db 2 TTPNSEGWHDGYYSWSWSDGGGSTYTNNSGTYEITWGNGNLVGKGWNPGLNARAIIH 61

Qy 93 FEGVYQPNNGNSYLAIVYGWTRNPLVEYYIIVENFGTYDPSSGATDLGTVCDGSIVRLGKTT 152

Db 62 FTGVQPNGSTYLSVYGMTRNPLVEYYIVENFGSSNPSSGSTDIGTSCDGSITYTGOST 121
QY 153 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLVNNGDHYQIVATEGYF 212
Db 122 RYNAPSIDGTQTFNQYWSVRQDKRSSGTVQTGCHFDAMASAGLVNTGDHYQIVATEGYF 181
QY 213 SSGYARITVADVG 225
Db 182 SSGYARITVADVG 194

RESULT 12

AAB48548 standard; protein; 221 AA.
ID AAB48548
XX
AC AAB48548;
XX
DT 05-MAR-2001 (first entry)
XX
DE Cochliobolus carbonum xylanase.
XX
KM Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
KM bleaching agent.
XX
OS Cochliobolus carbonum.
XX
PN WO200068396-A2.
XX
PD 16-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US013172.
XX
PR 12-MAY-1999; 99US-0133714P.
XX
PA (XENC-) XENCOR INC.
XX
PI Bentzien JM;
XX
DR WPI; 2000-679800/66.
XX
PT Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
PS Disclosure; Fig 16Q; 114pp; English.
XX
CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 221 AA;

Query Match 65.1%; Score 806.5; DB 3; Length 221;
Best Local Similarity 67.9%; Pred. No. 9e-68;
Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFAPAGNATELEKQRTTPNSEGWHGYYYSWWSGDGAQATYTN 60
Db 1 MVSFTSITTAVAATGALAAPATDVS-LVARQNTPNGEETHNGCFWSWWSGDGARATYTN 59
QY 61 LEGGTYEISWGDGNLVGKGWNPGLNARAIHFEGVYQPNGNSYLA VYGWTRNPLVEYYI 120
Db 60 GAGGSYSVSWSGGNLVGKGWNPGLNARAIHFEGVYQPNGNSYLA VYGWTRNPLVEYYI 118
QY 121 VENFGTYDPSSGATDLGTEVECDGSYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
Db 119 VENFGTYDPSSSQSNKGTVTSDDSSYKIAOSTRTNQP SIDGTRTFQOYWSVRQDKRSSGS 178

QY 181 VQTGCHPDAMARAGLVNNGDHYQIVATEGYFSSGYARITV 221
Db 179 VNMKTHPDAMASKGMNL-GQHYQIVATEGYFSTGNAQITV 218

RESULT 13

AAO18654
ID AAO18654 standard; protein; 221 AA.
XX
AC AAO18654;
XX
DT 24-OCT-2002 (first entry)
XX
DE C carbonum xylanase.
XX
KM Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KM liquid clarification; coffee extraction; plant oil extraction;
KM starch extraction; food thickener; animal food additive; mutant; mutein.
XX
OS Cochliobolus carbonum.
XX
PN WO200238746-A2.
XX
PD 16-MAY-2002.
XX
PF 09-NOV-2001; 2001WO-US048018.
XX
PR 10-NOV-2000; 2000US-00710050.
XX
PA (XENC-) XENCOR INC.
XX
PI Bentzien J, Dahiyat B;
XX
DR WPI; 2002-608200/65.
XX
PT Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX
PS Disclosure; Fig 16Q; 121pp; English.
XX
CC The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
described in the exemplification of the invention
XX
SQ Sequence 221 AA;

Query Match 65.1%; Score 806.5; DB 5; Length 221;
Best Local Similarity 67.9%; Pred. No. 9e-68;
Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFAPAGNATELEKQRTTPNSEGWHGYYYSWWSGDGAQATYTN 60
Db 1 MVSFTSITTAVAATGALAAPATDVS-LVARQNTPNGEETHNGCFWSWWSGDGARATYTN 59
QY 61 LEGGTYEISWGDGNLVGKGWNPGLNARAIHFEGVYQPNGNSYLA VYGWTRNPLVEYYI 120
Db 60 GAGGSYSVSWSGGNLVGKGWNPGLNARAIHFEGVYQPNGNSYLA VYGWTRNPLVEYYI 118
QY 121 VENFGTYDPSSGATDLGTEVECDGSYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180

Db 119 VENFGTYDPSSQSQNKGTVTSDGSSYKIAQSTRTNQPSIDGTRTFQQYWSVRQNKRSSGS 178

QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221

Db 179 VNMKTHFDAMASKGMNL-GQHYQIVATEGYFSTGNAQITV 218

RESULT 14

AD166756

ID AD166756 standard; protein; 221 AA.

XX

AC AD166756;

XX

DT 22-APR-2004 (first entry)

XX

DE C. carbonum xylanase.

XX

KM Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;

KW paper industry; food; animal feed; thermostability; alkaliphilic;

KM hot alkali treatment.

XX

OS Cochliobolus carbonum.

XX

PN US6682923-B1.

XX

PD 27-JAN-2004.

XX

PF 12-MAY-2000; 2000US-00570856.

XX

PR 12-MAY-1999; 99US-0133714P.

PR 07-JUN-1999; 99US-0138156P.

XX

PA (XENC-) XENCOR.

XX

PI Bentzien J, Dahlyat BI;

XX

DR WPI; 2004-118575/12.

XX

PT New mutant xylanase (XA) protein comprising at least four amino acid

PT substitutions as compared to Bacillus circulans xylanase, useful for

PT bleaching (paper) pulp, and in the food and animal feed industries.

XX

PS Disclosure; SEQ ID NO 29; 84pp; English.

XX

CC The invention relates to a mutant xylanase activity (XA, endo-1,4-beta

CC xylanase from Bacillus circulans) protein appearing as AD166730. Also

CC included is a bleaching agent comprising the XA protein. The non-

CC naturally occurring XA protein comprises at least four amino acid

CC substitutions as compared to Bacillus circulans xylanase AD166728. The

CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,

CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,

CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is

CC useful for bleaching pulp in the paper and related industries, but is

CC also useful in the food and animal feed industries. The new protein is

CC active at higher pH and temperature ranges than naturally occurring

CC xylanases, simplifying incorporation of the xylanase treatment step into

CC pulp processing, especially where the enzyme is added after hot alkali

CC treatment. The present sequence is a xylanase from another species

CC included for comparison.

XX

SQ Sequence 221 AA;

Query Match 65.1%; Score 806.5; DB 8; Length 221;

Best Local Similarity 67.9%; Pred. No. 9e-68;

Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

QY 1 MVGFTPVALAALATGALAFAPGNATELEKQTTPNSEGWHDGYYSWWSGDGAQATYTN 60

Db 1 MVSFTSIITAATAVATGALAPATDVS-LVARQNTPNGEETHNGCFWSWMSDGGARATYTN 59

QY 61 LEGGTYEISWGDGNLVCGKGNPGLNARAIHFEQVYQPNNGNSYLA VYGWTRNPLVEYYI 120

Db 60 GAGGSYSVSWGSGGNLVGKGKGNP-G-TARTITTYSGTYNNGNSYLA VYGWTRNPLVEYYV 118

QY 121 VENFGTYDPSSGATDGLTVECDGSYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180

Db 119 VENFGTYDPSSQSQNKGTVTSDGSSYKIAQSTRTNQPSIDGTRTFQQYWSVRQNKRSSGS 178

QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221

Db 179 VNMKTHFDAMASKGMNL-GQHYQIVATEGYFSTGNAQITV 218

RESULT 15

AEB00301

ID AEB00301 standard; protein; 227 AA.

XX

AC AEB00301;

XX

DT 08-SEP-2005 (first entry)

XX

DE Xylanase SEQ ID NO:11.

XX

KM enzyme; xylanase; feedstuff; alcohol; fermentation; brewing; filtration.

XX

OS Humicola insolens.

XX

PN WO2005059084-A1.

XX

PD 30-JUN-2005.

XX

PF 17-DEC-2004; 2004WO-DK00880.

XX

PR 19-DEC-2003; 2003DK-00001895.

XX

PA (NOVO) NOVOZYMES AS.

XX

PI Festeresen RM, Vlksoe-Nielsen A, Joergensen CT, Christensen LH;

XX

DR WPI; 2005-458778/46.

XX

PT Preparation of a mash (having enhanced filterability and/or improved

PT extract yield after filtration) comprises preparing a mash in the

PT presence of enzyme activities comprising xylanase of GH family 10 and

PT filtering to obtain wort.

XX

PS Disclosure; SEQ ID NO 11; 68pp; English.

XX

CC The invention relates to a process for preparing a mash (A) (having

CC enhanced filterability and/or improved extract yield after filtration)

CC which comprises preparing a mash in the presence of enzyme activities

CC (comprising a xylanase of GH family 10 at at least 15% w/w of the total

CC xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a

CC wort. Also described is a composition is useful for reducing the

CC viscosity of an aqueous solution comprising a starch hydrolyate, which

CC is a mash for beer making or a feed composition. The process is useful

CC for the production of an alcoholic beverage, such as beer or whiskey and

CC the composition is useful in the mashing and filtration step in brewing

CC process. The present sequence represents a xylanase used in the mashing

CC process of the invention.

XX

SQ Sequence 227 AA;

Query Match 55.7%; Score 689.5; DB 9; Length 227;

Best Local Similarity 55.8%; Pred. No. 1.1e-56;

Matches 126; Conservative 31; Mismatches 62; Indels 7; Gaps 3;

QY 1 MVGFTPVALAALATGALA-----FPAGNATELEKQTTPNSEGWHDGYYSWWSGDGAQ 55

Db 1 MSLKSVLAATAVASSAIAAPDFVPRDNSTALQARQVTNPAEGWHNGYFYSWWSDGCGQ 60

QY 56 ATYTNLEGTYEISWGDGNLVCGKGNPGLNARAIHFEQVYQPNNGNSYLA VYGWTRNPL 115

Db 61 VQYTNLEGSRRYQVRMRNTGNFVGKGKGNP-G-TGRTINVGYFNPQNGYLA VYGWTRNPL 119

QY 116 VYYIYVENFGTYDPSSGATDGLTVECDGSYRLGKTRVNAPSIDGTQTFDQYWSVRQDK 175

Db	120	VEYVIESYGTYNPGSQAQYKGFYTDGDQYDIFVSTRYNQPSIDGTRTFQQYWSIRKMK	179
Qy	176	RTSGTVQTCCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITV	221
Db	180	RVGGSVNMQNHFNAMQOHGMP-LGQHYQVVAATEGYQSSGESDITV	224

Search completed: February 10, 2006, 14:54:12
Job time : 153.432 secs

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OM protein - protein search, using sw model

Run on: February 10, 2006, 14:54:33 ; Search time 27.9236 Seconds
(without alignments)
775.285 Million cell updates/sec

Title: US-09-467-368-2

Perfect score: 1238

Sequence: 1 MVGFTPVLAALAAATGALAF.....VATEGYFSSGYARITVADVG 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	691.5	55.9	219	2	S71472 endo-1,4-beta-xyla
2	689.5	55.7	227	2	S43919 endo-1,4-beta-xyla
3	689	55.7	241	2	S71473 endo-1,4-beta-xyla
4	684.5	55.3	223	2	S39883 endo-1,4-beta-xyla
5	680.5	55.0	225	1	S57477 endo-1,4-beta-xyla
6	667	53.9	222	2	S39154 xylanase 1 - fungu
7	663	53.6	197	1	A44597 endo-1,4-beta-xyla
8	659	53.2	232	2	JC7577 endo-1,4-beta-xyla
9	637.5	51.5	221	1	S57469 endo-1,4-beta-xyla
10	636.5	51.4	190	1	A44593 endo-1,4-beta-xyla
11	636.5	51.4	190	1	A44595 endo-1,4-beta-xyla
12	634.5	51.3	190	1	A44594 endo-1,4-beta-xyla
13	599.5	48.4	221	2	JC7307 endo-1,4-beta-xyla
14	585.5	47.3	335	2	T50601 endo-1,4-beta-xyla
15	573	46.3	333	1	J50590 endo-1,4-beta-xyla
16	554.5	44.8	241	2	T37005 endo-1,4-beta-xyla
17	553	44.7	240	1	S47512 endo-1,4-beta-xyla
18	540	43.6	240	1	J50591 endo-1,4-beta-xyla
19	529	42.7	644	1	I40712 endo-1,4-beta-xyla
20	528	42.6	661	1	S59633 endo-1,4-beta-xyla
21	505.5	40.8	210	2	C83762 endo-1,4-beta-xyla
22	498	40.2	656	1	S59631 endo-1,4-beta-xyla
23	470.5	38.0	213	1	I40569 endo-1,4-beta-xyla
24	469.5	37.9	213	1	S48126 endo-1,4-beta-xyla
25	468.5	37.8	213	1	S01734 endo-1,4-beta-xyla
26	452	36.5	354	1	S51779 endo-1,4-beta-xyla
27	427	34.5	511	1	JQ1935 endo-1,4-beta-xyla
28	400	32.3	261	1	S12745 endo-1,4-beta-xyla
29	397.5	32.1	228	1	WWSXP endo-1,4-beta-xyla

30	390	31.5	211	2	S49542 endo-1,4-beta-xyla
31	389.5	31.5	789	2	S58235 endo-1,4-beta-xyla
32	388	31.3	211	1	JC1198 endo-1,4-beta-xyla
33	385	31.1	211	1	S48229 endo-1,4-beta-xyla
34	372	30.0	229	2	S39155 xylanase 2 - fungu
35	371	30.0	954	1	S20907 endo-1,4-beta-xyla
36	365	29.5	781	2	S51592 XyB precursor - R
37	356	28.8	209	2	JC4909 endo-1,4-beta-xyla
38	355.5	28.7	802	2	A36910 xylanase, beta(1,3
39	299.5	24.2	607	2	S49528 endoxylanase - rum
40	296	23.9	607	2	S24754 endo-1,4-beta-xyla
41	248	20.0	608	2	B53295 xylanase (EC 3.2.1
42	240.5	19.4	266	1	S48865 endo-1,4-beta-xyla
43	145	11.7	50	2	A61149 endo-1,4-beta-xyla
44	115	9.3	2817	2	B97033 uncharacterized pr
45	113	9.1	40	2	PQ0202 endo-1,4-beta-xyla

ALIGNMENTS

RESULT 1
S71472
endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile
N/Alternate names: xylanase A
C/Species: Chaetomium gracile
C/Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
C/Accession: S71472; S78206
R/Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
Curr. Genet. 29, 73-80, 1995
A/Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asp
A/Reference number: S71472; MUID:96118924; PMID:8595661
A/Accession: S71472
A/Molecule type: DNA
A/Residues: 1-219 <YOS>
A/Cross-references: UNIPROT:Q12579; UNIPARC:UPI00000421A6; EMBL:D49850; NID:Q1339857; PIR:
A/Accession: S78206
A/Molecule type: protein
A/Residues: 31-45;82-94;152-160 <YOH>
A/Cross-references: UNIPARC:UPI0000175A79; UNIPARC:UPI0000175A82; UNIPARC:UPI0000175A83
C/Genetics:
A/Introns: 81/2
C/Function:
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/1-30/Domain: signal sequence #status predicted <SIG>
F/31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F/42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
F/115,206/Active site: Glu #status predicted

Query Match 55.9%; Score 691.5; DB 2; Length 219;
Best Local Similarity 59.1%; Pred. No. 5.3e-48;
Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps 5;

Qy	1	MVGFTPVAAALAAATGALAF	PAGNAT--ELEKQOTTPNSEGMHDCGYYSWSDGAQAT	57
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RESULT 2

Db 121 YIVENFGTYNPSTGATKLGCVTSDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRNRSS 180

Qy 179 GTVQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVA 222

Db 181 GSVNTANHFNAWAQGGTLT-GTMDYQIVAVEGYFSSGSASITVS 223

RESULT 5

S57477

endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - Emericella nidulans

N/Alternate names: xylanase 1

C/Species: Emericella nidulans, Aspergillus nidulans

C/Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004

C/Accession: S57477

R/Perez-Gonzalez, J.A.

submitted to the EMBL Data Library, June 1995

A/Description: Expression in Saccharomyces cerevisiae of two xylanase encoding genes from

A/Reference number: S57469

A/Accession: S57477

A/Molecule type: DNA

A/Residues: 1-225 <PER>

A/Cross-references: UNIPROT:P55332; UNIPARC:UPI0000139073; EMBL:Z49892; NID:9870832; PID

C/Genetics:

A/Introns: 93/2

C/Function:

A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A/Pathway: xylan degradation

C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C/Keywords: glycosidase; hydrolase; polysaccharide degradation

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>

F/48-225/Domain: endo-1,4-beta-xylanase homology <XYL>

F/121,212/Active site: Glu #status predicted

Query Match 55.0%; Score 680.5; DB 1; Length 225;

Best Local Similarity 56.6%; Pred. No. 4.1e-47;

Matches 129; Conservative 31; Mismatches 57; Indels 11; Gaps 4;

Qy 1 MVGFTPVALLAATGALFPAGN-----ATLEKQTTPNSEGMHDGYYSWWSDDG 53

Db 1 MVSFSLVLLCCALGAFATFVGSSEDLAREASLER--STPSSTGWSNGYYTSFWTDGG 58

Qy 54 AQAATTNLEGGTYEISWGDGSLVGGKGNPGLNARAIHFEGVYQPNNGSYLAIVYGMTRN 113

Db 59 GGVYTTNGAGGSYTVQMSNVGNFVGKGMNPG-STRTINYGGSFNPSGNGYLAIVYGMTQN 117

Qy 114 PLVEYIVVENFGTYDPSSGATDLGTVECDGSIRLQKTRVNAPSIDGTQTFDQYWSVRQ 173

Db 118 PLIEYIVVESYGTYPGSGGHRGTVYSDGATYDIYATRYNAPSIEGTATFEQFWSVRQ 177

Qy 174 DKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221

Db 178 SKRTGCTVTANHFNAWAALGMRL-GTHNYQIVATEGYQSSGSASITV 224

RESULT 6

S39154

xylanase 1 - fungus (Trichoderma reesei)

C/Species: Trichoderma reesei

C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C/Accession: S39154

R/Toercoenen, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkinen, N.; Harkki, A.; Kubi

Biotechnology 10, 1461-1465, 1992

A/Title: The two major xylanases from trichoderma reesei: characterization of both enzym

A/Reference number: S39154

A/Accession: S39154

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-222 <TOE>

A/Cross-references: UNIPROT:P36217; UNIPARC:UPI00000421A9; EMBL:X69573; NID:9396563; PID

C/Genetics:

A/Gene: xyn1

A/Introns: 90/2

C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

F/44-222/Domain: endo-1,4-beta-xylanase homology <XYL>

Query Match 53.9%; Score 667; DB 2; Length 222;

Best Local Similarity 57.1%; Pred. No. 4.8e-46;

Matches 128; Conservative 32; Mismatches 60; Indels 4; Gaps 3;

Qy 1 MVGFTPVALLAATGALFPAG--NATELEKQTTPNSEGMHDGYYSWWSDDGAQATY 58

Db 1 MVSFTSL-LAASPPSRASCRPAEVESSAVERKQTIPGTGYNNGYTSYWNDSHGCVTY 59

Qy 59 TNLGGTYEISWGDGSLVGGKGNPGLNARAIHFEGVYQPNNGSYLAIVYGMTRNPLVEY 118

Db 60 TNGPGGQFSVNWNSGNFVGKGMQPGTKNRYNFSGSYNPNNGSYLSYVGWSRNPLEY 119

Qy 119 YIVENFGTYDPSSGATDLGTVECDGSIRLQKTRVNAPSIDGTQTFDQYWSVRQDKRTS 178

Db 120 YIVENFGTYNPSTGATKLGCVTSDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRNRSS 179

Qy 179 GTVQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVA 222

Db 180 GSVNTANHFNAWAQGGTLT-GTMDYQIVAVEGYFSSGSASITVS 222

RESULT 7

A44597

endo-1,4-beta-xylanase (EC 3.2.1.8) A - bracket fungus (Schizophyllum commune)

N/Alternate names: xylanase A

C/Species: Schizophyllum commune

C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004

C/Accession: A44597; S41411; A05147; S38973

R/Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A/Reference number: A44593

A/Accession: A44597

A/Molecule type: protein

A/Residues: 1-197 <YAG>

A/Cross-references: UNIPROT:P35809; UNIPARC:UPI0000034D33

A/Experimental source: strain Delmar ATCC 38548

R/Bray, M.R.; Clarke, A.J.

Eur. J. Biochem. 219, 821-827, 1994

A/Title: Identification of a glutamate residue at the active site of xylanase A from Sch

A/Reference number: S41411; MUID:94155888; PMID:7906649

A/Accession: S41411

A/Status: preliminary

A/Molecule type: protein

A/Residues: 83-123 <BRA>

A/Cross-references: UNIPARC:UPI0000172966

R/Paice, M.G.; Jurasek, L.; Carpenter, M.R.; Smillie, L.B.

Appl. Environ. Microbiol. 36, 802-808, 1978

A/Reference number: A05147; MUID:79102289; PMID:32833

A/Accession: A05147

A/Molecule type: protein

A/Residues: 1-27 <PAI>

A/Cross-references: UNIPARC:UPI0000172967

R/Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Campbell, R.; Yaguchi, M.; Jurasek, L.;

FEBS Lett. 334, 296-300, 1993

A/Title: Amino acid sequence and thermostability of xylanase A from Schizophyllum commune

A/Reference number: S38973; MUID:94063044; PMID:8243636

A/Accession: S38973

A/Molecule type: protein

A/Residues: 1-197 <OKU>

A/Cross-references: UNIPARC:UPI0000034D33

A/Experimental source: ATCC 38548

C/Function:

A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A/Pathway: xylan degradation

C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F/12-197/Domain: endo-1,4-beta-xylanase homology <XYL>

F/87,184/Active site: Glu #status predicted

F/111-160/Disulfide bonds: #status experimental

	Query Match	53.6%;	Score 663;	DB 1;	Length 197;	
	Best Local Similarity	61.3%;	Pred. No. 8.8e-46;			
	Matches 119;	Conservative	26;	Mismatches 43;	Indels 6;	Gaps 2
Qy	34	TPNSEGHMDGYYYSWMSDGAQATYTNLEGGTYEISW-GDGCNLVGKGWNPGLNARAIIH	92			
		: : : :				
Dd	3	TPTSSTGTGDGGYYYSWMTDAGADATIÖNNGGGSYTLLTWSGNNGNLVVGKGMWNPGAASRSIS	62			
Qy	93	FEGVVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTTYDPSSGATDLGTVECDGSIYRLGKTT	152			
		: : : : :				
Dd	63	YSGTYQPNGNSYLSVYGWTRSLIEYYIVESYGSYPSSAASHKGSVTCNGATYDILSTM	122			
Qy	153	RVNAPSIDGTÖTFDQYWSVRÖDKRT-----SGTVÖTGCHFDAMARAGLNVNGDHYYÖIVA	207			
		: : :				
Dd	123	RYNAPSIDGTÖTFEQFWSVRNPKAPBGSSISGTVDVÖCHFDAMKGLGMNLGSEHNYYÖIVA	182			
Qy	208	TEGYFFSSGYARITV	221			
Dd	183	TEGYÖSSGTAIITV	196			

RESULT 8

endo-1,4-beta-xylosanase (EC 3.2.1.8) G2 - *Aspergillus oryzae*
 N/Alternate names: endo-1,3-beta-xylosanase G2; xylosanase G2
 C/Species: *Aspergillus oryzae*
 C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
 C/Accession: J07577; PC7120
 R/Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka, T.; Blochl. Biotechnol. Biochem. 64, 2734-2738, 2000
 A/Title: Molecular cloning, overexpression, and purification of a major xylosanase from *Aspergillus oryzae*
 A/Reference number: J07577; MUID: 21077500; PMID:11210150
 A/Accession: J07577
 A/Molecule type: DNA
 A/Residues: 1-232 <KIM>
 A/Cross-references: UNIPROT:Q9HFA4; UNIPARC:UPI0000069976; DDBJ:AB044941
 A/Experimental source: strain KBN616
 A/Accession: PC7120
 A/Molecule type: protein
 A/Residues: 45-64 <KI2>
 A/Cross-references: UNIPARC:UPI0000175A84
 C/Comment: This enzyme has strong similarity to other fungal family 11 endoxylanases, de
 C/Genetics:
 A/Gene: xynG2
 A/Introns: 100/2
 C/Superfamily: endo-1,4-beta-xylosanase; endo-1,4-beta-xylosanase homology
 C/Keywords: glycosidase; hydrolase

Query

Query Match	53.2%;	Score 659;	DB 2;	Length 232;
Best Local Similarity	54.9%;	Pred. No. 2.2e-45;		
Matches 128; Conservative	30;	Mismatches 61;	Indels 14;	Gaps 4;

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Qy      1  MVGFTPVALLAALATGALAP-----AGNATELEK--RQTTPNSEGHMGYYYSW 48
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Db      1  MVSFSSILLACSAALGALATPIEPLADHPNEAFNETAFNDLVGRSTPSTGTYNNGYYYSF 60

Qy      49  WSDGAQATYTNLEGCTYEISWGDGNI VGCKWNPGLNARAIHEGVYQPNGNSYLAAY 108
      || : || | | | | | | | | | | | | | | | | : : : : || : : || : : || : :
Db      61  WTDGGADVITYTNGNGSGSYSVQWSNVGNFVGCKWNPGL--SRAITYSGSFNPSGNGYLAAY 119

Qy      109  GWTRNPLVEYYIVENFGTYDPPSSGATDLGTVECDSIYRLKTRVNAPSIDGTQTFDQY 168
      || : : || : || : || : || : || : || : || : || : || : || : || : || :
Db      120  GWTTDPLIEYIVESYGTYNPGSGGYTKQVTSDGSTYNIYTSVRTNAPSIIIGTATFTQF 179

Qy      169  MSVRQDKRTSGTYQTGCHFDAMARAGLNVNGDHYIYQIVATEGYFSSGYARITV 221
      || || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      180  MSVRTSKRVGGIVITTGHNHFENAMAKYGLTL--GTHNYQIVATEGYQSSGSSAITV 231

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RESULT 9

557469
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - *Emericella nidulans*
N;Alternate names: xylanase 2

C/Species: *Emericella nidulans*, *Aspergillus nidulans*
C/Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: S57469
R/Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A/Description: Expression in *Saccharomyces cerevisiae* of two xylanase encoding genes from
A/Reference number: S57469
A/Accession: S57469
A/Molecule type: DNA
A/Residues: 1-221 <PER>
A/Cross-references: UNIPROT:P55333; UNIPARC:UPI0000139075; EMBL:Z49893; NID:g870834; PID
C/Genetics:
A/Introns: 89/3
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/1-19/Domain: signal sequence #status predicted <SIG>
F/19-221/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>
F/44-221/Domain: endo-1,4-beta-xylanase homology <XYL>
F/117,208/Active site: Glu #status predicted

Query Match

Query Match	51.5%;	Score 637.5;	DB 1;	Length 221;
Best Local Similarity	54.0%;	Pred. No. 1.1e-43;		
Matches 122;	Conservative 36;	Mismatches 59;	Indels 9;	Gaps 4;

[illegible]

RESULT 10

endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (*Trichoderma harzianum*) (strain N/Alternate names: xylanase
C/Species: *Trichoderma harzianum*
C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000
C/Accession: A44593

submitted to the Protein Sequence Database, March 1994
A;Reference number: A44593
A;Accession: A44593
A;Molecule type: protein
A;Residues: 1-190 <YAG>
A;Cross-references: UNIPARC:UPI00000493CB
A;Experimental source: strain E58
R;Campbell, R.L.; Rose, D.R.
submitted to the Brookhaven Protein Data Bank, June 1994
A;Reference number: A52868; PDB:1XND
A;Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46, 'A'48-190
C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylians
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F;86,177/Active site: Glu #status experimental

Query Match

Query Match	51.4%;	Score 636.5;	DB 1;	Length 190;
Best Local Similarity	60.7%;	Pred. No. 1.1e-43;		

[illegible]

RESULT 11
A44595
endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (*Trichoderma viride*)
N/Alternate names: xylanase IIB
C/Species: *Trichoderma viride*
C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: A44595
R/Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A/Reference number: A44593

A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-190 <YAG>
A/Cross-references: UNIPROT:Q7M520; UNIPARC:UPI0000172968
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F/86,177/Active site: Glu #status predicted
F/126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted
F/129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match	51.4%	Score 636.5;	DB 1;	Length 190;
Best Local Similarity	60.2%;	Pred. No. 1.1e-43;		
Matches 115; Conservative	27;	Mismatches 48;	Indels 1;	Gaps 1;

[illegible]

RESULT 12
A44594
endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)
N/Alternate names: xylanase IIA
C/Species: Trichoderma viride
C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: A44594
R/Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A;Reference number: A44593

A;Accession: A44594

A;Molecule type: protein

A;Residues: 1-190 <YAG>

A;Cross-references: UNIPROT:Q7M519; UNIPARC:UPI0000034D34

C;Function:

A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A;Pathway: xylan degradation

C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>

F;77,88/Binding site: substrate (Tyr) #status predicted

F;86,177/Active site: Glu #status predicted

Query Match	51.3%;	Score 634.5;	DB 1;	Length 190;
Best Local Similarity	60.2%;	Pred. No. 1.6e-43;		
Matches 115;	Conservative 27;	Mismatches 48;	Indels 1;	Gaps 1;

QY	32 QTTPNSEGHMDGYIYSWMSDGAOATYTNLGGTYEISWDGGLNVGKGWNPLGNARAI	91
	:::: : : : : : :	
Dp	1 QTIGPGTGFNNNGFYFSYMNDDHGCVITYTNPGGQFSSVMNSNGNFVGKGMQPGRKNKI	60
QY	92 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIIYRLGKT	151
	: : : : :	
Dp	61 NFSGTYPNPNGNSYLSVYSGWSRNPLEIYYIVENFGTYNPSTGATFKLGEVTSIDGSIVDIYRT	120
QY	152 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDMARAGLNVNGDHYYQIVATEGY	211
	: : : :	
Dp	121 QRVNOPSIITIGSTIFYQYWSVRTRRSSGSVNTANHFNAAOGLTL-GTMDYQIVAVEGY	179
QY	212 FSSGYARITVA	222
	:	
Dp	180 FSSGSASITVS	190

RESULT 13
JC7307
endo-1,4-beta-xylanase (EC 3.2.1.8) - *Penicillium* sp.

C;/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;/Accession: JC7307; PC1086
R;/Kimura, T.; Ito, J.; Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka, K.; Ohmiya, B.; Biochem. Biotechnol. 64, 1230-1237, 2000
A;/Title: Purification, characterization, and molecular cloning of acidophilic xylanase
A;/Reference number: JC7307
A;/Accession: JC7307
A;/Molecule type: DNA
A;/Residues: 1-221 <KIM>
A;/Cross-references: UNIPROT:Q9UUQ2; UNIPARC:UPI00000421AD; DDBJ:AB035540
A;/Accession: PC7086
A;/Molecule type: protein
A;/Residues: 32-51 <KI2>
A;/Cross-references: UNIPARC:UPI0000175A85
C;/Genetics:
A;/Gene: xynA
A;/Introns: 89/2
C;/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;/Keywords: glycoprotein; glycosidase; hydrolase

Query Match	48.4%;	Score 599.5;	DB 2;	Length 221;
Best Local Similarity	51.1%;	Pred. No. 1.1e-40;		
Matches 114;	Conservative 41;	Mismatches 65;	Indels 3;	Gaps 3;

[illegible]

[illegible]

RESULT 14

endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor
 N/Alternate names: xylanase B
 C/Species: Streptomyces coelicolor
 C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
 C/Accession: T50601
 R/Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw
 Mol. Microbiol. 21, 77-96, 1996
 A/Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S
 A/Reference number: Z20556; MUID:97000351; PMID:8843436
 A/Accession: T50601
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-335 <RED>
 A/Cross-references: UNIPROT:Q9RXN6; UNIPARC:UPI00000DC56E; EMBL:AL133220; PIDN:CAB61738.
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: xlnB
 C/Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
 C/Keywords: glycosidase; hydrolase

Query Match

Best Local Similarity 51.5%; Pred. No. 2.4e-39;
Matches 117; Conservative 24; Mismatches 73; Indels 13; Gaps 4;

```
Qy      6 PVAL-----AALATGALAF PAGNATELEKROTTPNSEGMHDGYIYSSWSDGGAQATY   58
        ||| |||| | | | | | | : | | | | | | : | :
Db     14 PVTLLVRSAMAVALLAALAALMLP--GTAAQADTVTTNQEGTNNGYYISFWTDSQGTVSM   70
Qy     59 TNLGGTYEISWGDCGNLVGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEY   118
        ||| | | : | | | | | | : | : | : | | | | | | | | | | | | | | | |
Db     71 NMGS GGQYSTSWRNTGNFVAGKWANG-GRRTVQYSGSFNPSGNAYLALYGWTSNPLVEY   129
Qy    119 YIVENFGTYDPPSSGATDLGTEVCDSIYRLGKTRVRNAPSIDGTQTFDQYWSVRQDKRTS   178
        ||| : | | | : ||| | | : | | | | | | : | : | | | | | | | | | | | | |
Db    130 YIVDNMGTYRPTEYK--GTVTS DCGTYDYKTTRVNKPSEVGRTTFDQYWSVRQAKRTG   187
Qy    179 GTVQTGCHFDAMARACILNVNGDHYIQIYVALEGYFSSGYARITVADV G   225
        || : | | | | | | | | : | | : | | | | | | | | | | | | | | | | | | |
Db    188 GTITTGNHFDAMARACMPLGNFSYIMATEGYOSSGSSSINVGCTG   234
```

RESULT 15

endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans
N/Alternate names: xylanase B
C/Species: Streptomyces lividans
C/Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999
C/Accession: JS0590; PS0239
R/Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-82, 1991
A/Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A/Reference number: JS0589; MUID:92077439; PMID:1743521
A/Accession: JS0590
A/Molecule type: DNA
A/Residues: 1-333 <SHA>
A/Cross-references: UNIPARC:UPI000017296A; GB:M64552
A/Accession: PS0239
A/Molecule type: protein
A/Residues: 41-71 <SH2>
A/Cross-references: UNIPARC:UPI000017296B
C/Genetics:
A/Gene: xlnB

C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A;Pathway: xylan degradation
C;Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-40/Domain: signal sequence #status predicted <SIG>
F;41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>
F;54-230/Domain: endo-1,4-beta-xylanase homology <XYL>
F;127,217/Active site: Glu #status predicted

Query Match

Best Local Similarity 51.4%; Pred. No. 2.3e-38;
Matches 112; Conservative 24; Mismatches 76; Indels 6; Gaps 3;

Qy	8	ALALALATGALAF	PAGNATELEKROTTPN	SEGMHDGYIYSWS	SDGGAQATYTNL	EGGYIE	67
Db	22	AWAVALARSPMLP	--GTAQADTVTTN	QEGTNNGYIYSFW	ITDSQGTVMNMG	SGGOYS	78
Qy	68	ISWGDGNLVGKGW	MNPGLNABAIHEG	VYQPNGNSYLA	VGWTRNPLVEY	IYVENGTY	127
Db	79	TSWRNTGNFVAGK	GWANG-GRRTVQ	YSGSFNPSGNAL	YALYGWTSNPL	VEYIYIDNMGT	137
Qy	128	DPSSGATDLGVE	CDGSIYRLKTRV	NAPSIDGTQTFD	QWSVRQDKRTS	GTGTCGF	187
Db	138	RPTGEYK--GT	VTSDDGTYDIY	KTRVNKPSVEG	TRTFDQYWSV	RQSKRTGTIT	195
Qy	188	DAMARAGLNVN	GDIYQIVATEG	EYSSGARITV	ADVG	225	
Db	196	DAMARAGMPL	GNFYSYIMIM	ATEGYQSSGT	SSINVG	GTG	233

Search completed: February 10, 2006, 15:02:20
Job time : 28.9236 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 14:49:37 ; Search time 227.148 Seconds
(without alignments)
698.857 Million cell updates/sec

Title: US-09-467-368-2
Perfect score: 1238
Sequence: 1 MVGFPPVALAALATGALAF.....VATEGYFSSGYARITVADVG 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	1238	100.0	225	1 XYN_A_THELA	Q43097 thermomyces
2	965	77.9	194	1 XYN_A_PAEVA	P81536 paecilomyce
3	821.5	66.4	227	2 Q9UVZ3_9PLEO	Q9UVZ3 setosphaeri
4	806.5	65.1	221	1 XYN1_COCCA	Q06562 cochliobolu
5	785	63.4	295	2 Q9C1R2_FUSOX	Q9C1R2 fusarium ox
6	775.5	62.6	227	2 Q00263_9PEZI	Q00263 ascochyta p
7	728	58.8	231	2 Q92245_MAGGR	Q92245 magnaporthe
8	716.5	57.9	231	2 Q13447_COCSA	Q13447 cochliobolu
9	711	57.4	204	2 Q51SA1_MAGGR	Q51SA1 magnaporthe
10	710.5	57.4	231	2 Q70T28_9PLEO	Q70T28 setosphaeri
11	701.5	56.7	231	2 Q00350_COCCA	Q00350 cochliobolu
12	692.5	55.9	227	2 Q9HGE1_HUMGT	Q9HGE1 humicola gr
13	691.5	55.9	219	2 Q12579_9PEZI	Q12579 chaetomium
14	689.5	55.7	227	1 XYN1_HUMIN	P55334 humicola in
15	689	55.7	241	2 Q12580_9PEZI	Q12580 chaetomium
16	685.5	55.4	235	2 Q766V1_9ASCO	Q766V1 scytalidium
17	685	55.3	220	2 Q7SDQ1_NEUCR	Q7SDQ1 neurospora
18	684.5	55.3	223	2 Q02244_TRIRE	Q02244 trichoderma
19	684	55.3	293	2 Q871E8_NEUCR	Q871E8 neurospora
20	681.5	55.0	221	2 Q4WL2_9PEZI	Q4WL2 aspergillus
21	681	55.0	228	2 Q4WG11_ASPFU	Q4WG11 aspergillus
22	680.5	55.0	223	2 Q728Q3_TRIVI	Q728Q3 trichoderma
23	680.5	55.0	225	1 XYN_A_EMENT	P55332 emericella
24	680.5	55.0	225	2 Q5B767_EMENT	Q5B767 aspergillus
25	678.5	54.8	261	2 Q8J1V6_9PEZI	Q8J1V6 chaetomium
26	676.5	54.6	231	2 Q9C1R1_FUSOX	Q9C1R1 fusarium ox
27	672.5	54.3	231	2 Q4HVK9_GIBZE	Q4HVK9 gibberella
28	672.5	54.3	231	2 Q7ZA57_GIBZE	Q7ZA57 gibberella
29	672.5	54.3	267	2 Q6UN40_9PEZI	Q6UN40 chaetomium
30	671.5	54.2	223	2 Q99015_TRIRE	Q99015 trichoderma
31	670	54.1	220	2 Q8J0T4_9HYPO	Q8J0T4 trichoderma

32	667	53.9	222	1 XYN2_TRIRE	P36217 trichoderma
33	663	53.6	197	1 XYN_A_SCHCO	P35809 schizophyll
34	662.5	53.5	230	2 Q8J1V5_9PEZI	Q8J1V5 chaetomium
35	660.5	53.4	221	2 P87037_ASPOR	P87037 aspergillus
36	660	53.3	233	1 XYN2_MAGGR	P55335 magnaporthe
37	660	53.3	233	2 Q51XD0_MAGGR	Q51XD0 magnaporthe
38	659	53.2	232	2 Q9HFA4_ASPOR	Q9HFA4 aspergillus
39	648.5	52.4	228	2 Q4IGN4_GIBZE	Q4IGN4 gibberella
40	648.5	52.4	228	2 Q5NDZ1_GIBZE	Q5NDZ1 gibberella
41	642.5	51.9	221	2 Q5AQR5_EMENT	Q5AQR5 aspergillus
42	638	51.5	290	2 Q9HEY9_PHACH	Q9HEY9 phanerocha
43	638	51.5	290	2 Q9HEZ0_PHACH	Q9HEZ0 phanerocha
44	637.5	51.5	221	1 XYNB_EMENT	P55333 emericella
45	636.5	51.4	190	2 Q7M520_TRIVI	Q7M520 trichoderma

ALIGNMENTS

RESULT 1
XYNA_THELA STANDARD; PRT; 225 AA.
ID XYN_A_THELA
AC Q43097;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan xylanohydrolase).
GN Name=XYNA;
OS Thermomyces lanuginosus (Humicola lanuginosa).
OC Bacteria; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
OX NCBI_TaxID=5541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=97033440; PubMed=8879171; DOI=10.1016/0168-1656(96)01516-7;
RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;
RT "Cloning and characterization of the gene for the thermostable xylanase Xyna from Thermomyces lanuginosus.";
RL J. Biotechnol. 49:211-218(1996).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=98426042; PubMed=9753433; DOI=10.1021/bi9808641;
RA Gruber K., Klintschar G., Hayn M., Schlacher A., Steiner W.,
RA Kracky C.;
RT "Thermophilic xylanase from Thermomyces lanuginosus: high-resolution X-ray structure and modeling studies.";
RL Biochemistry 37:13475-13485(1998).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.
CC -!- BIOPHYSICOCHEMICAL PROPERTIES: Temperature dependence: Thermostable;
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G) family.

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EMBL; U35436; AAB94633.1; -; Genomic_DNA.
PDB; 1YNA; X-ray; @=32-225.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW 3D-structure; Glycosidase; Hydrolase; Pyrrolidone carboxylic acid; Signal; Xylan degradation.

FT SIGNAL 1 31
FT CHAIN 32 225
FT ACT_SITE 117 209
FT ACT_SITE 209 209
FT MOD_RES 32 32
FT DISULFID 141 185
FT STRAND 33 33
FT STRAND 37 41
FT TURN 42 43
FT TURN 44 50
FT STRAND 56 60
FT TURN 63 64
FT STRAND 65 70
FT STRAND 75 82
FT STRAND 90 100
FT STRAND 103 112
FT TURN 113 115
FT STRAND 116 124
FT TURN 129 132
FT STRAND 134 141
FT TURN 142 143
FT STRAND 144 158
FT TURN 159 160
FT STRAND 161 172
FT STRAND 179 182
FT HELIX 183 192
FT TURN 193 194
FT STRAND 200 211
FT STRAND 214 223
SQ SEQUENCE 225 AA; 24356 MW; FAA79A914C5C676C CRC64;

Query Match 100.0%; Score 1238; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.9e-96;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGFPPVALAALATGALAFAPGNATELEKROTPNSEGWHGYYYSWSDGGAQATYTN 60
DB 1 MVGFPPVALAALATGALAFAPGNATELEKROTPNSEGWHGYYYSWSDGGAQATYTN 60
QY 61 LEGGYEISWGDGGLVGGKWNPGLNARAIHFEQVYQPNNGNSYLAIVYGWTRNPLVEYYI 120
DB 61 LEGGYEISWGDGGLVGGKWNPGLNARAIHFEQVYQPNNGNSYLAIVYGWTRNPLVEYYI 120
QY 121 VENFGTYDPSSGATDLGTVCECDGSYRLKKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
DB 121 VENFGTYDPSSGATDLGTVCECDGSYRLKKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
QY 181 VQTGFHDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADVG 225
DB 181 VQTGFHDAMARAGLNVNGDHYQIVATEGYFSSGYARITVADVG 225

RESULT 2
XVNA_PAEVA STANDARD; PRT; 194 AA.
AC P81536;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
DE xylanohydrolase) (PVX).
OS Paecilomyces variotii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.
OX NCBI_TaxID=45996;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (1.59 ANGSTROMS), AND PROTEIN SEQUENCE OF 50-58
RP AND 123-128.
RC STRAIN=Bainier;
RX MEDLINE=20090955; PubMed=10623548; DOI=10.1006/jmbi.1999.3348;
RA Kumar P.R., Eswaramoorthy S., Vithayathil P.J., Viswamitra M.A.;
RT "The tertiary structure at 1.59 A resolution and the proposed amino
RT acid sequence of a family-11 xylanase from the thermophilic fungus

RT Paecilomyces variotii bainier.";
RL J. Mol. Biol. 295:581-593(2000).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- BIOPHYSICOCHEMICAL PROPERTIES:
CC Temperature dependence:
CC Thermostable;
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PDB; 1PVX; X-ray; A=1-194.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW 3D-structure; Acetylation; Direct protein sequencing; Glycosidase;
KW Hydrolase; Xylan degradation.
FT ACT_SITE 86 86 Nucleophile (By similarity).
FT ACT_SITE 178 178 Proton donor (By similarity).
FT MOD_RES 1 1 N-acetylglutamine.
FT DISULFID 110 154
SQ SEQUENCE 194 AA; 20947 MW; 1D5C50AA4F6EDB90 CRC64;

Query Match 77.9%; Score 965; DB 1; Length 194;
Best Local Similarity 87.6%; Pred. No. 3.8e-73;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 33 TTPNSEGWHHDGYYYSWSDGGAQATYTNLEGTYEISWGDGGLVGGKWNPGLNARAIH 92
DB 2 TTPNSEGWHHDGYYYSWSDGGSIDSTYTNNSGTYEITWNGGGLVGGKWNPGLNARAIH 61
QY 93 FEGVYQPNNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVCECDGSYRLKKT 152
DB 62 FTGVYQPNNGTSYLSVYGWTRNPLVEYYIVENFGSSNPSSGSTDLGTVSCGSTYTLGOST 121
QY 153 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGFHDAMARAGLNVNGDHYQIVATEGYF 212
DB 122 RVNAPSIDGTQTFNQYWSVRQDKRSSGTVQTGFHDAMASAGLNTGHDHYQIVATEGYF 181
QY 213 SSGYARITVADVG 225
DB 182 SSGYARITVADVG 194

RESULT 3
Q9UVZ3_9PLEO PRELIMINARY; PRT; 227 AA.
AC Q9UVZ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xylanase precursor.
GN Name=xyl1;
OS Setosphaeria turcica.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Setosphaeria.
OX NCBI_TaxID=93612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=H2;
RC Degefu Y., Paulin L., Lubbeck P.S.;
RT "Cloning, sequencing and expression of a xylanase gene from the maize
RT pathogen Helminthosporium turcicum Pass.";
RL Eur. J. Plant Pathol. 107:457-465(2001).
DR EMBL; AJ238895; CAB52417.1; -; Genomic_DNA.

DR HSSP; 043097; 1YNA.
DR SMR; 09UV23; 37-224.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Signal; Xylan degradation.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 227 xylanase.
SQ SEQUENCE 227 AA; 24123 MW; BA86FC075EE5306E CRC64;

Query Match 66.4%; Score 821.5; DB 2; length 227;
Best Local Similarity 67.7%; Pred. No. 5.3e-61;
Matches 153; Conservative 25; Mismatches 41; Indels 7; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFPAAGN-----ATELEKQRTPNSEGMHDGYYSWSDGCAQ 55
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
1 MVSFTSITTAVAATGALAAPATDIAARAPSDLVARQSTENGEGTHNGCFYSWSDGAR 60
QY 56 ATYTNLEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQYQPNGNSYLAIVGTRNPL 115
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
61 ATYTNAGGSYSVSWGTGGLVGGKGNPGLNARAIHFEQYQPNGNSYLAIVGTRNPL 119
QY 116 VEYIVENFGTYDPSSGATDLGVECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDK 175
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
120 VEYIVENFGTYDPSSQAQNKGTYSDDSSYKIAQSTRNQPSIDGTRTFQYWSVRQNK 179
Db 176 RTSGTVCCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
180 RSSGSVNMKTHFDAMASKGNL-GSHYQIVATEGYFSSGSASITV 224

RESULT 4
XYN1 COCCA STANDARD; PRT; 221 AA.

ID XYN1 COCCA
AC Q06562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I) (1,4-beta-D-xylan xylohydrolase 1).
GN Name=XYL1;
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Race 1 / Isolate SB111;
RX MEDLINE=94003417; PubMed=8400376;
RA Abel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
RT "Cloning and targeted gene disruption of XYL1, a beta 1,4-xylanase gene from the maize pathogen Cochliobolus carbonum.";
RL Mol. Plant Microbe Interact. 6:467-473(1993).
RN [2]
RP PARTIAL PROTEIN SEQUENCE.
RA Holden F.R., Walton J.D.;
RT "Xylanases from the fungal maize pathogen Cochliobolus carbonum.";
RL Physiol. Mol. Plant Pathol. 40:39-47(1992).
CC -1- FUNCTION: Major xylan-degrading enzyme. Contributes to the hydrolysis of arabinoxylan, the major component of maize cell-wall.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G) family.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----

DR EMBL; L13596; AAA33024.1; -; Genomic_DNA.
DR HSSP; 043097; 1YNA.
DR SMR; Q06562; 31-218.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Direct protein sequencing; Glycosidase; Hydrolase; Signal;
KW Xylan degradation.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 221 Endo-1,4-beta-xylanase I.
FT ACT_SITE 115 115 Nucleophile (By similarity).
FT ACT_SITE 206 206 Proton donor (By similarity).
FT CONFLICT 81 81 W -> I (in Ref. 2).
FT CONFLICT 107 107 G -> A (in Ref. 2).
FT CONFLICT 131 131 S -> W (in Ref. 2).
SQ SEQUENCE 221 AA; 23728 MW; 59DBD8983FC5B08C CRC64;

Query Match 65.1%; Score 806.5; DB 1; length 221;
Best Local Similarity 67.9%; Pred. No. 9.3e-60;
Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFPAAGNATELEKQRTPNSEGMHDGYYSWSDGCAQATYTN 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
1 MVSFTSITTAVAATGALAAPATDVS-LVARQNTPNGEETHNGCFYSWSDGARATYTN 59
QY 61 LEEGTYEISWGDGGLVGGKGNPGLNARAIHFEQYQPNGNSYLAIVGTRNPLVEYYI 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
60 GAGGSYSVSWSGGLVGGKGNPGLNARAIHFEQYQPNGNSYLAIVGTRNPLVEYYV 118
Db 121 VENFGTYDPSSGATDLGVECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
119 VENFGTYDPSSQSNKGTYSDDSSYKIAQSTRNQPSIDGTRTFQYWSVRQNKRSSGS 178
QY 181 VQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
179 VNMKTHFDAMASKGNL-GQHYQIVATEGYFSTGNAQITV 218
Db

RESULT 5
O9C1R2 FUSOX PRELIMINARY; PRT; 295 AA.

ID O9C1R2 FUSOX
AC O9C1R2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xylanase 5 protein.
GN Name=xyl5;
OS Fusarium oxysporum f. sp. lycopersici.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
OC Fusarium oxysporum complex.
OX NCBI_TaxID=59765;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21654148; PubMed=11795847; DOI=10.1007/s00294-001-0260-0;
RA Gomez-Gomez E., Roncero M.I.G., Di Pietro A., Hera C.;
RT "Molecular characterization of a novel endo-beta-1,4-xylanase gene from the vascular wilt fungus Fusarium oxysporum.";
RL Curr. Genet. 40:268-275(2001).
DR EMBL; AF246830; AAK27974.1; -; Genomic_DNA.
DR HSSP; 043097; 1YNA.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=45130;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Emami K., Hack E.;
RT "Characterisation of a xylanase gene from Cochliobolus sativus and its
RT expression.";
RL Mycol. Res. 105:352-359(2001).
DR EMBL; AJ004802; CAA06151.1; -; Genomic_DNA.
DR HSSP; Q8J1V6; 1H1A.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR01137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW xylan degradation.
SQ SEQUENCE 231 AA; 25577 MW; 333E6DD1F065A6BF CRC64;

Query Match 57.9%; Score 716.5; DB 2; Length 231;
Best Local Similarity 58.7%; Pred. No. 3.6e-52;
Matches 135; Conservative 29; Mismatches 55; Indels 11; Gaps 4;

QY 1 MVGFTPVALLAALATGALAP-----AGNATE-LEKROTTPNSEGMHGGYYSWMSD 51
DB 1 MVSFKSLLLAAVAATTSVLAAPFDPRLRRDDGNATALLKQSTPSSEGHANGYFYSWTWD 60
QY 52 GGAQATYTNLEGGTYEISWGDGSLVGGKGNPGLNARAIHFEVGYQPNNGSLAVYGMT 111
DB 61 GGGSAQYTMGEGRYSVTWRNTGNFVGKGNPGLNARAIHFEVGYQPNNGSLAVYGMT 119
QY 112 RNPLVEYIVENFGTYDPSGATDLGTECDGSIYRLGKTRVNAPSIDGTQTFDQYMSV 171
DB 120 RNPLVEYIVESYGTNPSSGAQYKGSFQTDGTYVNAVSTRYNQPSIDGTRTFQYMSV 179
QY 172 RQDKRTSGTYGTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221
DB 180 RQDKRVGGSVNMQNHFNAMSRGYNL-GQHYQIVATEGYQSSGSDIYV 228

RESULT 9

Q51SA1_MAGGR PRELIMINARY; PRT; 204 AA.
AC Q51SA1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG08424.4;
OS Magnaporthe oryzae 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nussbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armstrong J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Biye J., Boguslavskiy L.,
RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Chesnatsang Y., Citroen M.,
RA Collymore A., Conscience T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dookey K., Dorje P.,
RA Dorjee K., Dorje L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gerner S.,
RA Ghitke A., Goyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Huby E., Iliev I.,

RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,
RA Kelle C., Kien A., Kiser P., Kodira C., Kubokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Meneus L.,
RA Mesirov J., Mihailev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okawo O., O'leary S., Omotosho B.,
RA O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnuez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchinga P.,
RA Tenzing P., Testaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Zander E.;
RT "The genome sequence of Magnaporthe oryzae.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACU01001255; EAA49509.1; -; Genomic_DNA.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 204 AA; 22624 MW; 2396D83ED2B92260 CRC64;

Query Match 57.4%; Score 711; DB 2; Length 204;
Best Local Similarity 65.1%; Pred. No. 9.2e-52;
Matches 127; Conservative 26; Mismatches 40; Indels 2; Gaps 2;

QY 27 ELEKRTTPNSEGMHGGYYSWMSDGAQATYTNLEGGTYEISWGDGSLVGGKGNPGL 86
DB 10 DLHARGTTPSSTGTHDGFYYSWMTDNGAQAATYTNNAAGSYSITWSGNGNLVGGKGNPG- 68
QY 87 NARAIHFEVGYQPNNGSLAVYGMTNPLVEYIVENFGTYDPSGATDLGTECDGSIY 146
DB 69 SARNVITYSANTRPNGNSLYSVGWTNPLVEYIVENFGTYDPSGASRKGTINVDGATY 128
QY 147 RLKTRVNAPSIDGTQTFDQYMSVRQDKRTSGTYGTGCHFDAMARAGLNVNGDHYQIV 206
DB 129 QVAGSTRTPNSIDGTRTFQYMSVRQDKRTSGTYGTGCHFDAMARAGLNVNGDHYQIV 187
QY 207 ATEGYFSSGYARITV 221
DB 188 ATEGYFSSGSTVTI 202

RESULT 10
Q70T28_9PLEO

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ID Q70T28_9PLEO PRELIMINARY; PRT; 231 AA.
AC Q70T28;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Xylanase precursor.
GN Name=xyl12;
OS Setosphaeria turcica.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Setosphaeria.
OX NCBI_TaxID=93612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15016446; DOI=10.1016/j.biochi.2004.01.001;
RA Degefu Y., Lohrander K., Paulin L.G.;
RT "Expression patterns and phylogenetic analysis of two xylanase genes
RT (htxyl 1 and htxyl 2) from Helminthosporium turcicum, the cause of
RT leaf blight of maize."
RL Biochimie 86:83-90(2004).
DR EMBL; AJ548879; CAD70174.1; -; Genomic_DNA.
DR HSSP; P09850; 1BCX.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Signal; Xylan degradation.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 231 xyl12.
SQ SEQUENCE 231 AA; 25611 MW; 44078D5B52BAF15 CRC64;

Query Match 57.4%; Score 710.5; DB 2; Length 231;
Best Local Similarity 57.8%; Pred. No. 1.2e-51;
Matches 133; Conservative 30; Mismatches 56; Indels 11; Gaps 4;

QY 1 MVGFTPVALLAALATGALAFP-----AGNATE-LEKRQTPNSEGWHDGYYSWSD 51
DB 1 MVSFKSLLLAAVATTSVFAAPFDLERRDDGNATALLERKQSTPSSEGYHNQYFYSWTD 60

QY 52 GGAQATYTNLEGGTYEISWGDGNLVGKGNPGLNARAIHFEQVQPNNSYLAVYGMT 111
DB 61 GGSAQYTMGEESKYSVTWRNTGNFVGKGNPG-NGRITNYGGSFNPQNGYLAVYGMT 119

QY 112 RNPLVEYYIVENFGTYDPSSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYMSV 171
DB 120 RNPLVEYYIVIESGTYNPSSGAQIKGSFQTDGTYDIATSTRYNQPSIDGTRTFQYMSV 179

QY 172 RODKRTSGTVQTCGFDAWARAGLNVNGDHYQIVATEGYFSSGYARITV 221
DB 180 RTQKRVGGSVNMQNHFNAMSRKYNL-GTHYYQIVATEGYQSSGSEIYV 228

RESULT 11
Q00350 COCCA PRELIMINARY; PRT; 231 AA.
AC Q00350;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Xyl12 precursor.
GN Name=Xyl2;
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SB111;
RX MEDLINE=97055717; PubMed=8900004;
RA Apel-Birkhold P.C., Walton J.D.;
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RT "Cloning, disruption, and expression of two endo-beta 1, 4-xylanase
RT genes, Xyl2 and Xyl3, from Cochliobolus carbonum.";
RL Appl. Environ. Microbiol. 62:4129-4135(1996).
DR EMBL; U58915; AAC62815.1; -; Genomic_DNA.
DR HSSP; Q811V6; 1H1A.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Signal.
FT SIGNAL 1 41 Potential.
FT CHAIN 41 231 Xyl2.
SQ SEQUENCE 231 AA; 25576 MW; 237C3D49C4D0E871 CRC64;

Query Match 56.7%; Score 701.5; DB 2; Length 231;
Best Local Similarity 57.4%; Pred. No. 6.7e-51;
Matches 132; Conservative 31; Mismatches 56; Indels 11; Gaps 4;

QY 1 MVGFTPVALLAALATGALAPAG-----NATE-LEKRQTPNSEGWHDGYYSWSD 51
DB 1 MVSFKSLLLAAVATTSVLAAPFDLERRDPVNATALLERKQSTPSAEYHNQYFYSWTD 60

QY 52 GGAQATYTNLEGGTYEISWGDGNLVGKGNPGLNARAIHFEQVQPNNSYLAVYGMT 111
DB 61 GGSAQYTMGEESKYSVTWRNTGNFVGKGNPG-SGRVINYGGAFNQNGYLAVYGMT 119

QY 112 RNPLVEYYIVENFGTYDPSSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYMSV 171
DB 120 RNPLVEYYIVIESGTYNPSSGAQIKGSFQTDGTYNVAVSTRYNQPSIDGTRTFQYMSV 179

QY 172 RODKRTSGTVQTCGFDAWARAGLNVNGDHYQIVATEGYFSSGYARITV 221
DB 180 RTQKRVGGSVNMQNHFNAMSRKYNL-GQHYQIVATEGYQSSGSDIYV 228

RESULT 12
Q9HGE1_HUMGT
ID Q9HGE1_HUMGT PRELIMINARY; PRT; 227 AA.
AC Q9HGE1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Beta-1,4-xylanase.
GN Name=xyn2;
OS Humicola grisea var. thermoides.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_TaxID=5528;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=60849;
RA Faria F.P., Pocas-Fonseca M.J., Azevedo M.O.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF155594; AAG16891.1; -; Genomic_DNA.
DR HSSP; O43097; 1YNA.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation.
SQ SEQUENCE 227 AA; 25615 MW; 991815AD84EB2939 CRC64;

Query Match 55.9%; Score 692.5; DB 2; Length 227;
Best Local Similarity 56.6%; Pred. No. 3.7e-50;
Matches 128; Conservative 29; Mismatches 62; Indels 7; Gaps 3;

QY 1 MVGFTPVALLAALATGALA-----FPAGNATELEKRQTPNSEGWHDGYYSWSDGAQ 55
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Db 1 MVSIKSVLAATAVSSALAAPDFVPRDNSTALQARQVTNABEGWHNGYFYSWSDGGGQ 60

Qy 56 ATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAIHFEgyYQPNNGSYLAVYGMTNPL 115

Db 61 VQYTNLEGSRYQVRWRNTGNFVGKGWNP-GTGRITNYGgyFNPGNGYLAVYGMTNPL 119

Qy 116 VEYIIVENFGTYDPSSGATDLGTVBCDGSYRLGKTRVNAPSIDGTQTFDQYWSVRQDK 175

Db 120 VEYVIESYGTYNPGSQAYKGTFTYDGDQYDIFVSTRYNQPSIDGTRTFQYWSIRKNK 179

Qy 176 RTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221

Db 180 RVGGSVNMQNHFNAMQOHGMPL-GQHYQIVATEGYQSSGESDIYV 224

RESULT 13

Q12579_9PEZI PRELIMINARY; PRT; 219 AA.

AC Q12579; DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Endo-beta1,4-xylanase A (EC 3.2.1.8).

GN Name=cgXA;

OS Chaetomium gracile.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.

OX NCBI_TaxID=47794;

OK (1)

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=96118924; PubMed=8595661; DOI=10.1007/BF00313196;

RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;

RT "Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus nidulans.";

RL Curr. Genet. 29:73-80(1995).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Tsukagoshi N.;

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; D49850; BAA08649.1; -; Genomic_DNA.

DR PIR; S71472; S71472.

DR HSSP; P36217; 1XVO.

DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR GO; GO:0045493; P:xylan catabolism; IEA.

DR InterPro; IPR001137; Glyco_hydro_11.

DR Pfam; PF00457; Glyco_hydro_11; 1.

DR PRINTS; PR00911; GLHYDRLASE11.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KW Glycosidase; Hydrolase; Xylan degradation.

SQ SEQUENCE 219 AA; 23325 MW; 4729299E08FD9FBA CRC64;

Query Match 55.9%; Score 691.5; DB 2; Length 219;

Best Local Similarity 59.1%; Pred. No. 4.3e-50;

Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps 5;

Qy 1 MVGFTPVALLAALATGALAPFAGNAT--ELEKQTPNSEGWHDGYYSWSDGAQAT 57

Db 1 MVSFKAL---LLGAAGALAPFP-NVTQNELVARAGTSPSGTGNNGYFSFTWDGGGTVN 56

Qy 58 YTNLEGGTYEISWGDGNLVGKGWNPGLNARAIHFEgyYQPNNGSYLAVYGMTNPLVE 117

Db 57 YONGAGGSYSVQWQNCNFGVKGWNPGA-ARTINFGTFSPOGNGYLAIYGMTQNP LVE 115

Qy 118 YIIVENFGTYDPSSGATDLGTVBCDGSYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRT 177

Db 116 YIIVESFGTYDPSSQASKFTIQDGSYTYIAKTRVNPQPSIEGTSTFDQFWSVRQNHRS 175

Qy 178 SGTVQTCGHPDAMARAGLNVNGDHYQIVATEGYFSSGYARITVA 222

Db 176 SGSVNVAAHFNAMQAQGLK-LGSHNYQIVATEGYQSSGSSSITVS 219

RESULT 14

XYN1 HUMIN STANDARD; PRT; 227 AA.

ID XYN1 HUMIN DT 01-OCT-1996 (Rel. 34, Created)

AC P55334; Q12625; DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1) (1,4-beta-D-xylan xylanohydrolase 1).

GN Name=XYL1;

OS Humicola insolens.

OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.

OX NCBI_TaxID=34413;

OK [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=94247364; PubMed=8190078; DOI=10.1007/BF00301060;

RA Dalboege H., Hansen H.P.H.;

RT "A novel method for efficient expression cloning of fungal enzyme genes.";

RL Mol. Gen. Genet. 243:253-260(1994).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.

CC -1- PATHWAY: Xylan degradation.

CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G) family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

DR EMBL; X76047; CAA53632.1; -; mRNA.

DR PIR; S43919; S43919.

DR HSSP; O43097; 1YNA.

DR InterPro; IPR001137; Glyco_hydro_11.

DR Pfam; PF00457; Glyco_hydro_11; 1.

DR PRINTS; PR00911; GLHYDRLASE11.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KW Glycosidase; Hydrolase; Signal; Xylan degradation.

FT SIGNAL 1 19 Potential.

FT CHAIN 20 227 Endo-1,4-beta-xylanase 1.

FT ACT_SITE 121 121 Nucleophile (By similarity).

FT ACT_SITE 212 212 Proton donor (By similarity).

SQ SEQUENCE 227 AA; 25601 MW; 5C2FF6ADCFEAD1F CRC64;

Query Match 55.7%; Score 689.5; DB 1; Length 227;

Best Local Similarity 55.8%; Pred. No. 6.7e-50;

Matches 126; Conservative 31; Mismatches 62; Indels 7; Gaps 3;

Qy 1 MVGFTPVALLAALATGALA-----FPAGNATELEKQTPNSEGWHDGYYSWSDGAQ 55

Db 1 MVSIKSVLAATAVSSALAAPDFVPRDNSTALQARQVTNABEGWHNGYFYSWSDGGGQ 60

Qy 56 ATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAIHFEgyYQPNNGSYLAVYGMTNPL 115

Db 61 VQYTNLEGSRYQVRWRNTGNFVGKGWNP-GTGRITNYGgyFNPGNGYLAVYGMTNPL 119

Qy 116 VEYIIVENFGTYDPSSGATDLGTVBCDGSYRLGKTRVNAPSIDGTQTFDQYWSVRQDK 175

Db 120 VEYVIESYGTYNPGSQAYKGTFTYDGDQYDIFVSTRYNQPSIDGTRTFQYWSIRKNK 179

Qy 176 RTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221

Db 180 RVGGSVNMQNHFNAMQOHGMPL-GQHYQIVATEGYQSSGESDIYV 224

RESULT 15

Q12580_9PEZI PRELIMINARY; PRT; 241 AA.

AC Q12580;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Endo-beta1,4-xylanase (EC 3.2.1.8).
GN Name=cgxB;
OS Chaetomium gracile.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
OX NCBI_TaxID=47794;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118924; PubMed=8595661; DOI=10.1007/BF00313196;
RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
RT "Two family G xylanase genes from Chaetomium gracile and their
RT expression in Aspergillus nidulans.";
RL Curr. Genet. 29:73-80(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tsukagoshi N.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D49851; BAA08650.1; -, Genomic_DNA.
DR PIR; S71473; S71473.
DR HSSP; Q8J1V6; 1H1A.
DR SMR; Q12580; 31-220.
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 241 AA; 25564 MW; DCD4B012272F777F CRC64;

Query Match 55.7%; Score 689; DB 2; Length 241;
Best local Similarity 59.5%; Pred. No. 7.9e-50;
Matches 132; Conservative 31; Mismatches 55; Indels 4; Gaps 4;

QY 1 MVGFTPVALLAALATGALAFPAAGNATELEKROTTPNSE-GWHDGYYSWWSGGAQATYT 59
DB 1 MWNFSSIFLAASAAVVAAP-GEIPGMHKRQTLTSSQGTNNGYYSSFWDGQGNVQYT 59

QY 60 NLEGGTYEISWGDGGLVVGKGNPNGLNARAIHFEQVYQPNGNSYLAVYGWTRNPLVEY 119
DB 60 NEAGGGQYSVTWSGNGNWNVGGKGNWPG-SARTINYTANYNPNGNSYLAVYGWTRNPLIEY 118

QY 120 IVENFGTYDPSSGATDLGTVECDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSG 179
DB 119 VVENFGTYNPSTGATRLGSVTIDGSCYDIYRTQRVNQPSTIGTSTFYQFWSVRQNKRSRG 178

QY 180 TVQTGCHPDAMARAGLNVNGDHYQIVATEGYFSSGYARTV 221
DB 179 SVNMAAHFNAWAAAGLQL-GTHDYQIVATEGYSSGSATVNV 219

Search completed: February 10, 2006, 15:01:22
Job time : 230.148 secs

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OM protein - protein search, using SW model

Run on: February 10, 2006, 15:01:51 ; Search time 38.1265 Seconds
(without alignments)
487.903 Million cell updates/sec

Title: US-09-467-368-2
Perfect score: 1238
Sequence: 1 MVGFPTVALAALATGALAF.....VATEGYFSSGYARITVADVG 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	225	1 US-08-886-765-2	Sequence 2, Appl
2	1238	100.0	225	2 US-09-115-660-2	Sequence 2, Appl
3	1083	87.5	194	2 US-09-570-856B-24	Sequence 24, Appl
4	965	77.9	194	2 US-09-570-856B-23	Sequence 23, Appl
5	806.5	65.1	221	2 US-09-570-856B-29	Sequence 29, Appl
6	688.5	55.6	227	1 US-08-458-023B-4	Sequence 4, Appl
7	685.5	55.4	223	2 US-09-254-733-7	Sequence 7, Appl
8	684.5	55.3	223	1 US-08-121-436A-2	Sequence 2, Appl
9	678.5	54.8	261	2 US-08-768-373-2	Sequence 2, Appl
10	678.5	54.8	261	2 US-09-849-242A-2	Sequence 2, Appl
11	663	53.6	197	1 US-08-044-621D-29	Sequence 29, Appl
12	663	53.6	197	1 US-08-709-912-9	Sequence 9, Appl
13	663	53.6	197	1 US-09-047-370-9	Sequence 9, Appl
14	663	53.6	197	2 US-09-570-856B-18	Sequence 18, Appl
15	662.5	53.5	230	2 US-08-768-373-4	Sequence 4, Appl
16	662.5	53.5	230	2 US-09-849-242A-4	Sequence 4, Appl
17	636.5	51.4	190	1 US-08-044-621D-28	Sequence 28, Appl
18	636.5	51.4	190	1 US-08-709-912-14	Sequence 14, Appl
19	636.5	51.4	190	1 US-09-047-370-14	Sequence 14, Appl
20	635.5	51.3	190	1 US-08-044-621D-26	Sequence 26, Appl
21	635.5	51.3	190	1 US-08-709-912-16	Sequence 16, Appl
22	635.5	51.3	190	1 US-09-047-370-16	Sequence 16, Appl
23	634.5	51.3	190	1 US-08-044-621D-27	Sequence 27, Appl
24	634.5	51.3	190	2 US-09-570-856B-19	Sequence 19, Appl
25	632.5	51.1	190	1 US-08-709-912-17	Sequence 17, Appl
26	632.5	51.1	190	1 US-09-047-370-17	Sequence 17, Appl
27	632	51.1	225	2 US-09-570-856B-26	Sequence 26, Appl

28	630.5	50.9	190	2 US-09-570-856B-20	Sequence 20, Appl
29	630.5	50.9	190	2 US-09-570-856B-22	Sequence 22, Appl
30	628	50.7	225	1 US-08-290-979A-8	Sequence 8, Appl
31	610.5	49.3	223	2 US-09-462-246-2	Sequence 2, Appl
32	597.5	48.3	226	2 US-09-367-891A-2	Sequence 2, Appl
33	588.5	47.5	296	1 US-08-507-431-6	Sequence 6, Appl
34	588.5	47.5	296	2 US-09-116-622-6	Sequence 6, Appl
35	588.5	47.5	296	2 US-09-219-277-6	Sequence 6, Appl
36	588.5	47.5	296	2 US-09-599-661-6	Sequence 6, Appl
37	587.5	47.5	335	2 US-09-570-856B-15	Sequence 15, Appl
38	586.5	47.4	231	1 US-08-902-655A-6	Sequence 6, Appl
39	571.5	46.2	215	1 US-08-044-621D-34	Sequence 34, Appl
40	568	45.9	189	1 US-08-709-912-13	Sequence 13, Appl
41	568	45.9	189	1 US-09-047-370-13	Sequence 13, Appl
42	566.5	45.8	206	1 US-08-315-695-19	Sequence 19, Appl
43	566	45.7	344	1 US-08-468-812-2	Sequence 2, Appl
44	566	45.7	344	2 US-08-590-563-2	Sequence 2, Appl
45	566	45.7	344	2 US-09-770-621-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-886-765-2
; Sequence 2, Application US/08886765
; Patent No. 5817500
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; APPLICANT: Wagner, Peter
; APPLICANT: Mullertz, Anette
; APPLICANT: Knapp, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 58175000 No. 5817500disk of No. 5817500th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-886-765-2

Query Match 100.0%; Score 1238; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 7.9e-110;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVGFPTVALAALATGALAFPPAGNATELEKROTPNSEGWHDGYYSWSDGGAQATYTN 60
Db 1 MVGFPTVALAALATGALAFPPAGNATELEKROTPNSEGWHDGYYSWSDGGAQATYTN 60

[illegible]

RESULT 2

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US-09-115-660-2
; Sequence 2, Application US/09115660
; Patent No. 6245546
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; APPLICANT: Wagner, Peter
; APPLICANT: Mullertz, Anette
; APPLICANT: Knap, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 62455460 No. 6245546disk of No. 6245546th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,660
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/886,765
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-115-660-2

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	Query Match	100.0%;	Score 1238;	DB 2;	length 225;
	Best Local Similarity	100.0%;	Pred. No. 7.9e-110;		
	Matches 225;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 MVGFTVALAALATGALAFPAGNALEKRQTTPNSEGHWHDGYYSWSWSDGAQAATYTN				60
Dd	1 MVGFPPVALLAALATGALAFPAAGNATELEKRTTNPSEGMWDGYYSWSWSDGAAQATYTN				60
Qy	61 LEGGTVEISWGDGNLVGKGKNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI				120
Dd	61 LEGGTVEISWGDGNLVGGKGNPGLNARAIIHFEGVYQPNGNSYLAVYGWTRNPLVEYYI				120
Qy	121 VENFGTYDPSGSATDLGTVECDGSYRLGKTTRVNAPSIDGTQTFDQYMSVRQDKRTSGT				180
Dd	121 VENFGTYDPSGSATDLGTVECDGSYRLGKTTRVNAPSIDGTQTFDQYMSVRQDKRTSGT				180

[illegible]

RESULT 3

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US-09-570-856B-24
; Sequence 24, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570, 856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133, 714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3+"
US-09-570-856B-24

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Query Match	87.5%;	Score 1083;	DB 2;	Length 194;
Best Local Similarity	100.0%;	Pred. No. 3.6e-95;		
Matches 193; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY		33	TTPNSEGWHDDGYYYSSWMSDGAQATYTNLEGGTYEISWGDDGNLVGGKWNPLNARAIH	92
Dd		2	TTPNSEGWHDGYYSWSMSDGAQAITYNLNEGTYEISMGDGNNLVGGKWNPGLNARAIIH	61
QY		93	FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDSIYRLGKTJ	152
Dd		62	FEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIRLKGTT	121
QY		153	RVANAPSIDGTQTTFDQYWSVRQDKRTSGTGVQTGFCHFDAMARAGLNVGNDHYQIVATEGYF	212
Dd		122	RVANAPSIDGTQTTFDQYWSVRQDKRTSGTGVQTGFCHFDAMARAGLNVGNDHYQIVATEGYF	181
QY		213	SSGYARITVADVG 225	
Dd		182	SSGYARITVADVG 194	

RESULT 4

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US-09-570-856B-23
: Sequence 23, Application US/09570856B
: Patent No. 6682923
: GENERAL INFORMATION:
: APPLICANT: Bentzien, Joerg M
: APPLICANT: Dahiyat, Bassil I
: TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
: FILE REFERENCE: A-67478-1/RFT/RMS/RMK
: CURRENT APPLICATION NUMBER: US/09/570,856B
: CURRENT FILING DATE: 2002-04-15
: PRIOR APPLICATION NUMBER: US 60/133,714
: PRIOR FILING DATE: 1999-05-12
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 23
: LENGTH: 194
: TYPE: PRT
: ORGANISM: Paecilomyces variotii
US-09-570-856B-23

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Query Match	77.9%;	Score 965;	DB 2;	Length 194;
Best Local Similarity	87.6%;	Pred. No. 6e-84;		
Matches 169;	Conservative 11;	Mismatches 13;	Indels 0;	Gaps 0;

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Qy      33 TTPNSEGMHGDYXXSWMSDGGAAQTYYTLNKGCTIYEISWGDGGLVGGKGMNPGLNARAIH 92
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Db       2  TTPNSEGMHGDYXXSWMSDGGGDDSTYTNNSGCTIETLWGNGGNLVGGKGMNPGLNARAIH 61
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[illegible][illegible]

QY	213	SSGYARITVADVG	225
Db	182	SSGYARITVADVG	194

RESULT 5

US-09-570-856B-29
; Sequence 29, Application US/09570856B

```

: GENERAL INFORMATION:
: APPLICANT: Bentsen, Joerg M
: APPLICANT: Dahiyat, Bassil I
: TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
: FILE REFERENCE: A-67478-1/RFT/RMS/RMK
: CURRENT APPLICATION NUMBER: US/09/570,856B
: CURRENT FILING DATE: 2002-04-15
: PRIOR APPLICATION NUMBER: US 60/133,714
: PRIOR FILING DATE: 1999-05-12
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 29
: LENGTH: 221
: TYPE: PRT
: ORGANISM: Cochliobolus carbonum
: US-09-570-856B-29

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Query Match	65.1%;	Score 806.5;	DB 2;	Length 221;
Best Local Similarity	67.9%;	Pred. No. 8.4e-69;		
Matches 150;	Conservative 26;	Mismatches 42;	Indels 3;	Gaps 3;

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Oy      1 MVGFTPVAAALATGALAEPAGNATELEKQTTPNSEGMWDGYVYYSWMSDGAQATYTN    60
        ||| : ||:||||| | : : ||||| | : : ||||| | : |||||
Db      1 MVSFSTIITAAVAATGALAAPATDVSLVARONTPNGEGTHNGCFWSWMSGDGARATYTN    59
```

Oy 61 LEGGTVEISWBDGCGNLVGKGKMPGLNARAIHFEVGYQPNGNSYLAIVGWTRNPLVEYYI 120
||:||| ||||||||| :||| ||||||||| :
Db 60 GAGGSYSVSWSGCENLVGGKGMNPG-TARTITYSCTYNNGNSYLAIVGWTRNPLVEYYV 118

```
Oy      121 VENFGTYDESSGATDLGTVECDGSYRLKTRVRNAPSIDQTQFDQYWSVRQDKRTSGT 180
        ||||| : ||| ||| :: : || | ||||| : ||||| : ||| :
Db      119 VENFGTYDESSQSQNKGTVTSDDGSYKLAOSTRTNPISIDGTRTFQOYWSVRONKRSSGS 178
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Qy      181  VQTGCHPEAWARAGLVNNGDHYQIVATEGYFSSGARITV  221
      |  |||||  : : | ||||| ||||| : : |||
Db      179  VNMKTHPEDAWASKGMNL-GQHYQIVATEGYFSTGNAQITV  218

```

RESULT 6

US-08-458-023B-4
; Sequence 4, Application US/08458023B

```

; GENERAL INFORMATION:
; APPLICANT: Betka, Randy M.
; APPLICANT: Yoder, Wendy
; APPLICANT: Takagi, Shinobu
; APPLICANT: Boomhachan, Katuppan C.
; TITLE OF INVENTION: ASPERGILUS EXPRESSION SYSTEM
;

```

```

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 56679900 NO. 5667990disk of NO. 5667990th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6201
;

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: 1988/03/01 0000

```

; FILING DATE: 01-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US
TELECOMMUNICATION INFORMATION:

TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-458-023B-4

Query Match	55.64;	Score 688.5;	DB 1;	length 227;
Best Local Similarity	55.84;	Pred. No. 1.5e-57;		
Matches 126; Conservative	30;	Mismatches 63;	Indels 7;	Gaps 3;

Oy 1 MVGFTPVALLAALATGALA----FPAGNATELEKROTTPNSEGMHDIYYYSWMSDGAQ 55

Db 1 MVSLKSVTLLAATAVSSAIAPFDVFPRDNSTALQARQVTPNGEGWHNGYFYISWMSDGGGQ 60

Oy 56 ATYTNLEGGTYEISWGDGGLTVGGKGMNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNP.L 119
| | | | | : | | | | | : | | | | |
Db 61 VQYTNLBSRRYQWRMRNTGNFVGKGMPG-TGRITINYGGYFNPDGNGYLAVYGWTRNP.L 119

[illegible]

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Qy      176 RTSGTVQTGCHFDAMABAGLVNNGDHYQIVATEGYFSSGARITV 221
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Db      180 RVGGSVMNQNHENAMQDHGMP-LGQHYQVAVATEGYQSSGESDIYV 224

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RESULT 7

US-09-254-733-7
: Sequence 7, Application US/09254733

Patent No. 6277596
; GENERAL INFORMATION:
; ADDITIONAL MATERIALS

; APPLICANT: MORIYA, TATSUKI
 ; APPLICANT: AOYAGI, KAORU
 ; APPLICANT: SUMIDA, NAOMI
 ; ADDITIONAL APPLICANT: TAKEUCHI

```

1      TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBHI GENES ORIGINATING
2
3      TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
4
5      TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
6
7      PRT REFERENCE NO. 03667/15/EMC/00144

```

FILE REFERENCE: 99-0268*/LC(WMC)/00144
CURRENT APPLICATION NUMBER: US/09/254,733
CURRENT FILING DATE: 1999-05-07

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; COMMENT: FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0.0

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; SEQ ID NO 7
; LENGTH: 223


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/ TELEFAX: (202) 371-2540
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 261 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Chaetomium thermophilum
/ STRAIN: CBS730.95
/ FEATURE:
/ NAME/KEY: Protein
/ LOCATION: 1..261
/ OTHER INFORMATION: /label= XLNA
US-08-768-373-2

Query Match      54.8%; Score 678.5; DB 2; Length 261;
Best Local Similarity 57.7%; Pred. No. 1.6e-56;
Matches 128; Conservative 31; Mismatches 56; Indels 7; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFPAAGNATELEKROT-TPNSEGWHDGYYSWSDGGAQATYT 59
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Db 1 MWNFSTLFLAATAAAPS-----IEKQTLTSSATGTHNGYYSFWTDGQGNIRFN 55

QY 60 NLEGGTYEISWGDGGLVGGKGNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYY 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 56 LESGGQYSVTWSGNGMWVGKGNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLIEYY 115

QY 120 IVENFGTYDPSSGATDLGTVGCDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSG 179
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 116 VVESFGTYDPSTGATRMGSVTTDGGTYNIYRTQRVNAPSIETGKTFYQYWSVRISKRTGG 175

QY 180 TVQTGCHPDAMARAGLNVNGDHYIQIVATEGYFSSGYARITV 221
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 176 TVTMAHFNAWRQAGLQL-GSHDYQIVATEGYSSGSATVNV 216

RESULT 10
US-09-849-242A-2
/ Sequence 2, Application US/09849242A
/ Patent No. 6635464
/ GENERAL INFORMATION:
/   APPLICANT: PALOHEIMO, MARJA
/   HAKOLA, SATU
/   MONTYLO, ARJA
/   VEHMAANPERO, JARI
/   LANTTO, RAIJA
/   LAHTINEN, TARJA
/   FAGERSTRM, RICHARD
/   SUOMINEN, PIIRKO
/ TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
/   AND USES THEREOF
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
/   STREET: 1100 NEW YORK AVENUE, SUITE 600
/   CITY: WASHINGTON
/   STATE: DC
/   COUNTRY: US
/   ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/   MEDIUM TYPE: floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/09/849,242A
/   FILING DATE: 07-May-2001
/   CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 08/768,373
/   FILING DATE: 17-DEC-1996
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/ APPLICATION NUMBER: US 60/008,746
/ FILING DATE: 18-DEC-1995
/ APPLICATION NUMBER: US 60/020,839
/ FILING DATE: 28-JUN-1996
/ ATTORNEY/AGENT INFORMATION:
/   NAME: CIMBALA, MICHELE A.
/   REGISTRATION NUMBER: 33,851
/ REFERENCE/DOCKET NUMBER: 1716.0540004
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (202) 371-2600
/   TELEFAX: (202) 371-2540
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 261 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Chaetomium thermophilum
/ STRAIN: CBS730.95
/ FEATURE:
/ NAME/KEY: Protein
/ LOCATION: 1..261
/ OTHER INFORMATION: /label= XLNA
US-09-849-242A-2

Query Match      54.8%; Score 678.5; DB 2; Length 261;
Best Local Similarity 57.7%; Pred. No. 1.6e-56;
Matches 128; Conservative 31; Mismatches 56; Indels 7; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFPAAGNATELEKROT-TPNSEGWHDGYYSWSDGGAQATYT 59
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Db 1 MWNFSTLFLAATAAAPS-----IEKQTLTSSATGTHNGYYSFWTDGQGNIRFN 55

QY 60 NLEGGTYEISWGDGGLVGGKGNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYY 119
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Db 56 LESGGQYSVTWSGNGMWVGKGNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLIEYY 115

QY 120 IVENFGTYDPSSGATDLGTVGCDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSG 179
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Db 116 VVESFGTYDPSTGATRMGSVTTDGGTYNIYRTQRVNAPSIETGKTFYQYWSVRISKRTGG 175

QY 180 TVQTGCHPDAMARAGLNVNGDHYIQIVATEGYFSSGYARITV 221
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 176 TVTMAHFNAWRQAGLQL-GSHDYQIVATEGYSSGSATVNV 216

RESULT 11
US-08-044-621D-29
/ Sequence 29, Application US/08044621D
/ Patent No. 5405769
/ GENERAL INFORMATION:
/   APPLICANT: Warren W. Makarchuk
/   APPLICANT: Wing L. Sung
/   APPLICANT: Makoto Yaguchi
/   APPLICANT: Robert L. Campbell
/   APPLICANT: David R. Rose
/ TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
/   OF A LOW MOLECULAR MASS XYLANASE
/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
/   ADDRESSEE: Gowling, Strachy & Henderson
/   STREET: Suite 2600, 160 Elgin Street
/   CITY: Ottawa
/   STATE: Ontario
/   COUNTRY: Canada
/   ZIP: K1P 1C3
/ COMPUTER READABLE FORM:
/   MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
/   COMPUTER: IBM PC
/   OPERATING SYSTEM: PC-DOS
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1      SOFTWARE: WordPerfect 5.1
2
3      CURRENT APPLICATION DATA:
4      APPLICATION NUMBER: US/08/044,621D
5      FILING DATE: April 8, 1993
6      CLASSIFICATION: 435
7      PRIOR APPLICATION DATA:
8      APPLICATION NUMBER:
9
10     FILING DATE:
11
12     ATTORNEY/AGENT INFORMATION:
13     NAME: Judy A. Erratt
14     REGISTRATION NUMBER: 34,076
15     REFERENCE/DOCKET NUMBER: 08-863796
16     TELECOMMUNICATION INFORMATION:
17     TELEPHONE: 613-786-0199
18     TELEFAX: 613-563-9869
19     TELEX:
20
21     INFORMATION FOR SEQ ID NO: 29:
22     SEQUENCE CHARACTERISTICS:
23     LENGTH: 197
24     TYPE: Amino Acid
25     STRANDEDNESS: NO. 5405769 Relevant
26     TOPOLOGY: linear
27     MOLECULE TYPE:
28     DESCRIPTION: protein
29     HYPOTHETICAL: NO
30     ANTI-SENSE: NO
31     FRAGMENT TYPE: NO
32     ORIGINAL SOURCE:
33     ORGANISM: Schizophyllum commune
34     STRAIN: Schizophyllum commune, Xylanase A
35     IMMEDIATE SOURCE:
36     POSITION IN GENOME:
37     FEATURE:
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39     PUBLICATION INFORMATION:
40     AUTHORS: Oku T., Yaguchi M., Paice M., & Jurssek
41     AUTHORS: L.
42     TITLE:
43     JOURNAL: Canadian Fed. Biol. Soc. Annu. Meet.
44     VOLUME:
45     ISSUE:
46     PAGES: Abstract 676
47     DATE: 1988
48     DOCUMENT NUMBER:
49     FILING DATE:
50     PUBLICATION DATE:
51     RELEVANT RESIDUES IN SEQ ID NO:
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53     US-08-044-621D-29

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Query Match	53.6%	Score 663;	DB 1;	Length 197;
Best Local Similarity	61.3%	Pred. No. 3.2e-55;		
Matches 119; Conservative	26;	Mismatches 43;	Indels 6;	Gaps 2;

[illegible]

RESULT 12
US-08-709-912-9
; Sequence 9, Application US/08709912
; Patent No. 5759840


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1 STATE: DC
2
3 COUNTRY: US
4 ZIP: 20005-3934
5
6 COMPUTER READABLE FORM:
7
8 MEDIUM TYPE: floppy disk
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10 COMPUTER: IBM PC compatible
11
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13
14 SOFTWARE: PatentIn Release #1.0, Version #1.30
15
16 CURRENT APPLICATION DATA:
17
18 APPLICATION NUMBER: US/08/768,373
19
20 FILING DATE: 17-DEC-1996
21
22 CLASSIFICATION:
23
24 PRIOR APPLICATION DATA:
25
26 APPLICATION NUMBER: US 60/008,746
27
28 FILING DATE: 18-DEC-1995
29
30 PRIOR APPLICATION DATA:
31
32 APPLICATION NUMBER: US 60/020,839
33
34 FILING DATE: 28-JUN-1996
35
36 ATTORNEY/AGENT INFORMATION:
37
38 NAME: CIMBALA, MICHELE A.
39
40 REGISTRATION NUMBER: 33,851
41
42 REFERENCE/DOCKET NUMBER: 1050.0540003
43
44 TELECOMMUNICATION INFORMATION:
45
46 TELEPHONE: (202) 371-2600
47
48 TELEFAX: (202) 371-2540
49
50 INFORMATION FOR SEQ ID NO: 4:
51
52 SEQUENCE CHARACTERISTICS:
53
54 LENGTH: 230 amino acids
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56 TYPE: amino acid
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58 STRANDEDNESS: single
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60 TOPOLOGY: linear
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62 MOLECULE TYPE: protein
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64 ORIGINAL SOURCE:
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66 ORGANISM: Chaetomium thermophilum
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68 STRAIN: CBS730.95
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70 FEATURE:
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72 NAME/KEY: Protein
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74 LOCATION: 1..230
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76 OTHER INFORMATION: /label= XLNB
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Query Match	53.5%;	Score 662.5;	DB 2;	Length 230;
Best Local Similarity	58.8%;	Pred. No. 4.4e-55;		
Matches 130;	Conservative 23;	Mismatches 55;	Indels 13;	Gaps 4;

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QY      12 LAATGALAFP--AGNAT-----ELEKRQTTPNSEGMHGGYYISWMSDGAQATYTN 60
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Db      9  LTAATALAFPLEAFNATEGEFNATSLHLEIMVRAGTSSGCTGTHNGWYYSFMTDGGGIWYTN 68
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      61 LEGGTYEISWGDGNNLVGKGWNPGLNRAIHFEGVYQPNGNSYLAIVGWRNPLVEYI 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY      121 VENFGTYDPSGATDLGTVECDSIYRLGKTRRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      128 VESYGTYPDSSGAQNLGTFQSDGTYKIAKSTRYNAPSIEGTKFTQYWSVRTSKRVGT 187
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      181 VQTGCHFDAMARAGLNVNGDHYIQIVATEGYFSSGYARITV 221
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      188 VTVANHFNAMWKSGLNL-GSHDYQIVATEGYKSSGSASITV 227
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: February 10, 2006, 15:03:36
Job time : 39.1265 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 15:17:55 ; Search time 131.563 Seconds
(without alignments)
714.573 Million cell updates/sec

Title: US-09-467-368-2
Perfect score: 1238
Sequence: 1 MVGFPPVALAALATGALAF.....VATEGYFSSGYARITVADVG 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	225	3	US-09-467-368-2
2	1238	100.0	225	4	US-10-307-386-24
3	1088	87.9	194	4	US-10-307-441-20
4	1088	87.9	194	6	US-11-088-725A-46
5	821.5	66.4	227	4	US-10-237-386-21
6	806.5	65.1	221	4	US-10-237-386-20
7	794.5	64.2	227	4	US-10-425-115-221836
8	789.5	63.8	221	4	US-10-425-115-267585
9	775.5	62.6	227	4	US-10-237-386-22
10	772.5	62.4	234	4	US-10-425-115-361946
11	716.5	57.9	231	4	US-10-237-386-26
12	701.5	56.7	231	4	US-10-237-386-25
13	691.5	55.9	219	4	US-10-237-386-29
14	689.5	55.7	227	4	US-10-237-386-27
15	689	55.7	241	4	US-10-237-386-35
16	684.5	55.3	223	4	US-10-237-386-31
17	681.5	55.0	221	4	US-10-237-386-30
18	671.5	54.2	223	4	US-10-237-386-32
19	671	54.2	234	4	US-10-213-990-69
20	667	53.9	222	4	US-10-237-386-32
21	663	53.6	197	4	US-10-307-441-9
22	663	53.6	197	6	US-11-088-725A-36
23	663	53.6	201	4	US-10-237-386-23
24	660.5	53.4	221	4	US-10-237-386-44
25	660	53.3	233	4	US-10-237-386-28
26	636.5	51.4	190	4	US-10-307-441-14
27	636.5	51.4	190	6	US-11-088-725A-41

28	635.5	51.3	190	4	US-10-307-441-16	Sequence 16, Appl
29	633	51.1	189	4	US-10-307-441-19	Sequence 19, Appl
30	633	51.1	189	6	US-11-088-725A-28	Sequence 28, Appl
31	632.5	51.1	190	4	US-10-307-441-17	Sequence 17, Appl
32	632.5	51.1	190	6	US-11-088-725A-42	Sequence 42, Appl
33	632.5	51.1	223	4	US-10-237-386-34	Sequence 34, Appl
34	631	51.0	225	4	US-10-237-386-36	Sequence 36, Appl
35	630.5	50.9	190	4	US-10-237-386-33	Sequence 33, Appl
36	624.5	50.4	190	6	US-11-088-725A-1	Sequence 1, Appl
37	613.5	49.6	313	4	US-10-213-990-72	Sequence 72, Appl
38	611.5	49.4	217	3	US-09-790-070A-11	Sequence 11, Appl
39	610.5	49.3	223	4	US-10-299-393-2	Sequence 2, Appl
40	610.5	49.3	223	6	US-11-154-793-2	Sequence 2, Appl
41	599.5	48.4	221	4	US-10-237-386-37	Sequence 37, Appl
42	573	46.3	228	4	US-10-237-386-39	Sequence 39, Appl
43	573	46.3	240	4	US-10-237-386-42	Sequence 42, Appl
44	568	45.9	189	4	US-10-307-441-13	Sequence 13, Appl
45	568	45.9	189	6	US-11-088-725A-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-467-368-2
; Sequence 2, Application US/09467368
; Patent No. US20020160080A1
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; Wagner, Peter
; Mullertz, Anette
; Knap, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20020160080A1o No. US20020160080A1disk of No. US200201600
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,368
; FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-467-368-2
Query Match 100.0%; Score 1238; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-109;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 TRVNAPSIDGTQTFPDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 180
QY 212 FSSGYARITVADVG 225
DB 181 FSSGYARITVADVG 194

RESULT 5

US-10-237-386-21
; Sequence 21, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 227
; TYPE: PRT
; ORGANISM: H. turcicum
US-10-237-386-21

Query Match 66.4%; Score 821.5; DB 4; Length 227;
Best Local Similarity 67.7%; Pred. No. 7.3e-70;
Matches 153; Conservative 25; Mismatches 41; Indels 7; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFPAAGN-----ATELEKQRTTPNSEGWHDGYYYSWSDGGAQ 55
DB 1 MVSFTSIITAAVAATGALAAPATDIAARAPSDLVAROSTPNEGTHNGCFYSWSDGAR 60
QY 56 ATYTNLEGTYEISWGDGNLVGKGNPGLNARAIHFEVGYQPNNGNSYLAIVGWTNPL 115
DB 61 ATYTNAGGGSYSVSWGTGNLVGKGNPGLNARAIHFEVGYQPNNGNSYLAIVGWTNPL 119
QY 116 VEYIVENFGTYDPSSGATDLGTVCEGSIYRLGKTRVNAPSIDGTQTFPDQYWSVRQDK 175
DB 120 VEYIVENFGTYDPSSQAQNKGTYSDDSSYKIAQSTRNQPSIDGTRTFQQYWSVRQNK 179
QY 176 RTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221
DB 180 RSSGSVNMKTHFDAMASKGNL-GSHYYQIVATEGYFSSGSASITV 224

RESULT 6

US-10-237-386-20
; Sequence 20, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 221
; TYPE: PRT
; ORGANISM: C. carbonum
US-10-237-386-20

Query Match 65.1%; Score 806.5; DB 4; Length 221;
Best Local Similarity 67.9%; Pred. No. 1.9e-68;
Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFPAAGNATELEKQRTTPNSEGWHDGYYYSWSDGGAQATYTN 60
DB 1 MVSFTSIITAAVAATGALAAPATDVS-LVARQNTPEGEGTHNGCFWSWSDGARATYTN 59
QY 61 LEGTYEISWGDGNLVGKGNPGLNARAIHFEVGYQPNNGNSYLAIVGWTNPLVEYYI 120
DB 60 GAGGSYSVSWSGGNLVGKGNPGLNARAIHFEVGYQPNNGNSYLAIVGWTNPLVEYYI 118
QY 121 VENFGTYDPSSGATDLGTVCEGSIYRLGKTRVNAPSIDGTQTFPDQYWSVRQDKRTSGT 180
DB 119 VENFGTYDPSSQAQNKGTYSDDSSYKIAQSTRNQPSIDGTRTFQQYWSVRQNKRS 178
QY 181 VQTCGHPDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221
DB 179 VNMKTHFDAMASKGNL-GSHYYQIVATEGYFSTGNAQITV 218

RESULT 7

US-10-425-115-221836
; Sequence 221836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 221836
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_133906C.1.pep
US-10-425-115-221836

Query Match 64.2%; Score 794.5; DB 4; Length 227;
Best Local Similarity 63.7%; Pred. No. 2.7e-67;
Matches 144; Conservative 32; Mismatches 43; Indels 7; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFPAAGNAT-----ELEKQRTTPNSEGWHDGYYYSWSDGGAQ 55
DB 1 MVSFTSLITAAVAATGAFAPATDVAARSSGDLVAROSTPNAEGTHNGCFYSWWTGSGK 60
QY 56 ATYTNLEGTYEISWGDGNLVGKGNPGLNARAIHFEVGYQPNNGNSYLAIVGWTNPL 115
DB 61 VTYTNAGGGSYSVSWGSGNLFVGKGNPGLNARAIHFEVGYQPNNGNSYLAIVGWTNPL 119
QY 116 VEYIVENFGTYDPSSGATDLGTVCEGSIYRLGKTRVNAPSIDGTQTFPDQYWSVRQDK 175
DB 120 VEYIVENFGTYDPSSQAQNKGTYSDDSSYKIAQSTRNQPSIDGTRTFQQYWSVRQNK 179
QY 176 RTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221
DB 180 RSSGSVNMKTHFDAMASKGNL-GSHYYQIVATEGYFSTGSASITV 224

RESULT 8


```

; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 231
; TYPE: PRT
; ORGANISM: C. sativus
; US-10-237-386-26

```

```

Query Match      57.9%; Score 716.5; DB 4; Length 231;
Best Local Similarity 58.7%; Pred. No. 7.4e-60;
Matches 135; Conservative 29; Mismatches 55; Indels 11; Gaps 4;

```

```

Qy 1 MVGFTPVALLAATGALAF-----AGNATE-LEKQTPNSEGMHDGYYSWSD 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MVSFKSLLLAAVATTSVLAAPFDLBERDDGNATALEKQSTPSSEGYHNGYFYSWTD 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 52 GGAQATYTNLECGTYEISWGDGNLVGKGNPGLNARAIHEGVYQPNNGSYLAIVYGMT 111
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GGSAQYTMGEGRYSVTWRNTGNFVGKGNPGLNARAIHEGVYQPNNGSYLAIVYGMT 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 112 RNPLVEYIVENFGTYDPSGATDLGVECDGSIYRLGKTRVNAPSIDGTQTFDQYMSV 171
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 RNPLVEYIVESYGTYNPSSGAQYKGSFQTDGTYNNAVSTRYNQPSIDGTRTFQYMSV 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 172 RQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 RQDKRVGGSVMQNHFNAMSRYGLNL-GQHYQIVATEGYQSSGSSDIYV 228
    |||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 12

```

US-10-237-386-25
; Sequence 25, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 231
; TYPE: PRT
; ORGANISM: C. carbonum
; US-10-237-386-25

```

```

Query Match      56.7%; Score 701.5; DB 4; Length 231;
Best Local Similarity 57.4%; Pred. No. 2e-58;
Matches 132; Conservative 31; Mismatches 56; Indels 11; Gaps 4;

```

```

Qy 1 MVGFTPVALLAATGALAFAG-----NATE-LEKQTPNSEGMHDGYYSWSD 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MVSFKSLLLAAVATTSVLAAPFDLBERDDGNATALEKQSTPSAEGYHNGYFYSWTD 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

Qy 52 GGAQATYTNLECGTYEISWGDGNLVGKGNPGLNARAIHEGVYQPNNGSYLAIVYGMT 111
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GGSAQYTMGEGRYSVTWRNTGNFVGKGNPGLNARAIHEGVYQPNNGSYLAIVYGMT 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 112 RNPLVEYIVENFGTYDPSGATDLGVECDGSIYRLGKTRVNAPSIDGTQTFDQYMSV 171
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 RNPLVEYIVESYGTYNPSSGAQYKGSFQTDGTYNNAVSTRYNQPSIDGTRTFQYMSV 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 172 RQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGYFSSGYARITV 221
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 RQDKRVGGSVMQNHFNAMSRYGLNL-GQHYQIVATEGYQSSGSSDIYV 228
    |||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 13

```

US-10-237-386-29
; Sequence 29, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. gracile
; US-10-237-386-29

```

```

Query Match      55.9%; Score 691.5; DB 4; Length 219;
Best Local Similarity 59.1%; Pred. No. 1.7e-57;
Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps 5;

```

```

Qy 1 MVGFTPVALLAATGALAFAGNAT--ELEKQTPNSEGMHDGYYSWSDGAQAT 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MVSFKAL---LLGAAGALAFPF-NVTQMNELVARAGTSPGTGNNGYFYSFTWDGGGTVN 56
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 58 YTNLECGTYEISWGDGNLVGKGNPGLNARAIHEGVYQPNNGSYLAIVGWTNPLVE 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 YQNGAGGSYSVQWQNCNPFVGKGNPGLNARAIHEGVYQPNNGSYLAIVGWTNPLVE 115
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 118 YIYVENFGTYDPSGATDLGVECDGSIYRLGKTRVNAPSIDGTQTFDQYMSVRQDKRT 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 YIYVESFGTYDPSGASKFQTIQDGSYTTIAKTRVNQPSIEGTSTFDQFWSVRQNHRS 175
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 178 SGTVQTCGHPDAMARAGLNVNGDHYQIVATEGYFSSGYARITVA 222
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 SGSVNVAAHFNAWAQAGLKL-GSHNYQIVATEGYQSSGSSSITVS 219
    |||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 14

```

US-10-237-386-27
; Sequence 27, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426

```



```

; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 27
; LENGTH: 227
; TYPE: PRT
; ORGANISM: H. insolens
;
US-10-237-386-27

```

Query Match	55.7%;	Score 689.5;	DB 4;	Length 227;
Best Local Similarity	55.8%;	Pred. No. 2.7e-57;		
Matches 126;	Conservative 31;	Mismatches 62;	Indels 7;	Gaps 3;

Qy	1	MVGFTPVALLAALATGALA-----FPAGNATELEKROTPNSEGWHDDGYIYSWMSDGAQ	55
Db	1	MVSLKSVLAAATAVSSAIAAPDFVPRDNSTALQARQVTPNAEGWHNGYFYSWMSDGGGQ	60
Qy	56	ATYTNLEGGTYEISWGDGNLVGKGMNPLNARAIHFEGYQPNNGNSYLAVYGWTNPL	115
Db	61	VQYTNLEGRYQVRWRNTGNFVGKGWMPG-TGRTINYGGEYNPQNGYLAVYGWTNPL	119
Qy	116	VEYYIVENFGTYDPSSGATDLGTECDPSIYRLKTRVNAPSIDGTQTFDQYWSVRQDK	175
Db	120	VEYYIVESYGTYNPGSQAQYKGYFTDGDQYDIFVSTRYNQPSIDGTRTFQQYWSIRNKK	179
Qy	176	RTSGTVQTGCHFDAMARAGLNVNGDHYIQIVATEGYFSSGYARTV	221
Db	180	RVGGSVNMQNHFNAMQOHGMPL-GQHYOVVAATEGYQSSGESDITY	224

```

RESULT 15
US-10-237-386-35
; Sequence 35, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 241
; TYPE: PRT
; ORGANISM: C. gracile
US-10-237-386-35

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Query Match	55.7%;	Score 689;	DB 4;	Length 241;
Best Local Similarity	59.5%;	Pred. No. 3.3e-57;		
Matches 132;	Conservative 31;	Mismatches 55;	Indels 4;	Gaps 4;

[illegible]

Db 119 VVENFGTYNPSTGATRLGSAVTLDGSCYDIYRTQRVNPQPSIEGTSTFYQFWMSVRQNKSGG 178

QY 180 TVQTCGCHFDAMARAGLNVNGDHYQIVATEGYFSSGARITV 221

Db 179 SVNMAHFENMAAAAGLQI-GTHDYQIVATEGYSSGSAITNV 219

Search completed: February 10, 2006, 15:22:35
Job time : 132.563 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 15:18:39 ; Search time 11.2768 Seconds
(Without alignments)
261.826 Million cell updates/sec

Title: US-09-467-368-2
Perfect score: 1238
Sequence: 1 MVGFTPVLAALAAATGALP.....VATEGYFSSGYARITVADVG 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New: *
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep: *
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep: *
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep: *
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	225	7	US-11-170-653-24 Sequence 24, Appl
2	821.5	66.4	227	7	US-11-170-653-21 Sequence 21, Appl
3	806.5	65.1	221	7	US-11-170-653-20 Sequence 20, Appl
4	775.5	62.6	227	7	US-11-170-653-22 Sequence 22, Appl
5	716.5	57.9	231	7	US-11-170-653-26 Sequence 26, Appl
6	701.5	56.7	231	7	US-11-170-653-25 Sequence 25, Appl
7	691.5	55.9	219	7	US-11-170-653-29 Sequence 29, Appl
8	689.5	55.7	227	7	US-11-170-653-27 Sequence 27, Appl
9	689	55.7	241	7	US-11-170-653-35 Sequence 35, Appl
10	684.5	55.3	223	7	US-11-170-653-31 Sequence 31, Appl
11	671.5	54.2	223	7	US-11-170-653-30 Sequence 30, Appl
12	667	53.9	222	7	US-11-170-653-32 Sequence 32, Appl
13	663	53.6	201	7	US-11-170-653-23 Sequence 23, Appl
14	660.5	53.4	221	7	US-11-170-653-44 Sequence 44, Appl
15	660	53.3	233	7	US-11-170-653-28 Sequence 28, Appl
16	632.5	51.1	223	7	US-11-170-653-34 Sequence 34, Appl
17	631	51.0	225	7	US-11-170-653-36 Sequence 36, Appl
18	630.5	50.9	190	7	US-11-170-653-33 Sequence 33, Appl
19	608	49.1	432	6	US-10-517-939-178 Sequence 178, App
20	599.5	48.4	221	7	US-11-170-653-37 Sequence 37, App
21	585.5	47.3	335	6	US-10-517-939-232 Sequence 232, App
22	581	46.9	348	6	US-10-517-939-166 Sequence 166, App
23	573	46.3	228	7	US-11-170-653-39 Sequence 39, Appl
24	573	46.3	240	7	US-11-170-653-42 Sequence 42, Appl
25	567	45.8	344	7	US-11-108-163B-10 Sequence 10, Appl

26	563	45.5	239	7	US-11-170-653-40	Sequence 40, Appl
27	562.5	45.4	241	7	US-11-170-653-43	Sequence 43, Appl
28	561	45.3	242	7	US-11-170-653-41	Sequence 41, Appl
29	560	45.2	193	7	US-11-108-163B-14	Sequence 14, Appl
30	560	45.2	217	7	US-11-108-163B-13	Sequence 13, Appl
31	560	45.2	220	7	US-11-108-163B-12	Sequence 12, Appl
32	560	45.2	301	7	US-11-108-163B-11	Sequence 11, Appl
33	558.5	45.1	354	7	US-10-517-939-216	Sequence 216, App
34	553	44.7	240	7	US-11-170-653-38	Sequence 38, Appl
35	551	44.5	358	6	US-10-517-939-182	Sequence 182, App
36	541.5	43.7	347	6	US-10-517-939-196	Sequence 196, App
37	541	43.7	216	7	US-11-170-653-45	Sequence 45, Appl
38	540.5	43.7	542	6	US-10-517-939-262	Sequence 262, App
39	539.5	43.6	352	6	US-10-517-939-226	Sequence 226, App
40	532	43.0	445	6	US-10-517-939-368	Sequence 368, App
41	531.5	42.9	303	6	US-10-517-939-214	Sequence 214, App
42	531.5	42.9	358	6	US-10-517-939-370	Sequence 370, App
43	528	42.6	237	7	US-11-170-653-47	Sequence 47, Appl
44	527.5	42.6	346	6	US-10-517-939-160	Sequence 160, App
45	524	42.3	356	6	US-10-517-939-234	Sequence 234, App

ALIGNMENTS

RESULT 1
US-11-170-653-24
; Sequence 24, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor;
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170, 653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237, 386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 225
; TYPE: PRT
; ORGANISM: T. lanuginosus
US-11-170-653-24

Query Match 100.0%; Score 1238; DB 7; Length 225;
Best local Similarity 100.0%; Pred. No. 4.7e-106;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVGFTPVLAALAAATGALFPAGNATELEKQTTPNSEGMHGYYSWSDGAQATYTN	60
DB	1	MVGFTPVLAALAAATGALFPAGNATELEKQTTPNSEGMHGYYSWSDGAQATYTN	60
QY	61	LEGGTYEISWGDGNLVGKGWNPGLNARAIHFEQVYQPNGNSYLAVYGTWRNPLVEYYI	120
DB	61	LEGGTYEISWGDGNLVGKGWNPGLNARAIHFEQVYQPNGNSYLAVYGTWRNPLVEYYI	120
QY	121	VENFGTYDPSSGATDLGTYECDSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT	180
DB	121	VENFGTYDPSSGATDLGTYECDSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT	180
QY	181	VQTGCHPDAMARAGLVNGDHYIYQIVATEGYFSSGYARITVADVG	225
DB	181	VQTGCHPDAMARAGLVNGDHYIYQIVATEGYFSSGYARITVADVG	225

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RESULT 2
US-11-170-653-21
; Sequence 21, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 227
; TYPE: PRT
; ORGANISM: H. turcicum
US-11-170-653-21
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Query Match          66.4%; Score 821.5; DB 7; Length 227;
Best Local Similarity 67.7%; Pred. No. 4.7e-68;
Matches 153; Conservative 25; Mismatches 41; Indels 7; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFPAAGN-----ATELEKROQTTPNSEGWHDGYYSWSDGGAQ 55
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MVSFTSIITAAVAATGALAPATDIAARAPSDLVAROSTPGEETHNGCFYSWSDGAR 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 56 ATYTNLEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQYQPNNGNSYLAVYGTNRNPL 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ATYTNAGGGSYSVSWGTGGLVGGKGNPGLNARAIHFEQYQPNNGNSYLAVYGTNRNPL 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 VEYIVENFGTYDPSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDK 175
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 VEYIVENFGTYDPSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDK 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 RTSGTVQTCGHPDAMARAGLNVNGDHYIQIVATEGYFSSGYARITV 221
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 180 RSSGSVNMKTHFDAMASKGMNL-GSHYQIVATEGYFSSGSASITV 224
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 3
US-11-170-653-20
; Sequence 20, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
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; LENGTH: 221
; TYPE: PRT
; ORGANISM: C. carbonum
US-11-170-653-20
```

```
Query Match          65.1%; Score 806.5; DB 7; Length 221;
Best Local Similarity 67.9%; Pred. No. 1.1e-66;
Matches 150; Conservative 26; Mismatches 42; Indels 3; Gaps 3;

QY 1 MVGFTPVALLAALATGALAFPAAGNATELEKROQTTPNSEGWHDGYYSWSDGGAQATYTN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MVSFTSIITAAVAATGALAPATDVS-LVARQNTPEGEETHNGCFYSWSDGARATYTN 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 LBGTYEISWGDGGLVGGKGNPGLNARAIHFEQYQPNNGNSYLAVYGTNRNPLVEYYI 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 60 GAGGSYSVSWSGGGLVGGKGNPGLNARAIHFEQYQPNNGNSYLAVYGTNRNPLVEYYI 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VENFGTYDPSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 119 VENFGTYDPSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDKRTSGT 178
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 VQTCGHPDAMARAGLNVNGDHYIQIVATEGYFSSGYARITV 221
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 179 VNMKTHFDAMASKGMNL-GSHYQIVATEGYFSSGSASITV 218
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 4
US-11-170-653-22
; Sequence 22, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 227
; TYPE: PRT
; ORGANISM: A. pisi
US-11-170-653-22
```

```
Query Match          62.6%; Score 775.5; DB 7; Length 227;
Best Local Similarity 65.5%; Pred. No. 7.4e-64;
Matches 148; Conservative 25; Mismatches 46; Indels 7; Gaps 4;

QY 1 MVGFTPVALLAALATGALAFPAAGN-ATE---LEKROQTTPNSEGWHDGYYSWSDGGAQ 55
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MVSFTSIITAAVAATGALAVPTDLATRSGLALTARAGTPSSQGTTHNGCFYSWMTDGAQ 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 56 ATYTNLEGGTYEISWGDGGLVGGKGNPGLNARAIHFEQYQPNNGNSYLAVYGTNRNPL 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ATYTNAGGGSYSVNMKTGGLVGGKGNPGLNARAIHFEQYQPNNGNSYLAVYGTNRNPL 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 VEYIVENFGTYDPSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDK 175
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 VEYIVENFGTYDPSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYWSVRQDK 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 RTSGTVQTCGHPDAMARAGLNVNGDHYIQIVATEGYFSSGYARITV 221
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 180 RSSGSVNMKTHFDAMASKGMNL-GTHYQIVATEGYFSSGSASITV 224
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```
RESULT 5
US-11-170-653-26
; Sequence 26, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 231
; TYPE: PRT
; ORGANISM: C. sativus
US-11-170-653-26
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```
Query Match 57.9%; Score 716.5; DB 7; Length 231;
Best Local Similarity 58.7%; Pred. No. 1.8e-58;
Matches 135; Conservative 29; Mismatches 55; Indels 11; Gaps 4;

QY 1 MVGFTPVALLAALATGALAFP-----AGNATE-LEKRQTPNSEGMHGGYYSWMSD 51
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MVSFKSLLLAAVATTSLAAPDFLREDDGNATALLERKQSTPSSEGYHNGYFSWMTD 60

QY 52 GGAQATYTNLEGGTYEISWGDGNTLVGKGWNPGLNARAIHFEQVYQPNNGNSYLAAYGWT 111
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 GGSAQYTMGEGRSRYSTWRNTGNFVGKGWNP-GTGRVINYGAFFNPQNGYLAAYGWT 119

QY 112 RNPLVEYIVENFGTYDPSSGATDLGTVCECDGSYRLGKTRVNAPSIDGTQTFDQYMSV 171
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 RNPLVEYIVESYGTYNPSSGAQYKGSFQTDGTYNVAVSTRYNQPSIDGTRTFQYMSV 179

QY 172 RQDKRTSGTVQTCGHPDAMARAGLVNNGDHYQIVATEGYFSSGYARITV 221
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 180 RQDKRVGGSVNMQNHFNAMSRYGLNL-GQHYQIVATEGYQSSGSSDIYV 228
```

```
RESULT 6
US-11-170-653-25
; Sequence 25, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 25
; LENGTH: 231
; TYPE: PRT
; ORGANISM: C. carbonum
US-11-170-653-25

Query Match 56.7%; Score 701.5; DB 7; Length 231;
Best Local Similarity 57.4%; Pred. No. 4.2e-57;
Matches 132; Conservative 31; Mismatches 56; Indels 11; Gaps 4;

QY 1 MVGFTPVALLAALATGALAFPAAG-----NATE-LEKRQTPNSEGMHGGYYSWMSD 51
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MVSFKSLLLAAVATTSLAAPDFLREDDVNATALLERKQSTPSAEGYHNGYFSWMTD 60

QY 52 GGAQATYTNLEGGTYEISWGDGNTLVGKGWNPGLNARAIHFEQVYQPNNGNSYLAAYGWT 111
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 GGSAQYTMGEGRSRYSTWRNTGNFVGKGWNP-GSRVINYGAFFNPQNGYLAAYGWT 119

QY 112 RNPLVEYIVENFGTYDPSSGATDLGTVCECDGSYRLGKTRVNAPSIDGTQTFDQYMSV 171
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 RNPLVEYIVESYGTYNPSSGAQYKGSFQTDGTYNVAVSTRYNQPSIDGTRTFQYMSV 179

QY 172 RQDKRTSGTVQTCGHPDAMARAGLVNNGDHYQIVATEGYFSSGYARITV 221
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 180 RQDKRVGGSVNMQNHFNAMSRYGLNL-GQHYQIVATEGYQSSGSSDIYV 228
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RESULT 7
US-11-170-653-29
; Sequence 29, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. gracile
US-11-170-653-29
```

```
Query Match 55.9%; Score 691.5; DB 7; Length 219;
Best Local Similarity 59.1%; Pred. No. 3.2e-56;
Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps 5;

QY 1 MVGFTPVALLAALATGALAFPAAGNAT--ELEKRQTPNSEGMHGGYYSWSDGGAQAT 57
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MVSFKAL---LLGAAGALAFP-F-NVTQMNELVARAGTPTSGTNNGYFYSFTWDGGGTVN 56

QY 58 YTNLEGGTYEISWGDGNTLVGKGWNPGLNARAIHFEQVYQPNNGNSYLAAYGWTNPLVE 117
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 57 YQNGAGGSYSVQWQNCNMFVGKGWNPGA-ARTINFGSFTSPQNGYLAAYGWTQNPPLVE 115

QY 118 YVIVENFGTYDPSSGATDLGTVCECDGSYRLGKTRVNAPSIDGTQTFDQYMSVRODKRT 177
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 116 YVIVESFGTYDPSSQASKFGTIOGDSTYTIKTRVNQPSIEGTSTFDQFMSVROQNHRS 175

QY 178 SGTVQTCGHPDAMARAGLVNNGDHYQIVATEGYFSSGYARITVA 222
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

Db 176 SGSVVAAHFNAWAQAGLKL-GSHNYQIVATEGYQSSGSSSITVS 219

RESULT 8
US-11-170-653-27

; Sequence 27, Application US/11170653
; Publication No. US20050271769A1

; GENERAL INFORMATION:

; APPLICANT: Danisco A/S

; APPLICANT: Sibbesen, Ole

; APPLICANT: Sorensen, Jens

; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

; FILE REFERENCE: 674509-2046

; CURRENT APPLICATION NUMBER: US/11/170,653

; CURRENT FILING DATE: 2005-06-23

; PRIOR APPLICATION NUMBER: US/10/237,386

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: PCT/IB01/00426

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: GB 0005585.5

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 27

; LENGTH: 227

; TYPE: PRT

; ORGANISM: H. insolens

; US-11-170-653-27

Query Match 55.7%; Score 689.5; DB 7; Length 227;
Best Local Similarity 55.8%; Pred. No. 5.2e-56;
Matches 126; Conservative 31; Mismatches 62; Indels 7; Gaps 3;

QY 1 MVGFTPVALLAALATGALA-----FPAGNATELEKQRTTPNSEGWHDGYYSWMSDGAQ 55

Db 1 MVSLKSVLLAATAVSSAIAAPDFVPRDNSTALQARQVTPNAEGWHNGYFYSWMSDGGQ 60

QY 56 ATYTNLEGTYEISWGDGGLVGGKGNPGLNARAIHFEQYQPNNGSYLAVYGTNRNPL 115

Db 61 VQYTNLEGSRQYRWNRNTGNFVGGKGNPG-TGRTINYGYPNPGNGYLAVYGTNRNPL 119

QY 116 VEYIVENFGTYDPSSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYMSVRQDK 175

Db 120 VEYVIESYGTYPGSAQYKGTFTDQYDIFVSTRYNQPSIDGTRTFQQYWSIRKNK 179

QY 176 RTSGTVQTCGCHFDAMARAGLNVNGDHYIQIVATEGYFSSGYARITV 221

Db 180 RVGGSVMQNHFNAAQOHGMPL-GQHYQVVAATEGYQSSGESDIYV 224

RESULT 9

US-11-170-653-35

; Sequence 35, Application US/11170653

; Publication No. US20050271769A1

; GENERAL INFORMATION:

; APPLICANT: Danisco A/S

; APPLICANT: Sibbesen, Ole

; APPLICANT: Sorensen, Jens

; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

; FILE REFERENCE: 674509-2046

; CURRENT APPLICATION NUMBER: US/11/170,653

; CURRENT FILING DATE: 2005-06-23

; PRIOR APPLICATION NUMBER: US/10/237,386

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: PCT/IB01/00426

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: GB 0005585.5

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 35

; LENGTH: 241

; TYPE: PRT

; ORGANISM: C. gracile

; US-11-170-653-35

Query Match 55.7%; Score 689; DB 7; Length 241;
Best Local Similarity 59.5%; Pred. No. 6.1e-56;
Matches 132; Conservative 31; Mismatches 55; Indels 4; Gaps 4;

QY 1 MVGFTPVALLAALATGALAFPAAGNATELEKQRTTPNSE-GWHDGYYSWMSDGAQATYT 59

Db 1 MVNFSLLFLAASAAVVAAP-GELPGMHKQRTLTSSQGTNNGYYSFTWDGQGNVQYT 59

QY 60 NLEGTYEISWGDGGLVGGKGNPGLNARAIHFEQYQPNNGSYLAVYGTNRNPLVEY 119

Db 60 NEAGQYSVTWSGNGNWGGKGNPG-SARTINYTANYNPNGNSYLAVYGTNRNPLIEY 118

QY 120 IVENFGTYDPSSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYMSVRQDKRTSG 179

Db 119 VVENFGTYNPSTGATRLGSLTDDGSCYDIYRTQRVNQPSIEGTSTFYQFWSVRQDKRTSG 178

QY 180 TVQTCGCHFDAMARAGLNVNGDHYIQIVATEGYFSSGYARITV 221

Db 179 SVNMAAHFNMAAAGLQL-GTHDYQIVATEGYSSGSAITVNV 219

RESULT 10

US-11-170-653-31

; Sequence 31, Application US/11170653

; Publication No. US20050271769A1

; GENERAL INFORMATION:

; APPLICANT: Danisco A/S

; APPLICANT: Sibbesen, Ole

; APPLICANT: Sorensen, Jens

; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

; FILE REFERENCE: 674509-2046

; CURRENT APPLICATION NUMBER: US/11/170,653

; CURRENT FILING DATE: 2005-06-23

; PRIOR APPLICATION NUMBER: US/10/237,386

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: PCT/IB01/00426

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: GB 0005585.5

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 31

; LENGTH: 223

; TYPE: PRT

; ORGANISM: T. reesei

; US-11-170-653-31

Query Match 55.3%; Score 684.5; DB 7; Length 223;
Best Local Similarity 57.1%; Pred. No. 1.4e-55;
Matches 128; Conservative 32; Mismatches 61; Indels 3; Gaps 2;

QY 1 MVGFTPVALLAALATGALAPAG--NATELEKQRTTPNSEGWHDGYYSWMSDGAQATY 58

Db 1 MVSFTSLAGVAAISGVLAAPAEVSAVEKRQTIQPGTYNNGYFYSYWNDEHGGVTV 60

QY 59 TNLEGTYEISWGDGGLVGGKGNPGLNARAIHFEQYQPNNGSYLAVYGTNRNPLVEY 118

Db 61 TNGPGGQFSVWMSNSGNFVGGKGNPGLNARAIHFEQYQPNNGSYLAVYGTNRNPLIEY 120

QY 119 YIVENFGTYDPSSGATDLGTVECDSIYRLGKTRVNAPSIDGTQTFDQYMSVRQDKRTS 178

Db 121 YIVENFGTYNPSTGATKLGVTSDGSVYDIYRTQRVNQPSIIGTATFYQYMSVRNRHRS 180

QY 179 GTVQTCGCHFDAMARAGLNVNGDHYIQIVATEGYFSSGYARITVA 222

Db 181 GSVNTANHFNAWAQOGLTL-GTMDYQIVAVEGYFSSGSASITVS 223

RESULT 11

US-11-170-653-30
; Sequence 30, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-11-170-653-30

Query Match 54.2%; Score 671.5; DB 7; Length 223;
Best Local Similarity 56.2%; Pred. No. 2.2e-54;
Matches 126; Conservative 32; Mismatches 63; Indels 3; Gaps 2;

Qy 1 MVGFTPVALLAALATGALAPPAGNA--TELEKROTPNSEGWHGYYYSWMSDGAQATY 58
Db 1 MVSFTSLAGVAIAISGVLAAPAAEVEVAVEKQTIQPTGYNNGYFHSYWNDSHGCVTY 60
Qy 59 TNLEGGTYEISWGDGNLVGKGWNPGLNARAIHFEQVYQPNNGSYLAVYGWTRNPLVEY 118
Db 61 TNGPGGQFSVWNSNGNFGVGKGWQGTKNKVINFGSYNPNNGNSYLSVYGWNRNPLIEY 120
Qy 119 YIVENFGTYDPSSGATDLGTEVCDGSIYRLGKTRVNAPSIDGTQTFDQYMSVRQDKRTS 178
Db 121 YIVENFGTYNPSGTATKLGVTSDGSVYDIYRTQVNPQPSIIIGTATFYQYMSVRNRHRS 180
Qy 179 GTVQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVA 222
Db 181 GSVNTANHFNAWAQOGLTL-GTMDYQIVAVEGYFSSGSASITVS 223

RESULT 12

US-11-170-653-32
; Sequence 32, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 222
; TYPE: PRT
; ORGANISM: T. reesei
US-11-170-653-32

Query Match 53.9%; Score 667; DB 7; Length 222;
Best Local Similarity 57.1%; Pred. No. 5.7e-54;
Matches 128; Conservative 32; Mismatches 60; Indels 4; Gaps 3;

Qy 1 MVGFTPVALLAALATGALAPPAG--NATELEKROTPNSEGWHGYYYSWMSDGAQATY 58
Db 1 MVSFTSL-LAASPPSRASCRRPAEVSVAVEKQTIQPTGYNNGYFYSYWNDSHGCVTY 59
Qy 59 TNLEGGTYEISWGDGNLVGKGWNPGLNARAIHFEQVYQPNNGSYLAVYGWTRNPLVEY 118
Db 60 TNGPGGQFSVWNSNGNFGVGKGWQGTKNKVINFGSYNPNNGNSYLSVYGWNRNPLIEY 119
Qy 119 YIVENFGTYDPSSGATDLGTEVCDGSIYRLGKTRVNAPSIDGTQTFDQYMSVRQDKRTS 178
Db 120 YIVENFGTYNPSGTATKLGVTSDGSVYDIYRTQVNPQPSIIIGTATFYQYMSVRNRHRS 179
Qy 179 GTVQTGCHFDAMARAGLNVNGDHYQIVATEGYFSSGYARITVA 222
Db 180 GSVNTANHFNAWAQOGLTL-GTMDYQIVAVEGYFSSGSASITVS 222

RESULT 13

US-11-170-653-23
; Sequence 23, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 201
; TYPE: PRT
; ORGANISM: S. commune
US-11-170-653-23

Query Match 53.6%; Score 663; DB 7; Length 201;
Best Local Similarity 61.3%; Pred. No. 1.2e-53;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

Qy 34 TPNSGWHGYYYSWMSDGAQATYTNLEGGTYEISW-GDGNLVGKGWNPGLNARAIH 92
Db 5 TPSSGTGDDGYYYSWMTDAGDATYQNNGGSYTLTWSGNNGLVGGKWNPGAASRSIS 64
Qy 93 FEGVYQPNNGNSYLAVYGWTRNPLVEYIYVENFGTYDPSSGATDLGTEVCDGSIYRLGKTT 152
Db 65 YSGTYQPNNGNSYLSVYGWTRSSLIBIYIVESYSDPSSAASHKGSYTCNGATYDILSTW 124
Qy 153 RVNAPSIDGTQTFDQYMSVRQDKRT-----SGTVQTGCHFDAMARAGLNVNGDHYQIVA 207
Db 125 RVNAPSIDGTQTFEQFWSVNRNPKAPGSGISGTVDVQCHFDAMWKGIGMNLGSEHNYQIVA 184

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 10, 2006, 14:49:18 ; Search time 130.568 Seconds
(without alignments)
652.836 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225
Perfect score: 1088
Sequence: 1 QTTPNSEGMHDGYRYSWSD.....VATEGYFSSGYARITVADVG 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1088	100.0	194	5	AAE18456	Aae18456 Thermomyc
2	1088	100.0	225	2	AAW01112	Aaw01112 Xylanasae.
3	1088	100.0	225	2	AAW05187	Aaw05187 Endo-1,4-
4	1088	100.0	225	7	ABR63119	Abbr63119 Thermomyc
5	1088	100.0	225	9	AEB00305	Aeb00305 Xylanase
6	1083	99.5	194	3	AAAB48543	Aab48543 Thermomyc
7	1083	99.5	194	5	AAO18649	Aao18649 T. lanugin
8	1083	99.5	194	8	ADI66751	Adi66751 T. lanugi
9	965	88.7	194	3	AAAB48542	Aab48542 Paecilomy
10	965	88.7	194	5	AAO18648	Aao18648 P. varioti
11	965	88.7	194	8	ADI66750	Adi66750 P. varioti
12	742	68.2	221	3	AAAB48548	Aab48548 Cochliobo
13	742	68.2	221	5	AAO18654	Aao18654 C. carbonu
14	742	68.2	221	8	ADI66756	Adi66756 C. carbon
15	663	60.9	197	2	AAW60736	Aaw60736 Xylanase
16	663	60.9	197	3	AAAY98068	Aay98068 S. commun
17	663	60.9	197	3	AAAB48537	Aab48537 Schizophy
18	663	60.9	197	5	AAO18643	Aao18643 S. commune
19	663	60.9	197	5	AAE18445	Aae18445 Schizophy
20	663	60.9	197	8	ADI66745	Adi66745 S. commun
21	647.5	59.5	190	7	AAO30298	Aao30298 Trichoder
22	647.5	59.5	190	7	AAO30297	Aao30297 Trichoder
23	646.5	59.4	190	5	AAE18492	Aae18492 Trichophi
24	646.5	59.4	190	5	AEB47005	Aeb47005 Thermophi

25	646	59.4	227	9	AEB00301	Aeb00301 Xylanase
26	645	59.3	227	2	AAR75421	Aar75421 Humicola
27	645	59.3	227	2	AAR78231	Aar78231 Humicola
28	644.5	59.2	190	5	AAE18496	Aae18496 Trichoder
29	644.5	59.2	190	5	AAE18494	Aae18494 Trichoder
30	644.5	59.2	190	5	AEB47006	Aeb47006 Thermophi
31	643.5	59.1	190	7	AAO30285	Aao30285 Trichoder
32	643.5	59.1	190	7	AAO30284	Aao30284 Trichoder
33	643.5	59.1	190	7	AAO30286	Aao30286 Trichoder
34	643.5	59.1	190	7	AAO30283	Aao30283 Trichoder
35	643.5	59.1	190	7	AAO30293	Aao30293 Trichoder
36	643.5	59.1	190	7	AAO30294	Aao30294 Trichoder
37	641	58.9	234	6	ABB80186	Abb80186 A. fumiga
38	640.5	58.9	190	5	AEB47004	Aeb47004 Thermophi
39	640.5	58.9	190	5	AEB47001	Aeb47001 Thermophi
40	640.5	58.9	190	5	AAO30304	Aao30304 Trichoder
41	639.5	58.8	190	5	AAE18493	Aae18493 Trichoder
42	639.5	58.8	190	5	AAE18495	Aae18495 Trichoder
43	639.5	58.8	190	5	AEB47002	Aeb47002 Thermophi
44	639.5	58.8	190	7	AAO30307	Aao30307 Trichoder
45	639.5	58.8	190	7	AAO30306	Aao30306 Trichoder

ALIGNMENTS

RESULT 1
AAE18456
ID AAE18456 standard; protein; 194 AA.
XX
AC AAE18456;
XX
DT 16-MAY-2002 (first entry)
XX
DE Thermomyces lanuginosus xylanase, Xyn.
XX
KW Modified xylanase; thermostability; alkalophilicity; industrial process;
KW pulp manufacture; poultry; swine feed; enzyme; Xyn.
XX
OS Thermomyces lanuginosus.
XX
PN WO200192487-A2.
XX
PD 06-DEC-2001.
XX
PF 31-MAY-2001; 2001WO-CA000769.
XX
PR 31-MAY-2000; 2000US-0213803P.
XX
PA (CANA) NAT RES COUNCIL CANADA.
XX
PI Sung WL;
XX
DR WPI; 2002-171435/22.
XX
PT Modified xylanase exhibiting increased thermostability and
PT alkalophilicity useful for industrial processing e.g. for pulp
PT manufacturing.
XX
PS Disclosure; Page 83-84; 109pp; English.
XX
CC The present invention relates to a modified xylanase exhibiting increased
CC thermostability and alkalophilicity. Modified xylanase is useful in
CC industrial process such as pulp manufacturing. Modified xylanase is also
CC useful for bleaching of pulp, processing of precision devices and
CC improving digestibility of poultry and swine feed. Modified xylanase has
CC improved performance at conditions of high temperature and pH and
CC exhibits improved thermostability and/or alkalophilicity in comparison to
CC corresponding native xylanase. The present sequence is Thermomyces
CC lanuginosus xylanase, Xyn
XX
SQ Sequence 194 AA;

	Query Match	100.0%;	Score 1088;	DB 5;	Length 194;	
	Best Local Similarity	100.0%;	Pred. No. 1.8e-98;			
	Matches 194;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1 QTPNSEGWHDDGYYSWSWSDGAQATYTNLEGTYEISWGDCGNLVGKGWNPGLNARAI					60
Dd	1 QTTPNSEGWHDDGYYSWSWSDGAQATYTNLEGTYEISWGDCGNLVGKGWNPGLNARAI					60
Qy	61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTECDGSYYRLGKT					120
Dd	61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTECDGSYYRLGKT					120
Qy	121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCCHFDAMARAAGLNVNGDHYYYQIVATEGY					180
Dd	121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCCHFDAMARAAGLNVNGDHYYYQIVATEGY					180
Qy	181 FSSGYARITVADVG 194					
Dd	181 FSSGYARITVADVG 194					

RESULT 2
 AAW01112
 ID AAW01112 standard; protein; 225 AA.
 XX
 AC AAW01112;
 XX
 DT 21-MAY-1997 (first entry)
 XX
 DE Xylanase.
 XX
 KM Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermoascus;
 KM Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia;
 KM Byssoschlamus; Paecilomyces; animal feed additive; in-vivo breakdown;
 KM plant cell wall; growth rate; feed conversion.
 XX
 OS Thermomyces lanuginosus.
 XX
 PN WO9623062-A1.
 XX
 PD 01-AUG-1996.
 XX
 PF 26-JAN-1996; 96WO-DK000046.
 XX
 PR 26-JAN-1995; 95DK-00000094.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Hansen PK, Wagner P, Muelbertz A, Knap IH;
 XX
 DR WPI; 1996-454790/45.
 DR N-PSDB; AAT40742.
 XX
 PT Fungal xylanase preps. for use as animal feed additives - and DNA
 PT construct for producing recombinant Thermomyces xylanase.
 XX
 PS Claim 5; Page 45-46; 69pp; English.
 XX
 This sequence represents the xylanase from Thermomyces lanuginosus strain
 DSM 4109. This xylanase, and xylanases derived from Humicola,
 Thermoascus, Chaetomium, Mucor, Talaromyces, Malbranchea, Myceliophthora,
 Thielavia, Byssoschlamus or Paecilomyces strains can be used in the
 monocomponent xylanase preparations of the invention. The xylanase
 preparations and the recombinant Thermomyces xylanase are useful as
 animal feed additives, which promote in-vivo breakdown of plant cell wall
 material and thus improve digestibility, growth rate and/or feed
 conversion
 Sequence 225 AA;

Query Match	100.0%;	Score 1088;	DB 2;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 2.2e-98;		
Matches 194;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	I	QTTPNSEGMHWDGYIYSWMSDGAQATYTNNLEGGTYEISWGDDGNLVGKGMNPGLNARAI	60
Dd	32	QTTPNSEGMHWDGYIYSWMSDGAQATYTNNLEGGTYEISWGDDGNLVGKGMNPGLNARAI	91
QY	61	HFEGVYQPNGNSYLAVYGWTBNPLVEYYIVENFGTYDPSSGATDLGIVECDGSIRLGKT	120
Dd	92	HFEGVYQPNGNSYLAVYGWTBNPLVEYYIVENFGTYDPSSGATDLGIVECDGSIRLGKT	151
QY	121	TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFADAWARAGLNVNGDHYYQIVATEGY	180
Dd	152	TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFADAWARAGLNVNGDHYYQIVATEGY	211
QY	181	FSSGYARITVADV G 194	
Dd	212	FSSGYARITVADV G 225	

XX	RESULT 3
XX	AAW05187
ID	AAW05187 standard; protein; 225 AA.
XX	
AC	AAW05187;
XX	
DT	16-OCT-2003 (revised)
DT	22-FEB-1997 (first entry)
XX	
DE	Endo-1,4-beta-D-xylanase.
XX	
KM	Endo-1,4-beta-D-xylanase; xylanase; Thermomyces lanuginosus;
KW	Humicola lanuginosa; bread; enzyme; Saccharomyces cerevisiae; yeast;
KW	flour; baking; dough.
XX	
OS	Thermomyces lanuginosus; (strain DSM 4109).
XX	
PN	WO9632472-A1.
PD	
PD	17-OCT-1996.
XX	
PF	11-APR-1996; 96WO-DK000171.
XX	
PR	11-APR-1995; 95DK-00000435.
XX	
PA	(NOVO) NOVO-NORDISK AS.
XX	
PI	Jorgensen OB, Si JQ, Jakobsen TS;
XX	
DR	WPI; 1996-477123/47.
DR	N-PSDB; AAT43010.
XX	
PT	Bread improving additive contg. xylanase from Thermomyces - and opt.
PT	alpha-amylase, increases volume, improves anti-staling properties etc.
XX	
PS	Claim 4; Page 31-32; 41pp; English.
XX	
CC	The sequence represents an endo-1,4-beta-D-xylanase from Thermomyces
CC	lanuginosus (Humicola lanuginosa), which may be used as a bread-
CC	improving additive. The enzyme may be expressed recombinantly from a
CC	plasmid pYES2.0 vector in Saccharomyces cerevisiae DSM 10133 (claimed),
CC	and may be added to flour at 5-5,000 (preferably 20-2,000) FXU/kg flour,
CC	optionally along with other enzymes (amylase, maltogenase, lipase,
CC	cellulase, hemicellulase, pentosanase, glucose-oxidase, laccase,
CC	protease and/or peroxidase). The enzyme combines particularly well with
CC	amylolytic enzymes, and may be used to improve baking properties of flour
CC	and/or dough, by increasing volume and improving texture, flavour, crumb
CC	softness, freshness and anti-staling properties, while improving dough
CC	machinability and stability. (Updated on 16-OCT-2003 to standardise OS
CC	field)
XX	
SQ	Sequence 225 AA;

Query Match	100.0%;	Score 1088;	DB 2;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 2.2e-98;		

	Matches	194;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	QTTPNSEGMH	DGYYYSWMSDGAOATYTNLGGTYEISWGDSGNLVGKGWNPGLNARAI	60						
Db	32	QTTPNSEGMH	DGYRYSWMSDGAOATYTNLGGTYEISWGDSGNLVGKGWNPGLNARAI	91						
QY	61	HFEGVYQPNGNSYLAVYGWTBPLVEYIIVENFGTYDPSSGATDLGTVECDGSIRL	GKT	120						
Db	92	HFEGVYQPNGNSYLAVYGWTBPLVEYIIVENFGTYDPSSGATDLGTVECDGSIRL	GKT	151						
QY	121	TRVNAPSIDGTQTFPDQYWSVRDKRTSGTVQTGCHFDAMARAGLNVNGDHYIQIVATE	GCY	180						
Db	152	TRVNAPSIDGTQTFPDQYWSVRDKRTSGTVQTGCHFDAMARAGLNVNGDHYIQIVATE	GCY	211						
QY	181	FSSGYARITVADVG	194							
Db	212	FSSGYARITVADVG	225							

```

RESULT 4
ABR63119
ID ABR63119 standard; protein; 225 AA.
XX
XX ABR63119;
XX
XX 18-DEC-2003 (first entry)
XX
XX Thermomyces lanuginosus xylanase.
DE
XX Xylanase; thermostable; enzyme; feed additive.
XX
XX Thermomyces lanuginosus.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein /label= Signal_peptide
FT 31..225
FT /label= Mature_protein
PN WO2003062409-A2.
XX
XX 31-JUL-2003.
PD
XX
XX 23-JAN-2003; 2003WO-DK000039.
PF
PR 25-JAN-2002; 2002DK-00000130.
XX
XX (HOFF ) ROCHE VITAMINS AG.
XX
XX PI Wu W, Pettersson D, Fuglsang CC;
XX
XX WPI; 2003-731382/69.
XX
XX Composition useful as an animal feed additive comprises at least two
PT thermostable enzymes selected from endoglucanase, xylanase, phytase,
PT protease, galactanase, mannanase, dextranase and alpha-galactosidase.
XX
XX Disclosure; Page 60-61; Opp; English.
XX
XX The present sequence is the protein sequence of a thermostable xylanase
CC of Thermomyces lanuginosus. The xylanase has a melting temperature (Tm)
CC of 75.0 degrees C at pH 7.0. It is preferred for use in a claimed
CC composition of the invention, which comprises at least 2 thermostable
CC enzymes selected from an endoglucanase, xylanase, phytase, protease,
CC galactanase, mannanase, dextranase and alpha-galactosidase. The
CC composition is useful for improving the nutritional value of animal
CC feeds, especially those containing soya, wheat, barley, oats and/or rye
XX
XX Sequence 225 AA;

```

QY	1 QTTPNSEGMHDIYYYSWMSDGAQTATYNLEGGTYEISWGDDGNLVGKGKWNPLNARAI 60
Db	32 QTTPNSEGMHDGIYYYSWMSDGAQTATYNLEGGTYEISWGDDGNLVGKGKWNPLNARAI 91
QY	61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIYENFGTYPDSSGATDLGVECDGSIYRLGKT 120
Db	92 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIYENFGTYPDSSGATDLGVECDGSIYRLGKT 151
QY	121 TRVNAPSIDGTQTFEDQWSVRQDKRTSGTVOTGCHFDAMARAAGLNANGDHYYQIVATEGY 180
Db	152 TRVNAPSIDGTQTFEDQWSVRQDKRTSGTVOTGCHFDAMARAAGLNANGDHYYQIVATEGY 211
QY	181 FSSGYARITVADYC 194
Db	212 FSSGYARITVADYC 225

```

RESULT 5
AEB00305
ID AEB00305 standard; protein; 225 AA.
XX
AC AEB00305;
XX
DT 08-SEP-2005 (first entry)
XX
DE xylanase SEQ ID NO:15.
XX
KM enzyme; xylanase; feedstuff; alcohol; fermentation; brewing; filtration.
XX
OS Thermomyces lanuginosus.
XX
PN WO2005059084-A1.
XX
PD 30-JUN-2005.
XX
PF 17-DEC-2004; 2004WO-DK000880.
XX
PR 19-DEC-2003; 2003DK-00001895.
XX
PA (NOVO ) NOVOZYMES AS.
XX
PI Festeresen RM, Viksoe-Nielsen A, Joergensen CT, Christensen LLH;
XX
DR WPI; 2005-458778/46.
XX
PT Preparation of a mash (having enhanced filterability and/or improved
PT extract yield after filtration) comprises preparing a mash in the
PT presence of enzyme activities comprising xylanase of GH family 10 and
PT filtering to obtain wort.
XX
XX
PS Disclosure; SEQ ID NO 15; 68pp; English.
XX
XX
CC The invention relates to a process for preparing a mash (A) (having
CC enhanced filterability and/or improved extract yield after filtration)
CC which comprises preparing a mash in the presence of enzyme activities
CC (comprising a xylanase of GH family 10 at at least 15% w/w of the total
CC xylanase and endoglucanase enzyme protein) and filtering (A) to obtain a
CC wort. Also described is a composition is useful for reducing the
CC viscosity of an aqueous solution comprising a starch hydrolysate, which
CC is a mash for beer making or a feed composition. The process is useful
CC for the production of an alcoholic beverage, such as beer or whiskey and
CC the composition is useful in the mashing and filtration step in brewing
CC process. The present sequence represents a xylanase used in the mashing
CC process of the invention.
XX
SQ Sequence 225 AA;
XX
Query Match 100.0%; Score 1088; DB 9; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.2e-98;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 QTPNSEGWHDDGYRYSWSDGGAQATYTNLEGTYEISWGDGGLVGGKGMNPGLNARAI 60

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Db 32 QTPNSEGWHHDGYYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAI 91
Qy 61 HFEGYQPNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 120
Db 92 HFEGYQPNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 151
Qy 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYIQIVATEGY 180
Db 152 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYIQIVATEGY 211
Qy 181 FSSGYARITVADV 194
Db 212 FSSGYARITVADV 225

RESULT 6

AAB48543
ID AAB48543 standard; protein; 194 AA.
XX AAB48543;
AC
XX
DT 05-MAR-2001 (first entry)
XX
DE Thermomyces lanuginosus xylanase.
XX
KW Bacterial; Bacillus circulans; xylanase; xylanase activity; XA; bleaching agent.
XX
OS Thermomyces lanuginosus.
XX
PN WO200068396-A2.
XX
PD 16-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US013172.
XX
PR 12-MAY-1999; 99US-0133714P.
XX
PA (XENC-) XENCOR INC.
XX
PI Bentzien JM;
XX
DR WPI; 2000-679800/66.
XX
PT Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
PS Disclosure; Fig 16L; 114pp; English.
XX
CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 194 AA;

Query Match 99.5%; Score 1083; DB 3; Length 194;
Best Local Similarity 100.0%; Pred. No. 5.5e-98;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTPNSEGWHHDGYYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAIH 61
Db 2 TTPNSEGWHHDGYYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAIH 61
Qy 62 FEGVYQPNNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 121
Db 62 FEGVYQPNNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 121

Qy 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYIQIVATEGY 181
Db 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYIQIVATEGY 181
Qy 182 SSGYARITVADV 194
Db 182 SSGYARITVADV 194

RESULT 7

AAO18649
ID AAO18649 standard; protein; 194 AA.
XX AAO18649;
AC
XX
DT 24-OCT-2002 (first entry)
XX
DE T lanuginosus xylanase.
XX
KW Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching; liquid clarification; coffee extraction; plant oil extraction; starch extraction; food thickener; animal food additive; mutant; mutein.
XX
OS Thermomyces lanuginosus.
XX
PN WO200238746-A2.
XX
PD 16-MAY-2002.
XX
PF 09-NOV-2001; 2001WO-US048018.
XX
PR 10-NOV-2000; 2000US-00710050.
XX
PA (XENC-) XENCOR INC.
XX
PI Bentzien J, Dahiyat B;
XX
DR WPI; 2002-608200/65.
XX
PT Novel xylanase activity protein, useful in bleaching process of pulp and in food and animal feed industry, has enhanced thermostability and alkalophilicity.
XX
PS Disclosure; Fig 16L; 121pp; English.
XX
CC The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
XX
SQ Sequence 194 AA;

Query Match 99.5%; Score 1083; DB 5; Length 194;
Best Local Similarity 100.0%; Pred. No. 5.5e-98;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTPNSEGWHHDGYYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAIH 61
Db 2 TTPNSEGWHHDGYYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAIH 61
Qy 62 FEGVYQPNNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 121
Db 62 FEGVYQPNNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 121

Db 62 FEGVYQPNGNSYLA VYGWTRNPLVEYIIVENFGTYDPSSGATDLGTV ECDGSIYRLGKT 121
Qy 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVGTGCHFDAMARAGLNVNGDHYQIVATEGYF 181
Db 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVGTGCHFDAMARAGLNVNGDHYQIVATEGYF 181
Qy 182 SSGYARITVADVG 194
Db 182 SSGYARITVADVG 194

RESULT 8

AD166751
ID AD166751 standard; protein; 194 AA.

XX AC AD166751;

DT 22-APR-2004 (first entry)

DE T. lanuginosus xylanase.

KW Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;

KW paper industry; food; animal feed; thermostability; alkalophillic;
KW hot alkali treatment.

XX OS Thermomyces lanuginosus.

XX PN US6682923-B1.

XX PD 27-JAN-2004.

PF 12-MAY-2000; 2000US-00570856.

XX PR 12-MAY-1999; 99US-0133714P.

PR 07-JUN-1999; 99US-0138156P.

XX PA (XENC-) XENCOR.

XX PI Bentzien J, Dahlyat BI;

DR WPI; 2004-118575/12.

XX PT New mutant xylanase (XA) protein comprising at least four amino acid
PT substitutions as compared to Bacillus circulans xylanase, useful for
PT bleaching (paper) pulp, and in the food and animal feed industries.

XX PS Disclosure; SEQ ID NO 24; 84pp; English.

XX CC The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
CC xylanase from Bacillus circulans) protein appearing as AD166730. Also
CC included is a bleaching agent comprising the XA protein. The non-
CC naturally occurring XA protein comprises at least four amino acid
CC substitutions as compared to Bacillus circulans xylanase AD166728. The
CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
CC useful for bleaching pulp in the paper and related industries, but is
CC also useful in the food and animal feed industries. The new protein is
CC active at higher pH and temperature ranges than naturally occurring
CC xylanases, simplifying incorporation of the xylanase treatment step into
CC pulp processing, especially where the enzyme is added after hot alkali
CC treatment. The present sequence is a xylanase from another species

XX SQ Sequence 194 AA;

Query Match 99.5%; Score 1083; DB 8; Length 194;

Best Local Similarity 100.0%; Pred. No. 5.5e-98;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTPNSEGWHHDGYYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGGKGNPGLNARAIH 61
Db 2 TTPNSEGWHHDGYYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGGKGNPGLNARAIH 61

Qy 62 FEGVYQPNGNSYLA VYGWTRNPLVEYIIVENFGTYDPSSGATDLGTV ECDGSIYRLGKT 121
Db 62 FEGVYQPNGNSYLA VYGWTRNPLVEYIIVENFGTYDPSSGATDLGTV ECDGSIYRLGKT 121
Qy 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVGTGCHFDAMARAGLNVNGDHYQIVATEGYF 181
Db 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVGTGCHFDAMARAGLNVNGDHYQIVATEGYF 181
Qy 182 SSGYARITVADVG 194
Db 182 SSGYARITVADVG 194

RESULT 9

AAB48542
ID AAB48542 standard; protein; 194 AA.

XX AC AAB48542;

DT 05-MAR-2001 (first entry)

DE Paecilomyces variotii xylanase.

KW Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
KW bleaching agent.

XX OS Paecilomyces variotii.

XX PN WO200068396-A2.

XX PD 16-NOV-2000.

PF 12-MAY-2000; 2000WO-US013172.

XX PR 12-MAY-1999; 99US-0133714P.

XX PA (XENC-) XENCOR INC.

XX PI Bentzien JM;

DR WPI; 2000-679800/66.

XX PT Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.

XX PS Disclosure; Fig 16K; 114pp; English.

XX CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp

XX SQ Sequence 194 AA;

Query Match 88.7%; Score 965; DB 3; Length 194;

Best Local Similarity 87.6%; Pred. No. 2.2e-86;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 2 TTPNSEGWHHDGYYYSWSDGGAQATYTNLEGGTYEISWGDGNLVGGKGNPGLNARAIH 61

Db 2 TTPNSEGWHHDGYYYSWSDGGDSTYTNNSGGTYEITWNGGNLVGGKGNPGLNARAIH 61

Qy 62 FEGVYQPNGNSYLA VYGWTRNPLVEYIIVENFGTYDPSSGATDLGTV ECDGSIYRLGKT 121

Db 62 FEGVYQPNGTSYLSVYGWTRNPLVEYIIVENFGSSNPSSGSTDLGYSCDGSYTLGQST 121

Qy 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVGTGCHFDAMARAGLNVNGDHYQIVATEGYF 181

Db 122 RYNAPSIDGTQTFNQYWSVRQDKRSSGTVQTCGHPDAMASAGLNVGDPHYQIVATEGYF 181
Qy 182 SSGYARITVADVG 194
182 SSGYARITVADVG 194
Db 182 SSGYARITVADVG 194

RESULT 10
AA018648
ID AA018648 standard; protein; 194 AA.
XX
AC AA018648;
XX
DT 24-OCT-2002 (first entry)
XX
DE P variotii xylanase.

XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KW liquid clarification; coffee extraction; plant oil extraction;
KW starch extraction; food thickener; animal food additive; mutant; mutein.
XX
OS Paecilomyces variotii.

XX WO200238746-A2.
XX
XX 16-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US048018.
XX
XX 10-NOV-2000; 2000US-00710050.
XX
XX (XENC-) XENCOR INC.
XX
XX Bentzien J, Dahiyat B;
XX
XX WPI; 2002-608200/65.

PT Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX
XX Disclosure; Fig 16K; 121pp; English.

XX The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductor. The present sequence is a xylanase protein
CC described in the exemplification of the invention
XX
XX Sequence 194 AA;

Query Match 88.7%; Score 965; DB 5; Length 194;
Best Local Similarity 87.6%; Pred. No. 2.2e-86;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 2 TTPNSEGWHDGYYSWSDGGAQATYTNLEGGTYEISWGDGSLVGKGMNPGINARAIIH 61
Db 2 TTPNSEGWHDGYYSWSDGGDSTYTNNSGTYEITWNGGNLVGKGMNPGINARAIIH 61
Qy 62 FEGVYQPNNGNSYLAIVGWTNRNPLVEYYIVENFGTYDPSSGATDLGTVCECDGSIYRLGKTT 121
Db 62 FTGVYQPNNGTSYLSVYGWTRNPLVEYYIVENFGSSNPSGSGTDLGTVSCDGSYTLTGQST 121

Qy 122 RYNAPSIDGTQTFPDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVGDPHYQIVATEGYF 181
Db 122 RYNAPSIDGTQTFNQYWSVRQDKRSSGTVQTCGHPDAMASAGLNVGDPHYQIVATEGYF 181
Qy 182 SSGYARITVADVG 194
182 SSGYARITVADVG 194
Db 182 SSGYARITVADVG 194

RESULT 11
AD166750
ID AD166750 standard; protein; 194 AA.
XX
AC AD166750;
XX
DT 22-APR-2004 (first entry)
XX
DE P. variotii xylanase.

XX Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
KW paper industry; food; animal feed; thermostability; alkalophilic;
KW hot alkali treatment.

XX Paecilomyces variotii.
XX
XX US6682923-B1.
XX
XX 27-JAN-2004.
XX
XX 12-MAY-2000; 2000US-00570856.
XX
XX 12-MAY-1999; 99US-0133714P.
XX
XX 07-JUN-1999; 99US-0138156P.

XX (XENC-) XENCOR.

XX Bentzien J, Dahiyat BI;
XX
XX WPI; 2004-118575/12.

PT New mutant xylanase (XA) protein comprising at least four amino acid
PT substitutions as compared to Bacillus circulans xylanase, useful for
PT bleaching (paper) pulp, and in the food and animal feed industries.

XX Disclosure; SEQ ID NO 23; 84pp; English.

XX The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
CC xylanase from Bacillus circulans) protein appearing as AD166730. Also
CC included is a bleaching agent comprising the XA protein. The non-
CC naturally occurring XA protein comprises at least four amino acid
CC substitutions as compared to Bacillus circulans xylanase AD166728. The
CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
CC useful for bleaching pulp in the paper and related industries, but is
CC also useful in the food and animal feed industries. The new protein is
CC active at higher pH and temperature ranges than naturally occurring
CC xylanases, simplifying incorporation of the xylanase treatment step into
CC pulp processing, especially where the enzyme is added after hot alkali
CC treatment. The present sequence is a xylanase from another species
CC included for comparison.
XX
XX Sequence 194 AA;

Query Match 88.7%; Score 965; DB 8; Length 194;
Best Local Similarity 87.6%; Pred. No. 2.2e-86;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 2 TTPNSEGWHDGYYSWSDGGAQATYTNLEGGTYEISWGDGSLVGKGMNPGINARAIIH 61
Db 2 TTPNSEGWHDGYYSWSDGGDSTYTNNSGTYEITWNGGNLVGKGMNPGINARAIIH 61
Qy 62 FEGVYQPNNGNSYLAIVGWTNRNPLVEYYIVENFGTYDPSSGATDLGTVCECDGSIYRLGKTT 121

Db 62 FTGVYQNGTSTYLSVYGMTRNPLVEYIIVENFGSSNPNSSGSTDLGTVSCDGSITTLGQST 121
QY 122 RVNAPSIDGTQTEDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGYF 181
Db 122 RYNAPSIDGTQTENQYWSVRQDKRSSGTVQTGCHFDAMASAGLNTGDHYQIVATEGYF 181
QY 182 SSGYARITVADV 194
Db 182 SSGYARITVADV 194

RESULT 12

AAB48548
ID AAB48548 standard; protein; 221 AA.
XX AAB48548;
AC
XX
XX
DT 05-MAR-2001 (first entry)
XX
XX
DE Cochliobolus carbonum xylanase.
XX
XX
KW Bacterial; Bacillus circulans; xylanase; xylanase activity; XA; bleaching agent.
XX
OS Cochliobolus carbonum.
XX
PN WO200068396-A2.
XX
PD 16-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US013172.
XX
PR 12-MAY-1999; 99US-0133714P.
XX
PA (XENC-) XENCOR INC.
XX
PI Bentzien JM;
XX
DR WPI; 2000-679800/66.
XX
PT Non naturally occurring XA protein with enhanced thermostability,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX
PS Disclosure; Fig 16Q; 114pp; English.
XX
XX
CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermostability, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 221 AA;

Query Match 68.2%; Score 742; DB 3; Length 221;
Best Local Similarity 70.0%; Pred. No. 2.2e-64;
Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 1 QTPNSEGMHDGYYSWSDGGAQATYTNLEGGTYEISWGDGNTLVGKGWNPGLNARAI 60
Db 31 QNTPNGEETHNGCFWMSWSDGARATYTNAGGSYSVSWGSGNLVGGKWNPG-TARTI 89
QY 61 HFEGVYQPNNGNSYLA VYGWTRNPLVEYIIVENFGTYDPSSGATDLGTYECDGSYRLGKT 120
Db 90 TYSGTYYNNGNSYLA VYGWTRNPLVEYIIVENFGTYDPSSSQSNKGTITS DSSSYKIAQS 149
QY 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGY 180
Db 150 TRTNQPSIDGTTRTFQGYWSVRQDKRSSGSVNMKTHFDAMASKGMNL-CGHYYQIVATEGY 208

QY 181 FSSGYARITV 190
Db 209 FSTGNAQITV 218

RESULT 13

AAO18654
ID AAO18654 standard; protein; 221 AA.
XX AAO18654;
AC AAO18654;
XX
XX
DT 24-OCT-2002 (first entry)
XX
XX
DE C carbonum xylanase.
XX
KW Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KW liquid clarification; coffee extraction; plant oil extraction;
KW starch extraction; food thickener; animal food additive; mutant; mutein.
XX
OS Cochliobolus carbonum.
XX
PN WO200238746-A2.
XX
PD 16-MAY-2002.
XX
PF 09-NOV-2001; 2001WO-US048018.
XX
PR 10-NOV-2000; 2000US-00710050.
XX
PA (XENC-) XENCOR INC.
XX
PI Bentzien J, Dahiyat B;
XX
DR WPI; 2002-608200/65.
XX
XX
PT Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX
XX
PS Disclosure; Fig 16Q; 121pp; English.
XX
XX
CC The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermostability,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductor. The present sequence is a xylanase protein
CC described in the exemplification of the invention
XX
SQ Sequence 221 AA;

Query Match 68.2%; Score 742; DB 5; Length 221;
Best Local Similarity 70.0%; Pred. No. 2.2e-64;
Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 1 QTPNSEGMHDGYYSWSDGGAQATYTNLEGGTYEISWGDGNTLVGKGWNPGLNARAI 60
Db 31 QNTPNGEETHNGCFWMSWSDGARATYTNAGGSYSVSWGSGNLVGGKWNPG-TARTI 89
QY 61 HFEGVYQPNNGNSYLA VYGWTRNPLVEYIIVENFGTYDPSSGATDLGTYECDGSYRLGKT 120
Db 90 TYSGTYYNNGNSYLA VYGWTRNPLVEYIIVENFGTYDPSSSQSNKGTITS DSSSYKIAQS 149
QY 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYQIVATEGY 180

Db 150 TRTNQPSIDGTRTFQQYWSVRQNKRSSGSVNMKTHFDAMASKGMNL-GQHYVQIVATEGY 208
QY 181 FSSGYARITV 190
||:| |:||
Db 209 FSTGNAQITV 218

RESULT 14
ADI66756

ID ADI66756 standard; protein; 221 AA.

XX AC ADI66756;

DT 22-APR-2004 (first entry)

DE C. carbonum xylanase.

XX Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;

KW paper industry; food; animal feed; thermostability; alkaliphilic;

KW hot alkali treatment.

OS Cochliobolus carbonum.

XX PN US6682923-B1.

XX PD 27-JAN-2004.

XX PF 12-MAY-2000; 2000US-00570856.

XX PR 12-MAY-1999; 99US-0133714P.

XX PR 07-JUN-1999; 99US-0138156P.

XX PA (XENC-) XENCOR.

XX PI Bentzien J, Dahiyat BI;

XX DR WPI; 2004-118575/12.

XX PT New mutant xylanase (XA) protein comprising at least four amino acid

XX PT substitutions as compared to Bacillus circulans xylanase, useful for

XX PT bleaching (paper) pulp, and in the food and animal feed industries.

XX PS Disclosure; SEQ ID NO 29; 84pp; English.

XX CC The invention relates to a mutant xylanase activity (XA, endo-1,4-beta

XX CC xylanase from Bacillus circulans) protein appearing as ADI66730. Also

XX CC included is a bleaching agent comprising the XA protein. The non-

XX CC naturally occurring XA protein comprises at least four amino acid

XX CC substitutions as compared to Bacillus circulans xylanase ADI66728. The

XX CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,

XX CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,

XX CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is

XX CC useful for bleaching pulp in the paper and related industries, but is

XX CC also useful in the food and animal feed industries. The new protein is

XX CC active at higher pH and temperature ranges than naturally occurring

XX CC xylanases, simplifying incorporation of the xylanase treatment step into

XX CC pulp processing, especially where the enzyme is added after hot alkali

XX CC treatment. The present sequence is a xylanase from another species

XX CC included for comparison.

XX SQ Sequence 221 AA;

Query Match 68.2%; Score 742; DB 8; Length 221;

Best Local Similarity 70.0%; Pred. No. 2.2e-64;

Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 1 QTPNSEGMDGYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGWNPGLNARAI 60

Db 31 QNTPNSEGTDNGCFWSWMSDGAARATYTNAGAGGSYSVSWGSGNLVGGKGMNPG-TARTI 89

QY 61 HPEGVYQPNNGNSYLAIVGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDSIYRLGKT 120

Db 90 TYSGTYYNNGNSYLAIVGWTRNPLVEYYIVENFGTYDPSSQGNKGTVTSDGSSYKIAQS 149

QY 121 TRVNAPSIDGTQTFPDQYWSVRQDKRTSGTVQTCGHFDAMARAGLNVNGDHYVQIVATEGY 180
Db 150 TRTNQPSIDGTRTFQQYWSVRQNKRSSGSVNMKTHFDAMASKGMNL-GQHYVQIVATEGY 208
QY 181 FSSGYARITV 190
||:| |:||
Db 209 FSTGNAQITV 218

RESULT 15
AAW60736

ID AAW60736 standard; protein; 197 AA.

XX AC AAW60736;

DT 02-SEP-1998 (first entry)

DE Xylanase A of Schizophyllum commune.

XX Family 11 xylanase; improve; thermophilicity; alkalophilicity;

KW thermotolerance; bleach; wood pulp; processing; wheat; maize;

KW digestibility-improving animal feed additive; starch production; mutant.

XX OS Schizophyllum commune.

XX PN EP828002-A2.

XX PD 11-MAR-1998.

XX PF 05-SEP-1997; 97EP-00115412.

XX PR 09-SEP-1996; 96US-00709912.

XX PA (CANA) NAT RES COUNCIL CANADA.

XX PI Sung WL, Yaguchi M, Ishikawa K;

XX DR WPI; 1998-161100/15.

XX PT Modified xylanase enzymes - useful for improving wood pulp bleaching,

XX PT etc.

XX PS Disclosure; Page 40; 84pp; English.

XX CC AAW60728-44 represent family 11 xylanases. The specification describes a

XX CC method for modifying a Family 11 xylanase to improve its thermophilicity,

XX CC alkalophilicity and or thermotolerance. This method comprises

XX CC modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase

XX CC II or corresponding aligned amino acids of another Family 11 xylanase,

XX CC replacement of one or more amino acid sequences in the N-terminal region

XX CC with corresponding aligned sequences from another Family 11 xylanase to

XX CC form a chimeric xylanase and/or upstream extension of the N terminus by

XX CC addition of upto 10 amino acids. The modified xylanases are useful for

XX CC improving the bleachability of wood pulp by treatment at 55-75 degrees

XX CC celsius and pH 7.5-9.0 for 5-180 minutes. They might also be useful as

XX CC digestibility-improving animal feed additives. They might also be useful

XX CC in the processing of wheat or maize for starch production

XX SQ Sequence 197 AA;

Query Match 60.9%; Score 663; DB 2; Length 197;

Best Local Similarity 61.3%; Pred. No. 1.1e-56;

Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

QY 3 TPNSEGMDGYYSWMSDGAQATYTNLEGTYEISW-GDGNLVGKGWNPGLNARAIH 61

Db 3 TPNSTGTDGYYYSWWTGDAGDATYQNNGGSYTLTWSGNNGNLVGKGWNPGLAASRSIS 62

QY 62 FEGVYQPNNGNSYLAIVGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDSIYRLGKT 121

Db 63 YSGTYQPNNGNSYLAIVGWTRNPLVEYYIVESYGSYDPSAASHKGSVTCNGATYDILSTW 122

Oy	122	RVNAPSIDGTQT	FDQW	SVRQDKRT	-----	SGTVQ	TGCH	PDAM	ARAGL	NTVNG	DHYQ	IYA	176
Db	123	RVNAPSIDGTQT	FEQFWS	VRNPKAPG	SGIS	GTVDVQCH	PDAM	KGLG	MNTLG	SEHNYQ	IYA	182	
Oy	177	TEGYFSSGYAR	ITV	190									
Db	183	TEGYQSSGTAT	ITV	196									

Search completed: February 10, 2006, 14:54:12
Job time : 130.568 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 14:54:33 ; Search time 24.0764 Seconds
(without alignments)
775.285 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225

Perfect score: 1088

Sequence: 1 QTPNSEGWHDGYYSWSD.....VATEGYFSSGYARITVADV G 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	60.9	197	1 A44597	endo-1,4-beta-xy1a
2	656	60.3	219	2 S71472	endo-1,4-beta-xy1a
3	648	59.6	225	1 S57477	endo-1,4-beta-xy1a
4	646	59.4	227	2 S43919	endo-1,4-beta-xy1a
5	642.5	59.1	241	2 S71473	endo-1,4-beta-xy1a
6	636.5	58.5	190	1 A44593	endo-1,4-beta-xy1a
7	636.5	58.5	190	1 A44595	endo-1,4-beta-xy1a
8	635.5	58.4	222	2 S39154	endo-1,4-beta-xy1a
9	635.5	58.4	223	1 S39883	endo-1,4-beta-xy1a
10	634.5	58.3	190	1 A44594	endo-1,4-beta-xy1a
11	625	57.4	232	2 JC7577	endo-1,4-beta-xy1a
12	615	56.5	221	1 S57469	endo-1,4-beta-xy1a
13	571.5	52.5	333	1 JS0590	endo-1,4-beta-xy1a
14	569.5	52.3	335	2 TS0601	endo-1,4-beta-xy1a
15	555.5	51.1	221	2 JC7307	endo-1,4-beta-xy1a
16	544	50.0	241	2 T37005	endo-1,4-beta-xy1a
17	543.5	50.0	240	1 S47512	endo-1,4-beta-xy1a
18	529.5	48.7	240	1 JS0591	endo-1,4-beta-xy1a
19	522.5	48.0	661	1 S59633	endo-1,4-beta-xy1a
20	509	46.8	644	1 I40712	endo-1,4-beta-xy1a
21	503	46.2	210	2 C83762	endo-1,4-beta-xy1a
22	491	45.1	656	1 S59631	endo-1,4-beta-xy1a
23	470.5	43.2	213	1 S40569	endo-1,4-beta-xy1a
24	469.5	43.2	213	1 S48126	endo-1,4-beta-xy1a
25	468.5	43.1	213	1 S01734	endo-1,4-beta-xy1a
26	451.5	41.5	354	1 S51779	endo-1,4-beta-xy1a
27	426.5	39.2	511	1 JQ1935	endo-1,4-beta-xy1a
28	395	36.3	261	1 S12745	endo-1,4-beta-xy1a
29	393.5	36.2	228	1 WWSXP	endo-1,4-beta-xy1a

30	388	35.7	211	1 JC1198	endo-1,4-beta-xy1a
31	387	35.6	211	2 S49542	endo-1,4-beta-xy1a
32	385	35.4	211	1 S48229	endo-1,4-beta-xy1a
33	371	34.1	954	1 S20907	endo-1,4-beta-xy1a
34	369.5	34.0	789	2 S58235	endo-1,4-beta-xy1a
35	361	33.2	781	2 S51592	XyNB precursor - R
36	353.5	32.5	802	2 A36910	xy1anase, beta(1,3
37	352	32.4	229	2 S39155	xy1anase 2 - fungu
38	348.5	32.0	209	2 JC4909	endo-1,4-beta-xy1a
39	285.5	26.2	607	2 S49528	endoxy1anase - rum
40	280.5	25.8	607	2 S24754	endo-1,4-beta-xy1a
41	247.5	22.7	608	2 B53295	xy1anase (EC 3.2.1
42	236.5	21.7	266	1 S48865	endo-1,4-beta-xy1a
43	145	13.3	50	2 A61149	endo-1,4-beta-xy1a
44	115	10.6	2817	2 B97033	uncharacterized pr
45	113	10.4	40	2 PQ0202	endo-1,4-beta-xy1a

ALIGNMENTS

RESULT 1

A44597

endo-1,4-beta-xy1anase (EC 3.2.1.8) A - bracket fungus (Schizophyllum commune)

N:Alternate names: xy1anase A

C:Species: Schizophyllum commune

C>Date: 27-Jun-1994 #sequence revision 22-Nov-1996 #text_change 09-Jul-2004

C:Accession: A44597; S41411, A05147; S38973

R:Yaguchi, M.

submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593

A:Accession: A44597

A:Molecule type: protein

A:Residues: 1-197 <YAG>

A:Cross-references: UNIPROT:P35809; UNIPARC:UPI0000034D33

A:Experimental source: strain Delmar ATCC 38548

R:Bray, M.R.; Clarke, A.J.

Bur. J. Biochem. 219, 821-827, 1994

A:Title: Identification of a glutamate residue at the active site of xy1anase A from Sch

A:Reference number: S41411, MUID:94155888; PMID:7906649

A:Accession: S41411

A:Status: preliminary

A:Molecule type: protein

A:Residues: 83-123 <BRA>

A:Cross-references: UNIPARC:UPI0000172966

R:Paice, M.G.; Jurasek, L.; Carpenter, M.R.; Smillie, L.B.

Appl. Environ. Microbiol. 36, 802-808, 1978

A:Reference number: A05147; MUID:79102289; PMID:32833

A:Accession: A05147

A:Molecule type: protein

A:Residues: 1-27 <PAI>

A:Cross-references: UNIPARC:UPI0000172967

R:Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Campbell, R.; Yaguchi, M.; Jurasek, L.;

FEBS Lett. 334, 296-300, 1993

A:Title: Amino acid sequence and thermostability of xy1anase A from Schizophyllum commune

A:Reference number: S38973; MUID:94063044; PMID:8243636

A:Accession: S38973

A:Molecule type: protein

A:Residues: 1-197 <OKU>

A:Cross-references: UNIPARC:UPI0000034D33

A:Experimental source: ATCC 38548

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xy1ans

A:Pathway: xy1an degradation

C:Superfamily: endo-1,4-beta-xy1anase; endo-1,4-beta-xy1anase homology

C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F:12-197/Domain: endo-1,4-beta-xy1anase homology <XYL>

F:87,184/Active site: Glu #status predicted

F:111-160/Disulfide bonds: #status experimental

Query Match 60.9%; Score 663; DB 1; Length 197;

Best Local Similarity 61.3%; Pred. NO. 5e-47;

Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;

OY	3	T P N S E G M H D G Y I Y S W M S D G A O A T Y T N L E G G T Y E I S W - G D G G N L V G K G M N P G L N A R A I H	61
D b	3	T P S T G T D G G Y I Y S W M T D G A G D A T Y Q N N G C G S Y T L T W S G N N G N L V G K G M N P G A A S R S I S	62
OY	62	F E G V Y Q P N G N S Y L A V Y G W T R N P L V E Y Y I V E N F G T Y D P S S G A T D I G T V E C D G S I Y R L G K T T	121
D b	63	Y S G T Y Q P N G N S Y L S V Y G W T R R S L I E Y Y I V E S Y G S Y D P S S A A S H K S V T C N G A T Y D I L S T W	122
OY	122	R V N A P S I D G T Q F D Q Y W S V R Q D K R T -----S G T V Q T G C H F D A W A R A G L N V N G D H Y Y Q I V A	176
D b	123	R Y N A P S I D G T Q F E Q F W S V R N P K K A P G S T S G T V D V Q C H F D A W K G L G M N L G S E H N Y Q I V A	182
OY	177	T E G Y F S S G Y A R I T V	190
D b	183	T E G Y Q S S G T A I T V	196

RESULT 2
S71472
endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile
N/Alternate names: xylanase A
C/Species: Chaetomium gracile
C/Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
C/Accession: S71472; S78206
R/Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
Curr. Genet. 29, 73-80, 1995
A/Title: Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus
A/Reference number: S71472; MUID:96118924; PMID:8595661
A/Accession: S71472
A/Molecule type: DNA
A/Residues: 1-219 <YOS>
A/Cross-references: UNIPROT:Q12579; UNIPARC:UPI00000421A6; EMBL:D49850; NID:G1339857; PI
A/Accession: S78206
A/Molecule type: protein
A/Residues: 31-45;82-94;152-160 <YOH>
A/Cross-references: UNIPARC:UPI0000175A79; UNIPARC:UPI0000175A82; UNIPARC:UPI0000175A83
C/Genetics:
A/Introns: 81/2
C/Function:
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/1-30/Domain: signal sequence #status predicted <SIG>
F/31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F/42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
F/115,206/Active site: Glu #status predicted

	Query Match	60.3%;	Score 656;	DB 2;	Length 219;	
	Best Local Similarity	61.9%;	Pred. No. 2.1e-46;			
	Matches 117; Conservative	28;	Mismatches 42;	Indels 2;	Gaps 2;	
OY	3 TPNSEGWHDYYYYSWWSGGAQATYTNLGGTYEISWGEGNVLVGKGMNPGLARAIHF	62				
Dd	33 TPSTGTNTNGYFYFSFWTIDGGGTVNYQNAGAGSYSVQWNCGNFVGGKWMPGA-AARTINF	91				
OY	63 EGVYQPNGNSYLAVYGWRPLVEYYIVENFGTYDPSSGATDLGTECDGSIIYRLGKTTR	122				
Dd	92 SGTSPQGNGYLAIYGMTQLPVEYYIVESFPTYDSPSQSKFTIQDDGSTYTIAKTTR	151				
OY	123 VNAPSIDQTQFPDYWSVRQDKRTSGTVQTGCHPDAWARAGLNVNGDHYYQIVATEGYFS	182				
Dd	152 VNOPSIEGTSTFDQFWSVRQHRRSSGSVNVAAHFNAMAQAQIKLI-GSHNYQIVATEGYQS	210				
OY	183 SGYARITVA 191					
Dd	211 GSSSSITTVS 219					
RESULT 3	S57477					
N;Alternate names:	xylanase (EC 3.2.1.8) 1 precursor - Emericella nidulans xylanase 1					

C/Species: *Emericella nidulans*, *Aspergillus nidulans*
C/Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: S57477
R/Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A/Description: Expression in *Saccharomyces cerevisiae* of two xylanase encoding genes from
A/Reference number: S57469
A/Accession: S57477
A/Molecule type: DNA
A/Residues: 1-225 <PER>
A/Cross-references: UNIPROT:P55332; UNIPARC:UPI0000139073; EMBL:Z49892; NID:g870832; PDB:
C/Genetics:
A/Introns: 93/2
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>
F/48-225/Domain: endo-1,4-beta-xylanase homology <XYL>
F/121,212/Active site: Glu #status predicted

[illegible]

RESULT 4
S43919
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (*Humicola insolens*)
C/Species: *Humicola insolens*
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S43919
R;Dalboge, H.; Heldt-Hansen, H.P.
Mol. Gen. Genet. 243, 253-260, 1994
A/Title: A novel method for efficient expression cloning of fungal enzyme genes.
A/Reference number: S43919; MUID:94247364; PMID:8190078
A/Accession: S43919
A/Molecule type: mRNA
A/Residues: 1-227 <DAL>
A/Cross-references: UNIPROT:P55334; UNIPARC:UPI00000421A4; EMBL:X76047; NID:G505260; PDB:
C/Genetics:
A/Gene: XYL1
C/Function:
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>
F;48-225/Domain: endo-1,4-beta-xylanase homology <XYL>
F;112,123,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted
F;121,212/Active site: Glu #status predicted

Query Match	59.4%	Score 646;	DB 2;	Length 227;
Best Local Similarity	59.5%	Pred. No. 1.4e-45;		
Matches 113; Conservative	27;	Mismatches 48;	Indels 2;	Gaps 2;

Db 1 QTIGPGTGFNNNGYFYSYWMDGHGVTYTNPGGQFVSVMNSNGNFVGGKMGPGTKNKVI 60
QY 61 HFEGVYQPNNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSGATDLGTVECDGSYRLGKT 120
61 NFSGTYNPNNGNSYLSVYGWSRNP LI EYIVENFGTYNPSTGATKLG EVTSDGSVYDIYRT 120
QY 121 TRVNAPSIDGTQTDPQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYIQIVATEGY 180
Db 121 QRVNQPSTIEGTSTFYQYWSVRRTRRSSGSVNTANHFNAWAASHGLTL-GTMDYQIVAVEGY 179
QY 181 FSSGYARITVA 191
Db 180 FSSGSASITVS 190

RESULT 8
S39154
xylanase 1 - fungus (Trichoderma reesei)
C/Species: Trichoderma reesei
C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C/Accession: S39154
R/Toeroenen, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkinen, N.; Harkki, A.; Kubi
Biotechnology 10, 1461-1465, 1992
A/Title: The two major xylanases from trichoderma reesei: characterization of both enzym
A/Reference number: S39154
A/Accession: S39154
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-222 <TOE>
A/Cross-references: UNIPROT:P36217; UNIPARC:UPI00000421A9; EMBL:X69573; NID:g396563; PID
C/Genetics:
A/Gene: xyn1
A/Intons: 90/2
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
F/44-222/Domain: endo-1,4-beta-xylanase homology <XYL>

Query Match 58.4%; Score 635.5; DB 2; Length 222;
Best Local Similarity 60.2%; Pred. No. 9.9e-45;
Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;
QY 1 QTTPNSEGMHDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAI 60
Db 33 QTIGPGTGYNNNGYFYSYWMDGHGVTYTNPGGQFVSVMNSNGNFVGGKMGPGTKNKVI 92
QY 61 HFEGVYQPNNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSGATDLGTVECDGSYRLGKT 120
Db 93 NFSGTYNPNNGNSYLSVYGWSRNP LI EYIVENFGTYNPSTGATKLG EVTSDGSVYDIYRT 152
QY 121 TRVNAPSIDGTQTDPQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYIQIVATEGY 180
Db 153 QRVNQPSTIEGTATFYQYWSVRNRHSSGSVNTANHFNAWAQGLTL-GTMDYQIVAVEGY 211
QY 181 FSSGYARITVA 191
Db 212 FSSGSASITVS 222

RESULT 9
S39883
endo-1,4-beta-xylanase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)
N/Alternate names: endoxylanase II
C/Species: Trichoderma reesei
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S39883; S39884
R/Saarelainen, R.; Paloheimo, M.; Fagerstroem, R.; Suominen, P.L.; Nevalainen, K.M.H.
Mol. Gen. Genet. 241, 497-503, 1993
A/Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxylan
A/Reference number: S39883; MUID:94088442; PMID:8264524
A/Accession: S39883
A/Molecule type: DNA
A/Residues: 1-223 <SAA>
A/Cross-references: UNIPROT:Q02244; UNIPARC:UPI00000421A8; EMBL:S67387; NID:g4555906; PID

A/Experimental source: strain QM6a
A/Accession: S39884
A/Molecule type: protein
A/Residues: 34-43/49-57/121-151/178-191 <SAF>
A/Cross-references: UNIPARC:UPI0000175A7C; UNIPARC:UPI0000175A7D; UNIPARC:UPI0000175A7E;
C/Genetics:
A/Gene: xln2
A/Intons: 91/2
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-33/Domain: propeptide #status predicted <PRO>
F/34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>
F/45-223/Domain: endo-1,4-beta-xylanase homology <XYL>
F/71,94/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/110,121/Binding site: substrate (Tyr) #status predicted
F/119,210/Active site: Glu #status predicted

Query Match 58.4%; Score 635.5; DB 2; Length 223;
Best Local Similarity 60.2%; Pred. No. 1e-44;
Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;
QY 1 QTTPNSEGMHDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAI 60
Db 34 QTIGPGTGYNNNGYFYSYWMDGHGVTYTNPGGQFVSVMNSNGNFVGGKMGPGTKNKVI 93
QY 61 HFEGVYQPNNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSGATDLGTVECDGSYRLGKT 120
Db 94 NFSGTYNPNNGNSYLSVYGWSRNP LI EYIVENFGTYNPSTGATKLG EVTSDGSVYDIYRT 153
QY 121 TRVNAPSIDGTQTDPQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYIQIVATEGY 180
Db 154 QRVNQPSTIEGTATFYQYWSVRNRHSSGSVNTANHFNAWAQGLTL-GTMDYQIVAVEGY 212
QY 181 FSSGYARITVA 191
Db 213 FSSGSASITVS 223

RESULT 10
A44594
endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)
N/Alternate names: xylanase IIA
C/Species: Trichoderma viride
C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: A44594
R/Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A/Reference number: A44593
A/Accession: A44594
A/Molecule type: protein
A/Residues: 1-190 <YAG>
A/Cross-references: UNIPROT:Q7M519; UNIPARC:UPI0000034D34
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F/12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F/77,88/Binding site: substrate (Tyr) #status predicted
F/86,177/Active site: Glu #status predicted

Query Match 58.3%; Score 634.5; DB 1; Length 190;
Best Local Similarity 60.2%; Pred. No. 1e-44;
Matches 115; Conservative 27; Mismatches 48; Indels 1; Gaps 1;
QY 1 QTTPNSEGMHDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNLVGKGWNPGLNARAI 60
Db 1 QTIGPGTGFNNNGYFYSYWMDGHGVTYTNPGGQFVSVMNSNGNFVGGKMGPGTKNKVI 60

D_b 45 TTNQEGTNNGGYYSFWMTDSQGTVSMNMGSGGQYSTSWRNTGNFVAGKGMANG--GRRTVQY 103
QY 63 EGVYQPNGNSYLAVYGCTRNPFLVEYYIVENFGTYDPSSCATDLGTEVEDGSILRLGKTR 122
D_b 104 SGSFNPSGNAYLALYGWTSNPLVEYYIVDNWGTYRPTEGYK--GTVTSDGGTYDIYKTTIR 161
QY 123 VNAPSIDGTQTDFQYWSVRQDKRTSGTVQTCGHFDAMARAGLVNNGDHYIQLIATEGYFS 182
D_b 162 VNKPSVEGTRTFDQYWSVROSKRKTGTTTGNHFDAMARAQMPLGNFSYIMIMATEGYQS 221
QY 183 SGYARITVADVG 194
D_b 222 SGTSSINVGCTG 233

```

RESULT 14
T50601
endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor
N/Alternate names: xylanase B
C/Species: Streptomyces coelicolor
C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C/Accession: T50601
R/Redenbach, M.; Kleser, H.M.; Denapalte, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw
Mol. Microbiol. 21, 77-96, 1996
A/Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S
A/Reference number: Z20556; MUID:97000351; PMID:8843436
A/Accession: T50601
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-335 <RED>
A/Cross-references: UNIPROT:Q9RKN6; UNIPARC:UPI00000DC56E; EMBL:AL133220; PIDN:CAB61738.
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: xlnB
C/Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase

```

Query Match	52.3%;	Score 569.5;	DB 2;	Length 335;
Best Local Similarity	55.2%;	Pred. No. 3.8e-39;		
Matches 106;	Conservative 24;	Mismatches 59;	Indels 3;	Gaps 2;
QY	3	TPNSEGWHDGYRYSWSWDGAQATYTNLEGTYEISWGDGNLVGKGWNPGLNARAIHF	62	
		: : : : : :		
Db	46	TTNQEGTNNGYYSFMTDSOGTVSMNMWGGQYSTWRNTGNFVAKGWANG-GRRTVQY	104	
QY	63	EGVYQPNGNSYLAIVGWTRNPLVEYYIVENFGTYDPSSGATDLGTVBCDSIYRLGKTR	122	
		: : : : : : :		
Db	105	SGSFNPSGNAYLALYGWTSNPLVEYYIVDNMGTYRPTGEYK--GTVTSDCGTYDIKTR	162	
QY	123	VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVNGDHYIYQIVATEGYES	182	
		: : : : : :		
Db	163	VNKPVSVEGTRTFDQYWSVRQAKRTGCTITTGNHFDAMARAGMPLGNFSYIMIMATEGYQS	222	
QY	183	SGYARITVADVQ	194	
		: :		
Db	223	SGSSSINVGGTG	234	

```

RESULT 15
JC7307
endo-1,4-beta-xylanase (EC 3.2.1.8) - Penicillium sp.
N;Alternate names: endo-1,3-beta-xylanase; xylanase
C;Species: Penicillium sp.
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: JC7307; PC7086
R;Kimura, T.; Ito, J.; Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka, K.; Ohmura,
Biosci. Biotechnol. Biochem. 64, 1230-1237, 2000
A;Title: Purification, characterization, and molecular cloning of acidophilic xylanase from
A;Reference number: JC7307
A;Accession: JC7307
A;Molecule type: DNA
A;Residues: 1-221 <KIM>
A;Cross-references: UNIPROT:Q9UUC2; UNIPARC:UPI00000421AD; DDBJ:AB035540

```

A;Accession: PC7086
A;Molecule type: protein
A;Residues: 32-51 <KI2>
A;Cross-references: UNIPARC:UPI0000175A85
C;Genetics:
A;Gene: xynA
A;Intons: 89/2
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycoprotein; glycosidase; hydrolase

	Query Match	51.1%;	Score 555.5;	DB 2;	length 221;
	Best Local Similarity	53.6%;	Pred. No. 3.3e-38;		
	Matches 103;	Conservative 37;	Mismatches 49;	Indels 3;	Gaps 3.
QY	1 QTPNSE-GWHDGYYYSWWSDDGAQATYTNLBEGTVEIISWDGGLVGGKGMNPLNARA	59			
Dd	32 QTITSSQTGTNNGYYSFWTNNGGTVTQYLTNGAAGEYSVTWENCGDFTSGKGWSTG-SARD	90			
QY	60 IHFEGVYQPNGNSYLAVYGWTRNP LVEYYIVENFGTYDPSSGATDLGTVBCDSIYRLGK	119			
Dd	91 ITFEGTFNPSGNAYLAVYGWTTSP LVEYYIILEDYGDYNPENGSMTYKGTVTSDSGVYDIYE	150			
QY	120 TTRVNAPSIDGTOTFPDYMSVRQDKRTSGTVQTGCHEFDANARACLNVGNDHYQIVATEG	179			
Dd	151 HQOVNQPSISGTATFNQYWSIRQNTRRSSGTVTTHNFHNAWLGMNL-GSFNYQIVSTEG	209			
QY	180 YFSSGYARITVA	191			
Dd	210 YESSGSSTITVS	221			

Search completed: February 10, 2006, 15:02:21
Job time : 25.0764 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2006, 14:49:37 ; Search time 195.852 Seconds
(without alignments)
698.857 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225

Perfect score: 1088

Sequence: 1 QTPNSEGMHGDGYYYSWSD.....VATEGYFSSGYARITVADVG 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1088	100.0	225	1 XYNA_THELA	Q43097 thermomyces
2	965	88.7	194	1 XYNA_PAEVA	P81536 paecilomyce
3	758	69.7	227	2 Q9UVZ3_9PLEO	Q9uvz3 betosphaeri
4	750	68.9	295	2 Q9C1R2_FUSOX	Q9c1r2 fusarium ox
5	742	68.2	221	1 XYN1_COCCA	Q06562 cochliobolu
6	721	66.3	227	2 Q00263_9PEZI	Q00263 ascochyta p
7	705	64.8	204	2 Q51SA1_MAGGR	Q51sa1 magnaporthe
8	705	64.8	231	2 Q92245_MAGGR	Q92245 magnaporthe
9	665	61.1	235	2 Q766V1_NASCO	Q766v1 acytalidium
10	663	60.9	197	1 XYNA_SCHCO	P35809 schizophy11
11	656	60.3	219	2 Q12579_9PEZI	Q12579 chaetomium
12	656	60.3	231	2 Q13447_COCSA	Q13447 cochliobolu
13	654	60.1	231	2 Q70T28_9PLEO	Q70t28 setosphaeri
14	651	59.8	220	2 Q7SDQ1_NEUCR	Q7sdq1 neurospora
15	651	59.8	228	2 Q4WG11_ASPFU	Q4wg11 aspergillus
16	650	59.7	293	2 Q871E8_NEUCR	Q871e8 neurospora
17	648	59.6	225	1 XYNA_EMENT	P55332 emericeila
18	648	59.6	225	2 Q5B767_EMENT	Q5b767 aspergillus
19	648	59.6	231	2 Q00350_COCCA	Q00350 cochliobolu
20	647	59.5	227	2 Q9HGE1_HUMGT	Q9hge1 humicola gr
21	646	59.4	227	1 XYN1_HUMIN	P55334 humicola in
22	642.5	59.1	241	2 Q12580_9PEZI	Q12580 chaetomium
23	637.5	58.6	261	2 Q8J1V6_9PEZI	Q8j1v6 chaetomium
24	636.5	58.5	190	2 Q7M520_TRIVI	Q7m520 trichoderma
25	635.5	58.4	222	1 XYN2_TRIRE	P36217 trichoderma
26	635.5	58.4	223	2 Q02244_TRIRE	Q02244 trichoderma
27	634.5	58.3	190	2 Q7M519_TRIVI	Q7m519 trichoderma
28	634	58.3	230	2 Q8J1V5_9PEZI	Q8j1v5 chaetomium
29	631.5	58.0	267	2 Q6UN40_9PEZI	Q6un40 chaetomium
30	630.5	58.0	190	1 XYN TRIHA	P48793 trichoderma
31	630	57.9	221	2 Q4WLv2_ASPFU	Q4wlv2 aspergillus

32	629.5	57.9	220	2 Q8J0T4_9HYPO	Q8j0t4 trichoderma
33	627.5	57.7	223	2 Q7Z8Q3_TRIVI	Q7z8q3 trichoderma
34	625	57.4	232	2 Q9HFA4_ASPOR	Q9hfa4 aspergillus
35	623.5	57.3	223	2 Q99015_TRIRE	Q99015 trichoderma
36	621	57.1	225	1 XYNB_ASPKA	P48824 aspergillus
37	620	57.0	221	2 Q5AQR5_EMENT	Q5agr5 aspergillus
38	619	56.9	231	2 Q4HVK9_GIBZE	Q4hvk9 gibberella
39	619	56.9	231	2 Q7ZA57_GIBZE	Q7za57 gibberella
40	617	56.7	225	2 Q8TG22_ASPNG	Q8tg22 aspergillus
41	617	56.7	225	2 Q6QA21_9EURO	Q6qa21 aspergillus
42	617	56.7	231	2 Q9C1R1_FUSOX	Q9c1r1 fusarium ox
43	616	56.6	225	1 XYN2_ASPNG	P55330 aspergillus
44	615	56.5	221	1 XYNB_EMENT	P55333 emericeila
45	609	56.0	233	1 XYN2_MAGGR	P55335 magnaporthe

ALIGNMENTS

RESULT 1
ID XYNA_THELA STANDARD; PRT; 225 AA.
AC Q43097;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan xylohydrolase).
GN Name=XYNA;
OS Thermomyces lanuginosus (Humicola lanuginosa).
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
OX NCBI_TaxID=5541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=97033440; PubMed=9753433; DOI=10.1016/0168-1656(96)01516-7;
RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;
RT "Cloning and characterization of the gene for the thermostable xylanase Xyna from Thermomyces lanuginosus.";
RL J. Biotechnol. 49:211-218(1996).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=98426042; PubMed=9753433; DOI=10.1021/bi9808641;
RA Gruber K., Klintschar G., Hayn M., Schlacher A., Steiner W., Kracky C.;
RT "Thermophilic xylanase from Thermomyces lanuginosus: high-resolution X-ray structure and modeling studies.";
RL Biochemistry 37:13475-13485(1998).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xyans.
CC -!- BIOPHYSICOCHEMICAL PROPERTIES: Temperature dependence: Thermostable;
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G) family.

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CC EMBL, U35436; AAB94633.1; -; Genomic_DNA.
DR PDB; 1YNA; X-ray; @=32-225.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW 3D-structure; Glycosidase; Hydrolase; Pyrrolidone carboxylic acid; Signal; Xylan degradation.

FT SIGNAL 1 31
FT CHAIN 32 225
FT ACT_SITE 117 209
FT ACT_SITE 209 209
FT ACT_SITE 32 32
FT MOD_RES 32 32
FT DISULFID 141 185
FT STRAND 33 33
FT STRAND 37 41
FT TURN 42 43
FT STRAND 44 50
FT STRAND 56 60
FT TURN 63 64
FT STRAND 65 70
FT STRAND 75 82
FT STRAND 90 100
FT STRAND 103 112
FT TURN 113 115
FT STRAND 116 124
FT TURN 129 132
FT STRAND 134 141
FT TURN 142 143
FT STRAND 144 158
FT TURN 159 160
FT STRAND 161 172
FT STRAND 179 182
FT STRAND 183 192
FT HELIX 193 194
FT TURN 200 211
FT STRAND 214 223
SQ SEQUENCE 225 AA; 24356 MW; FAA79A914C5C676C CRC64;

Query Match 100.0%; Score 1088; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 7.3e-87;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTPNSEGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGWNPGLNARAI 60
DB 32 QTPNSEGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGWNPGLNARAI 91
QY 61 HFEGVYQPNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSGATDLGTVECDSIYRLGKT 120
DB 92 HFEGVYQPNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSGATDLGTVECDSIYRLGKT 151
QY 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNNGDHYIQIVATEGY 180
DB 152 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNNGDHYIQIVATEGY 211
QY 181 FSSGYARITVADV 194
DB 212 FSSGYARITVADV 225

RESULT 2
XYNA_PAEVA STANDARD; PRT; 194 AA.
AC P81536;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylosylase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
DE xylosylase) (PXY).
OS Paecilomyces variotii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.
OX NCBI_TaxID=45996;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (1.59 ANGSTROMS), AND PROTEIN SEQUENCE OF 50-58
RP AND 123-128.
RC STRAIN=Bainier;
RX MEDLINE=20090955; PubMed=10623548; DOI=10.1006/jmbi.1999.3348;
RA Kumar P.R., Eswaramoorthy S., Vithayathil P.J., Vismamitra M.A.;
RT "The tertiary structure at 1.59 A resolution and the proposed amino
RT acid sequence of a family-11 xylanase from the thermophilic fungus

RT Paecilomyces variotii bainier.";
RL J. Mol. Biol. 295:581-593 (2000).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- BIOPHYSICOCHEMICAL PROPERTIES:
CC Temperature dependence:
CC Thermotable;
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PDB; 1PVX; X-ray; A=1-194.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW 3D-structure; Acetylation; Direct protein sequencing; Glycosidase;
KW Hydrolase; Xylan degradation.
FT ACT_SITE 86 86 Nucleophile (By similarity).
FT ACT_SITE 178 178 Proton donor (By similarity).
FT MOD_RES 1 1 N-acetylglucine.
FT DISULFID 110 154
SQ SEQUENCE 194 AA; 20947 MW; 1D5C50AA4F6EDB90 CRC64;

Query Match 88.7%; Score 965; DB 1; Length 194;
Best Local Similarity 87.6%; Pred. No. 3.3e-76;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 2 TTPNSEGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGWNPGLNARAIH 61
DB 2 TTPNSEGMHDGYYYSWMSDGGDSTYTNNSGGTYEITWNGGNNLVGKGWNPGLNARAIH 61
QY 62 FEGVYQPNGNSYLA VYGWTRNPLVEYYIVENFGTYDPSGATDLGTVECDSIYRLGKT 121
DB 62 FEGVYQPNGNSYLA VYGWTRNPLVEYYIVENFGSSNPSSGSTDLGTVSCDSTYTLGOST 121
QY 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNNGDHYIQIVATEGY 181
DB 122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMASAGLNVTGDHYIQIVATEGY 181
QY 182 SSGYARITVADV 194
DB 182 SSGYARITVADV 194

RESULT 3
Q9UVZ3_9PLEO PRELIMINARY; PRT; 227 AA.
AC Q9UVZ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xylanase precursor.
GN Name=xy11;
OS Setosphaeria turcica.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Setosphaeria.
OX NCBI_TaxID=93612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=H2;
RA Degefu Y., Paulin L., Lubbeck P.S.;
RT "Cloning, sequencing and expression of a xylanase gene from the maize
RT pathogen Helminthosporium turcicum Pass.";
RL Eur. J. Plant Pathol. 107:457-465 (2001).
DR EMBL; AJ238895; CAB52417.1; -; Genomic_DNA.

DR	HSSP; Q43097; 1YNA.
DR	SMR; Q9UVZ3; 37-224.
DR	GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR	GO; GO:0045493; P:xylan catabolism; IEA.
DR	InterPro; IPR001137; Glyco_hydro_11.
DR	Pfam; PF00457; Glyco_hydro_11; 1.
DR	PRINTS; PR00911; GLHYDRLASE11.
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW	Signal; Xylan degradation.
FT	SIGNAL 1 19 Potential.
FT	CHAIN 20 227 xylanase.
GO	SEQUENCE 227 AA; 24123 MW; BA86FC075EE5306E CRC64;

Query Match	69.7%	Score 758;	DB 2;	Length 227;
Best Local Similarity	71.6%	Pred. No. 4.7e-58;		
Matches 136; Conservative	20;	Mismatches 32;	Indels 2;	Gaps 2;

Qy	1 QTTPNSEGHWDGYIYYSWMSDGGAAQTYYTNLEGGTYEISWGDCGNLVGKGWNPGLNARAI	60
Dd	37 QSTPNEGTHNGCFYSWSWDGARATYYTNGAGGSYSVSWGTGNNLVGKGMNPG-TARTI	95
Qy	61 HFEGVYQDNNGNSYLAVYGWTRNPIVEYYIVENFGTYDPSSGATDLCTVECDGSIYRLGKT	120
Dd	96 TYSGQYNBNGNSYLAIFYGWTRNPIVEYYVENFPTYDPSSQAQNKGTVTSDDSSYXIAQS	155
Qy	121 TRVNAPSIDGTQTDFDYWSVRQDKRTSGTVQTGFADAWABAGLNVNGDHYYQIVATEGY	180
Dd	156 TRTNQPSIDGTRTFQQYWSVRQNKRSSGSVMNMKTHFDAMASKMNL-GSHYYQIVATEGY	214
Qy	181 FSSGYARITV	190
Dd	215 FSSGSASITV	224

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RESULT 4
09C1R2_FUSOX
ID Q9C1R2_FUSOX PRELIMINARY; PRT; 295 AA.
AC Q9C1R2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE xylanase 5 protein.
GN Name=xyl5;
OS Fusarium oxysporum f. sp. lycopersici.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
OC Fusarium oxysporum complex.
OX NCBI_TaxId=59765;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21654148; PubMed=11795847; DOI=10.1007/s00294-001-0260-0;
RA Gomez-Gomez E., Roncero M.I.G., Di Pietro A., Hera C.;
RT "Molecular characterization of a novel endo-beta-1,4-xylanase gene
RT from the vascular wilt fungus Fusarium oxysporum.";
RL Curr. Genet. 40:268-275(2001).
DR EMBL; AF246830; AAK27974.1; -; Genomic_DNA.
DR HSSP; O43097; 1YNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA..
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHTRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR xylan degradation.
KW SEQUENCE 295 AA; 30858 MW; CA441056DCD3C104 CRC64;

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Query Match	68.9%	Score 750;	DB 2;	Length 295;
Best Local Similarity	70.5%	Pred. No. 3.2e-57;		
Matches 134;	Conservative 25;	Mismatches 29;	Indels 2;	Gaps 2;

QY	3	T P N S E G H M D G Y I Y S W M S D G G A O A T Y T N L E G G T Y E I S W G D G N U V G K G W N P G L N A R A I H F	62
Dd	36	T P N S S G T I N N G F Y I S W M S D G G A D A T Y T N G E G G S Y S M E W K D G G N V V C G K W S P G - K A R T I S Y	94
QY	63	E G V Y Q P N G N S Y L A V Y G W T R N P L V E Y I V E N F G T Y D P S S G A T D L G T V E C D G S I Y R L G K T T R	122
Dd	95	E G E Y K P N G N S Y L S V Y G W T R N P L V E Y I V E S F G T Y N P S S G A T P K K G T V E A D G S T Y D I F E T T R	154
QY	123	V N A P S I D G T Q T F D Q Y W S V R Q D K R T S G T V Q T G C H F D A W A R A G L V N G D H Y Y Q I V A T E G Y S	182
Dd	155	T N A P S I D G T Q T F Q Q Y W S V R Q G H N S T G S V D T G L H F D A W E K A G M K L - G T H D Y Q I L A T E G Y S	213
QY	183	S G Y A R I T V A D	192
Dd	214	S G S S H M T V S E	223

RESULT 5			
XYN1_COCCA			
ID	XYN1_COCCA	STANDARD;	PRT; 221 AA.
AC	Q06562;		
DT	01-FEB-1995 (Rel. 31, Created)		
DT	01-FEB-1995 (Rel. 31, Last sequence update)		
DT	10-MAY-2005 (Rel. 47, Last annotation update)		
DE	Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I) (1,4-beta-D-xylan xylanohydrolase 1).		
GN	Name=XYL1;		
OS	Cochliobolus carbonum (Bipolaris zeicola).		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;		
OC	Pleosporales; Pleosporaceae; Cochliobolus.		
OX	NCBI_TaxId=5017;		

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Race 1 / Isolate SB111;
RX MEDLINE=94003417; Pubmed=8400376;
RA Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
RT "Cloning and targeted gene disruption of XYL1, a beta 1,4-xylanase
RT gene from the maize pathogen Cochliobolus carbonum.";
RL Mol. Plant Microbe Interact. 6:467-473(1993).
RN [2]
RP PARTIAL PROTEIN SEQUENCE.
RA Holden F.R., Walton J.D.;
RT "Xylanases from the fungal maize pathogen Cochliobolus carbonum.";
RL Physiol. Mol. Plant Pathol. 40:39-47(1992).
CC -1- FUNCTION: Major xylan-degrading enzyme. Contributes to the
CC hydrolysis of arabinoxylan, the major component of maize cell-
CC walls.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; L13596; AAA33024.1; -; Genomic_DNA.
DR HSSP; O43097; 1YNA.
DR SMR; Q06562; 31-218.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHTRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Direct protein sequencing; Glycosidase; Hydrolase; Signal;
KW Xylan degradation.
FT SIGNAL 1 30 Potential.

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACU01001255; EAA49509.1; -; Genomic_DNA.
DR Interpro; IPR002453; Beta_tubulin.
DR Interpro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 204 AA; 22624 MW; 2396D83ED2B92260 CRC64;

Query Match	64.8%	Score 705;	DB 2;	Length 204;
Best Local Similarity	66.5%	Pred. No. 1.7e-53;		
Matches 125; Conservative	25;	Mismatches 36;	Indels 2;	Gaps 2;

Qy	3	TPNSEGMDHGYIYSWMSDGAQATYTNLEGGTYEISWGDGGLVGGKWNPGLNAPAIHF	62
Db	17	TPSSGTGHDGFYYSWMTDNGAQATYTNNAAGSYSITWSGNGNLVGGKWNPG-SARNVTY	75
Qy	63	EGVYQPNGNSYLAVYGMTRNPLVEYYIYENFGTYDPSSGATDLGVECDGSIYRLGKTR	122
Db	76	SANYRPNGNSYLSVYGMTRNPLVEYYIYENFGTYDPSSQASRKGTINVDGATYQVAQSTR	135
Qy	123	VNAPSIDGTQTFDQYWSVRQDKRTSGTYQTGCHFADAWARAGLNVNGDHYIYQIVATEGYFS	182
Db	136	TNQPISIDGTRTFQOQYWSVRQOKRSSGYIVDMKKHFDAMASMGKML-GTHDYQIVATEGYFS	194
Qy	183	SGYARITV	190
Db	195	SGSSTVTI	202

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RESULT 8
ID Q92245 MAGGR PRELIMINARY; PRT; 231 AA.
AC Q92245;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Endo-Beta-1,4-D-xylanase.
GN Name=XYL4;
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea) .
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes Incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mycelium;
RA Wu S.-C., Darvill A.G., Alberthelm P.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY144349; AAB06573.2; -; Genomic_DNA.
DR HSSP; Q43097; 1YNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW xylan degradation.
SQ SEQUENCE 231 AA; 25305 MW; CECF024A9D5A795B CRC64;

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Query Match	64.8%	Score 705;	DB 2;	Length 231;
Best Local Similarity	66.5%	Pred. No. 2e-53;		
Matches 125;	Conservative 25;	Mismatches 36;	Indels 2;	Gaps 2;

[illegible]

RESULT 9
Q766V1_9ASCO
ID Q766V1_9ASCO PRELIMINARY; PRT; 235 AA.

```

DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
DE G/11 family xylanase.
GN Name=sxy11;
OS Scytalidium thermophilum.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Scytalidium.
OX NCBI_TaxID=85995;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af101-3;
RA Morinaga T., Boonlue S., Aimi T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
EMBL AB114442; BAD07040.1; -; Genomic_DNA.
DR HSSP; P09850; 1BCX.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA..
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW xylan degradation.
SQ SEQUENCE 235 AA; 25526 MW; C929BBE7FD73682CA CRC64;

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Query Match	61.1%;	Score 665;	DB 2;	Length 235;
Best Local Similarity	63.8%;	Pred. No. 6.4e-50;		
Matches 120;	Conservative 24;	Mismatches 42;	Indels 2;	Gaps 2;

OY		3	TPNSEGHWDGYYYSWMSDGGAAQTNTNLEGCTYEISWGDEGNLVGKGMPGLNARAIHF	62
			: : : : : : : : : : : : : : : : :	
Db		49	TPSSTGMHGGEYFSFWTDGGGEVNVNMGNNNGNYGVNWRNCGNFVGKGMKPGA-ARTINY	107
OY		63	EGVYQPNGNSXYLAVYGWTRNPVEYYIVENFGTYDPSSGATDLGTVECDGSIVRLGKTR	122
			: : : : : : : :	
Db		108	SGTFNPSGNGYLAIYGMTTNPLVEYYIVENFGTYDPSSQAQNLTGYVDGSNYKLAKSTR	167
OY		123	VNAPSIDGTQTFDQYWSVRQDKRSTGTVQTGCHFDMARAGLNVGNDHYQIVATEGYES	182
			: : : : : : : : : : : : : :	
Db		168	YNQPSITIGTATFNQYWSVRQNKRSSGSVNVAHGFQAMAQRLNL-GNHDIQIVATEGYQS	226
OY		183	SGYARITV	190
Db		227	SGSASITV	234

RESULT 10		
XYNA_SCHCO		
ID_XYNA_SCHCO	STANDARD;	PRT; 197 AA.
AC P35809;		

DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
DE xylanohydrolase A).
GN Name=XVNA;
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
OX NCBI_TaxID=5334;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=ATCC 38548 / Delmar;
RA Yaguchi M., Roy C., Ujlie M., Watson D.C., Wakarchuk W.;
RL (In) Visser J., Beldman G., Kusters-van Someren M.A., Voragen A.G.J.
RL (eds.);
RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
RN [2]
RP PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RC STRAIN=ATCC 38548 / Delmar;
RX MEDLINE=94063044; Pubmed=8243636; DOI=10.1016/0014-5793(93)80698-T;
RA Oku T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
RA Jurasek L., Paice M.G.;
RT "Amino acid sequence and thermostability of xylanase A from
RT Schizophyllum commune.";
RL FEBS Lett. 334:296-300(1993).
RN [3]
RP PARTIAL PROTEIN SEQUENCE, AND ACTIVE SITE GLU-87.
RC STRAIN=ATCC 38548 / Delmar;
RX MEDLINE=94155888; Pubmed=7906649;
RA Bray M.R., Clarke A.J.;
RT "Identification of a glutamate residue at the active site of xylanase
RT A from Schizophyllum commune.";
RL Eur. J. Biochem. 219:821-827(1994).
CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- BIOPHYSICOCHEMICAL PROPERTIES:
CC pH dependence:
CC Active over a very broad pH range;
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A44597; A44597.
DR HSSP; P81536; 1PVX.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Direct protein sequencing; Glycosidase; Hydrolase; Xylan degradation.
FT ACT_SITE 87 Nucleophile (Probable).
FT ACT_SITE 184 Proton donor (By similarity).
FT DISULFID 111 160
SQ SEQUENCE 197 AA; 20979 MW; 42C8074E67C1FBB9 CRC64;
Query Match 60.9%; Score 663; DB 1; Length 197;
Best Local Similarity 61.3%; Pred. No. 7.7e-50;
Matches 119; Conservative 26; Mismatches 43; Indels 6; Gaps 2;
QY 3 TPNSEGWHDGYYSWSDGGAQATYTNLEGTYEISW-GDGNLVGKGWNPGLNARAIFH 61
DB 3 TPSSGTGIDGGYYYSWWTGAGDATYQNNGGGSYTLTWSGANGNLVGGKGWNPGAASRSIS 62
QY 62 FEGVYQPNNGNSYLAIVGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDSIYRLGKTT 121

DB 63 YSGTYQPNNGNSYLAIVGWTRSSLIIEYIVESYGSYDPSSAASHKGSVTCNGATYDILSTW 122
QY 122 RVNAPSIDGTQTFDQYWSVRQDKRT-----SGTVQTGCHFDAMARAGLNVNGDHYQIYA 176
DB 123 RVNAPSIDGTQTFEQFWSVRNPKKAPGSGTSGTDVQCHFDAMKGLGMNLGSEHNYQIYA 182
QY 177 TEGYFSSGYARITV 190
DB 183 TEGYQSSGTATITV 196
RESULT 11
Q12579_9PEZI
ID Q12579_9PEZI PRELIMINARY; PRT; 219 AA.
AC Q12579;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Endo-beta1,4-xylanase A (EC 3.2.1.8).
GN Name=cgxA;
OS Chaetomium gracile.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
OX NCBI_TaxID=47794;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96118924; Pubmed=8595661; DOI=10.1007/BF00313196;
RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
RT "Two family G xylanase genes from Chaetomium gracile and their
RT expression in Aspergillus nidulans.";
RL Curr. Genet. 29:73-80(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tsukagoshi N.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; D49850; BAA08649.1; -; Genomic_DNA.
DR PIR; S71472; S71472.
DR HSSP; P36217; 1XYO.
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 219 AA; 23325 MW; 4729299E08FDF9FBA CRC64;
Query Match 60.3%; Score 656; DB 2; Length 219;
Best Local Similarity 61.9%; Pred. No. 3.6e-49;
Matches 117; Conservative 28; Mismatches 42; Indels 2; Gaps 2;
QY 3 TPNSEGWHDGYYSWSDGGAQATYTNLEGTYEISWGDGNLVGKGWNPGLNARAIFH 62
DB 33 TPSSGTGTTNGYFYFSFTDGGGTVNYQNGAGGSYSVQWQNCGNPFVGGKGWNPGA-ARTINF 91
QY 63 BGVYQPNNGNSYLAIVGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDSIYRLGKTT 122
DB 92 SGTFSPOGNGYLAIVGWTONPLVEYYIVESFGTYDPSSQASKFGTTIQDDSTYTIKTT 151
QY 123 VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAMARAGLNVDHYQIVATEGYFS 182
DB 152 VNQPSIEGTSTFDQFWSVRQNHRS SVNVAAHFNAWAQAGLKL-GSHNYQIVATEGYQS 210
QY 183 SGYARITVA 191
DB 211 SGSSSITVS 219
RESULT 12
O13447_COCOA

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ID 013447_COCOA PRELIMINARY; PRT; 231 AA.
AC 013447;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Beta-1,4-xylosanase.
GN Name=xy12;
OS Cochliobolus sativus (Bipolaris sorokiniana).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=45130;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Emami K., Hack E.;
RT "Characterisation of a xylosanase gene from Cochliobolus sativus and its
RT expression.";
RL Mycol. Res. 105:352-359 (2001).
DR EMBL; AJ004802; CAA06151.1; -; Genomic_DNA.
DR HSSP; Q8JIV6; 1H1A.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylosan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PRO0911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation.
SQ SEQUENCE 231 AA; 25577 MW; 333E6DD1F065A6BF CRC64;

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Query Match	60.3%	Score 656;	DB 2;	Length 231;
Best Local Similarity	61.1%	Pred. No. 3.8e-49;		
Matches 116;	Conservative 27;	Mismatches 45;	Indels 2;	Gaps 2

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QY      1 QTPNSEGMHDGYIYSWMSDGAQATYNLFGCTYEISWGDGSLVGGKGNPGLNAPAI 60
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Db      41 QSTPSSEGHNGYFYSWMTDGGGSAQITMGEGSRYSVTRNRTGNFVGGKGNPG-TGRVI 99

QY      61 HFEGVYQPNNGSYLAVYGTNRNPLVEYYIVENFGTYDPSSGATDLGTECDGSYIRLCKT 120
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      100 NYGAFNPQNGYLAIVYGTNRNPLVEYYIESYGTYNPSSGAYKGSFQTDGTYNVAVS 159

QY      121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTQTGCHFDAWARAGLNVNGDHYQIVATEGY 180
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      160 TRYNQPSIDGTRTFQQYWSVRQKRVGGSVNMQNHFNAWSRYGLNL-GQHYIYQIVATEGY 218

QY      181 FSSGYARITV 190
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Db      219 QSSGSSDIYV 228

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RESULT 13
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ID Q70T28_9PLEO PRELIMINARY; PRT; 231 AA.
AC Q70T28;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Xylanase precursor.
OS Name=xy12;
GN Setosphaeria turcica.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Setosphaeria.
OX NCBI_TaxID=93612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15016446; DOI=10.1016/j.blochi.2004.01.001;
RA Degefu Y., Lohlander K., Paulin L.G.;
RT "Expression patterns and phylogenetic analysis of two xylanase genes
RT (htxy1 1 and htxy1 2) from Helminthosporium turcicum, the cause of
RT leaf blight of maize."
RL Biochimie 86:83-90(2004).
DR EMBL; AJ548879; CAD70174.1; -; Genomic DNA.

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DR HSSP; P09850; 1BCX.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Signal; Xylan degradation.
FT SIGNAL 1 19 potential.
FT CHAIN 20 231 xy12.
SQ SEQUENCE 231 AA; 25611 MW; 44078055B52BAF15 CRC64;

Query Match	60.1%;	Score 654;	DB 2;	Length 231;
Best Local Similarity	60.5%;	Pred. No. 5.7e-49;		
Matches 115; Conservative	28;	Mismatches 45;	Indels 2;	Gaps 2

[illegible]

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QY      181 FSSGVARITV 190
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Db      219 QSSGNSEIYV 228
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ID 07SDQ1_NEUCR PRELIMINARY; PRT; 220 AA.
AC 07SDQ1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, last annotation update)
DE Hypothetical protein (Probable endo-1, 4-beta-xylanase A).
GN Name=NCU02855.1; Synonyms=B10D6.120;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Jaffe D., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Seitremlkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseis M., Manceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Manhaupt G., Ebbola D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Manhaupt G.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [3]

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 10, 2006, 15:01:51 ; Search time 32.8735 Seconds
(without alignments)
487.903 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225

Perfect score: 1088
Sequence: 1 QTPNSEGWHGYYYSWMSD.....VATEGYFSSGYARITVADVG 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1088	100.0	225	1	US-08-886-765-2 Sequence 2, Appl1
2	1088	100.0	225	2	US-09-115-660-2 Sequence 2, Appl1
3	1083	99.5	194	2	US-09-570-856B-24 Sequence 24, Appl1
4	965	88.7	194	2	US-09-570-856B-23 Sequence 23, Appl1
5	742	68.2	221	2	US-09-570-856B-29 Sequence 29, Appl1
6	663	60.9	197	1	US-08-044-621D-29 Sequence 29, Appl1
7	663	60.9	197	1	US-08-709-912-9 Sequence 9, Appl1
8	663	60.9	197	1	US-09-047-370-9 Sequence 9, Appl1
9	663	60.9	197	2	US-09-570-856B-18 Sequence 18, Appl1
10	645	59.3	227	1	US-08-458-023B-4 Sequence 4, Appl1
11	638.5	58.7	223	2	US-09-254-733-7 Sequence 7, Appl1
12	637.5	58.6	261	2	US-08-768-373-2 Sequence 2, Appl1
13	637.5	58.6	261	2	US-09-849-242A-2 Sequence 2, Appl1
14	636.5	58.5	190	1	US-08-044-621D-28 Sequence 28, Appl1
15	636.5	58.5	190	1	US-08-709-912-14 Sequence 14, Appl1
16	636.5	58.5	190	1	US-09-047-370-14 Sequence 14, Appl1
17	635.5	58.4	190	1	US-08-044-621D-26 Sequence 26, Appl1
18	635.5	58.4	190	1	US-08-709-912-16 Sequence 16, Appl1
19	635.5	58.4	190	1	US-09-047-370-16 Sequence 16, Appl1
20	635.5	58.4	223	1	US-08-121-436A-2 Sequence 2, Appl1
21	634.5	58.3	190	1	US-08-074-621D-27 Sequence 27, Appl1
22	634.5	58.3	190	2	US-09-570-856B-19 Sequence 19, Appl1
23	634	58.3	230	2	US-08-768-373-4 Sequence 4, Appl1
24	634	58.3	230	2	US-09-849-242A-4 Sequence 4, Appl1
25	632.5	58.1	190	1	US-08-709-912-17 Sequence 17, Appl1
26	632.5	58.1	190	1	US-09-047-370-17 Sequence 17, Appl1
27	630.5	58.0	190	2	US-09-570-856B-20 Sequence 20, Appl1

28	630.5	58.0	190	2	US-09-570-856B-22	Sequence 22, Appl1
29	621	57.1	225	2	US-09-570-856B-26	Sequence 26, Appl1
30	617	56.7	225	1	US-08-290-979A-8	Sequence 8, Appl1
31	586.5	53.9	226	2	US-09-367-891A-2	Sequence 2, Appl1
32	576	52.9	223	2	US-09-462-246-2	Sequence 2, Appl1
33	574.5	52.8	296	1	US-08-507-431-6	Sequence 6, Appl1
34	574.5	52.8	296	2	US-09-116-622-6	Sequence 6, Appl1
35	574.5	52.8	296	2	US-09-219-277-6	Sequence 6, Appl1
36	574.5	52.8	296	2	US-09-599-661-6	Sequence 6, Appl1
37	572.5	52.6	231	1	US-08-902-655A-6	Sequence 6, Appl1
38	571.5	52.5	215	1	US-08-044-621D-34	Sequence 34, Appl1
39	571.5	52.5	335	2	US-09-570-856B-15	Sequence 15, Appl1
40	568	52.2	189	1	US-08-709-912-13	Sequence 13, Appl1
41	568	52.2	189	1	US-09-047-370-13	Sequence 13, Appl1
42	566.5	52.1	206	1	US-08-315-695-19	Sequence 19, Appl1
43	562.5	51.7	191	1	US-08-709-912-10	Sequence 10, Appl1
44	562.5	51.7	191	1	US-09-047-370-10	Sequence 10, Appl1
45	559	51.4	344	1	US-08-468-812-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-886-765-2
; Sequence 2, Application US/08886765
; Patent No. 5817500
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; APPLICANT: Wagner, Peter
; APPLICANT: Mullert, Peter
; APPLICANT: Knapp, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESS: No. 58175000 No. 5817500disk of No. 5817500th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/886,765
; FILING DATE: 1-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-886-765-2

Query Match 100.0%; Score 1088; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTPNSEGWHGYYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGMNPGINARAI 60
DB 32 QTPNSEGWHGYYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGMNPGINARAI 91

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QY      61 HFEGVYQPNNGNSYLAVYGWTRNPLVEYIIVENFGTYDPSSGATDLGTVCECDGSYRLGKT 120
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Db      92 HFEGVYQPNNGNSYLAVYGWTRNPLVEYIIVENFGTYDPSSGATDLGTVCECDGSYRLGKT 151
QY      121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGCHFDAMARAGLNVNGDHYQIVATEGY 180
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Db      152 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGCHFDAMARAGLNVNGDHYQIVATEGY 211
QY      181 FSSGYARITVADVG 194
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Db      212 FSSGYARITVADVG 225

RESULT 2
US-09-115-660-2
; Sequence 2, Application US/09115660
; Patent No. 6245546
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter Kamp
; APPLICANT: Wagner, Peter
; APPLICANT: Mulertz, Anette
; APPLICANT: Knap, Inge Helmer
; TITLE OF INVENTION: Animal Feed Additives
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 62455460 No. 6245546disk of No. 6245546th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,660
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/886,765
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4324.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-115-660-2

Query Match      100.0%; Score 1088; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 4e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGCHFDAMARAGLNVNGDHYQIVATEGY 180
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QY      181 FSSGYARITVADVG 194
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Db      212 FSSGYARITVADVG 225

RESULT 3
US-09-570-856B-24
; Sequence 24, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3+"
US-09-570-856B-24
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Query Match      99.5%; Score 1083; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 1e-96;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TTPNSEGWHHDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNLVGGKGNPGLNARAIH 61
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Db      2 TTPNSEGWHHDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNLVGGKGNPGLNARAIH 61
QY      62 FEGVYQPNNGNSYLAVYGWTRNPLVEYIIVENFGTYDPSSGATDLGTVCECDGSYRLGKT 121
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QY      122 RVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGCHFDAMARAGLNVNGDHYQIVATEGY 181
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RESULT 4
US-09-570-856B-23
; Sequence 23, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Paecilomyces variotii
US-09-570-856B-23
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RESULT 5
US-09-570-856B-29
; Sequence 29, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahlyac, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Cochliobolus carbonum
US-09-570-856B-29

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Query Match	68.2%	Score 742;	DB 2;	Length 221;
Best Local Similarity	70.0%	Pred. No. 9.6e-64;		
Matches 133;	Conservative 22;	Mismatches 33;	Indels 2;	Gaps 2;

QY 1 QTTPNSEGHNDGYYYSWMSDGAQATYTNLEGGTYEISWGDCGNLVGGKGMNPGLNARAI 60
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QY 121 TRVNAPSIDGTOTFDQYWSVRQDKRTSGTYQTGFADAWARAGLNVNGDHYYQIVATEGY 180
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Db 150 TRTNQPSIDGTRTFQGYWSVRQNKRRSSGVNMKTHFDAMASIGMNL-GQHYYQIVATEGY 208

QY 181 FSSGYARITV 190
|| : || : |||
Db 209 FSTGNAQITV 218

RESULT 6
US-08-044-621D-29
; Sequence 29, Application US/08044621D
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. Wakarchuk
; APPLICANT: Wing L. Sung
; APPLICANT: Makoto Yaguchi
; APPLICANT: Robert L. Campbell
; APPLICANT: David R. Rose

```

1  TITLE OF INVENTION:  CONSTRUCTION OF THERMOSTABLE MUTANTS
2  TITLE OF INVENTION:  OF A LOW MOLECULAR MASS XYLANASE
3  NUMBER OF SEQUENCES:  37
4  CORRESPONDENCE ADDRESSES:
5  ADDRESSEE:  Gowling, Strathby & Henderson
6  STREET:  Suite 2600, 160 Elgin Street
7  CITY:  Ottawa
8  STATE:  Ontario
9  COUNTRY:  Canada
10 ZIP:  K1P 1C3
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE:  Diskette, 5.25 in., 360KB storage
14 COMPUTER:  IBM PC
15 OPERATING SYSTEM:  PC-DOS
16 SOFTWARE:  WordPerfect 5.1
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER:  US/08/044,621D
19 FILING DATE:  April 8, 1993
20 CLASSIFICATION:  435
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER:
23 FILING DATE:
24 ATTORNEY/AGENT INFORMATION:
25 NAME:  Judy A. Erratt
26 REGISTRATION NUMBER:  34,076
27 REFERENCE/DOCKET NUMBER:  08-863796
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE:  613-786-0199
30 TELEFAX:  613-563-9869
31
32 TELEX:
33
34 INFORMATION FOR SEQ ID NO:  29:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH:  197
37 TYPE:  Amino Acid
38 STRANDEDNESS:  No. 5405769 Relevant
39 TOPOLOGY:  linear
40 MOLECULE TYPE:
41 DESCRIPTION:  protein
42 HYPOTHETICAL:  No
43 ANTI-SENSE:  No
44 FRAGMENT TYPE:  No
45 ORIGINAL SOURCE:
46 ORGANISM:  Schizophyllum commune
47 STRAIN:  Schizophyllum commune, Xylanase A
48 IMMEDIATE SOURCE:
49 POSITION IN GENOME:
50 FEATURE:
51 PUBLICATION INFORMATION:
52 AUTHORS:  Oku T., Yaguchi M., Paice M., & Jurssek
53
54 TITLE:
55 JOURNAL:  Canadian Fed. Biol. Soc. Annu. Meet.
56 VOLUME:
57 ISSUE:
58 PAGES:  Abstract 676
59 DATE:  1988
60 DOCUMENT NUMBER:
61 FILING DATE:
62 PUBLICATION DATE:
63 RELEVANT RESIDUES IN SEQ ID NO:
64
65 US-08-044-621D-29

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Query Match	60.9%;	Score 663;	DB 1;	Length 197;
Best Local Similarity	61.3%;	Pred. No. 3.4e-56;		
Matches 119; Conservative	26;	Mismatches 43;	Indels 6;	Gaps 2;

[illegible]

;
; PAGES: Abstract #676
! DATE: 1988
US-09-047-370-9

Query Match	60.9%	Score 663;	DB 1;	Length 197;
Best Local Similarity	61.3%	Pred. No. 3.4e-56;		
Matches 119;	Conservative 26;	Mismatches 43;	Indels 6;	Gaps 2;

Qy	3	TPNSEGMHDXYYXSWMSDGAQATYTNLEGTYEISW-GDGENLVGKGWNPGLNARATH	61
Db	3	TPSSTGTGCGYYXSWMTDAGADATYQNNCGGSYTLTWSGNNGNLVGKGWNPGAASRSTIS	62
Qy	62	PEGVYQPNNGNSYLAVYGWTRNPLVEYIYIVENFGTYDPSSGATDICTVECDGSIYRLGKTT	121
Db	63	YSGTYQPNNGNSYLSVYGWTRSSLIEYIYIVESYGSYDPSAASHKGSVTCNGATYDILSTW	122
Qy	122	RVNAPSIDGTQTFDQYWSVRQDKRT-----SGTVQTCGHPDAMARAGLNVNGDHYQIYA	176
Db	123	RYNAPSIDGTQTFEQFWSVRNPKKAPGSGISGTVDVQCHFDAMKGLGMNLGSEHNYQIYA	182
Qy	177	TEGYFSSSGYARITV	190
Db	183	TEGYQSSGTATITV	196

RESULT 9
US-09-570-056B-10
; Sequence 10, Application US/09570856B

```

; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahljac, Basill I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Schizophyllum commune
US-09-570-856B-18

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Query Match	60.9%	Score 663;	DB 2;	Length 197;
Best Local Similarity	61.3%	Pred. No. 3.4e-56;		
Matches 119; Conservative	26;	Mismatches 43;	Indels 6;	Gaps 2

Oy	3	TPNSEGMDGYYSWMWSDGAQATYTNLGGTYEISW-GDGGNULVGKGWNPGLNARA	61
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Oy	62	FEGVYQPNNSYLAIVGWTNRNPLVEYIIVENFGTYDPPSSGATDGLGVECDGSIYRLGKT	121
		: : : : :	
Db	63	YSGTYQPNNSYLSVYGWTRSLIETIYIVESYGSYDPPSSASHKGSVTCNGATYDILSTW	122
Oy	122	RVNAPSIDGTQTFEDQYWSVRQDKRT-----SGTVQTGCHFPDAMARAGLNVNGDHHYQIVA	176
		: : : :	
Db	123	RYNAPSIDGTQTFEQFWSVRNPKKABGSGISGTVDVQCHFPDAMKGLGMNLGSEHNYQIVA	182
Oy	177	TEGYFSSGYARITV	190
Db	183	TEGYQSSGTATITV	196

RESULT 10
US-08-458-023B-4
Sequence 4, Application US/08458023B
Patent No. 5667990
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.

APPLICANT: Yoder, Wendy
 APPLICANT: Takagi, Shinobu
 APPLICANT: Boomnathan, Karuppan C.
 TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 56679900 No. 5667990disk of No. 56679900th America, Inc
 STREET: 405 Lexington Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10174-6201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,023B
 FILING DATE: 01-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lowney Dr., Karen A.
 REGISTRATION NUMBER: 31,274
 REFERENCE/DOCKET NUMBER: 4086.010-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 227 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-458-023B-4

Query Match	59.3%;	Score 645;	DB 1;	length 227;
Best Local Similarity	59.5%;	Pred. No. 2.3e-54;		
Matches 113;	Conservative 26;	Mismatches 49;	Indels 2;	Gaps 2;

Qy	1 QTTPNSEGHMDGYYSWSWSDGGAOATYTNLEGGTYEISWGDSGNLVGGKWNPGLNARAI 60 : : : : : :
Dd	37 QVTPNGECHMNGIFYSWMSDGGGOYTNLBGSRYQVRMRNTGNFVGKGWNPg-TGRTI 95 : : :
Qy	61 HFEGVOPDNNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLCTVECDSIYRLCKT 120 : : : : : : : : : :
Dd	96 NYGFYNPQNGCYLAVYGWTRNPLVEYYVIESYGTYPGSGAQYKGFYTDGDQYDI FVS 155 : : :
Qy	121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGFHFDAMARAGLNVNGDHYYQLVATEGY 180 : : : : : : : :
Dd	156 TRYNPSPSIDGTRTFQQYWSIRKNRKRGVGSVMNQNHFNMQHGMP-L-GQHYYQVVATEGY 214 : : : :
Qy	181 FSSGYARITV 190 : :
Dd	215 QSSGESDITY 224 : :

RESULT 11
 ; US-09-254-733-7
 ; Sequence 7, Application US/09254733
 ; Patent No. 6277596
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: WATANABE, MANABU
 ; APPLICANT: MORIYA, TATSUKI
 ; APPLICANT: AOYAGI, KAORU
 ; APPLICANT: SUMIDA, NAOMI
 ; APPLICANT: MURAKAMI, TAKESHI
 ; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE cbh1 GENES ORIGINATING
 ; TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
 ; TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
 ; FILE REFERENCE: 99-0266*/LC(WMC)/00144
 ; CURRENT APPLICATION NUMBER: US/09/254, 733
 ; CURRENT FILING DATE: 1999-05-07


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1 APPLICATION NUMBER: US 60/008,746
2 FILING DATE: 18-DEC-1995
3 APPLICATION NUMBER: US 60/020,839
4 FILING DATE: 28-JUN-1996
5 ATTORNEY/AGENT INFORMATION:
6 NAME: CIMBALA, MICHAEL A.
7 REGISTRATION NUMBER: 33,851
8 REFERENCE/DOCKET NUMBER: 1716.0540004
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (202) 371-2600
11 TELEFAX: (202) 371-2540
12 INFORMATION FOR SEQ ID NO: 2:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 261 amino acids
15 TYPE: amino acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: protein
19 ORIGINAL SOURCE:
20 ORGANISM: Chaetomium thermophilum
21 STRAIN: CBS730.95
22 FEATURE:
23 NAME/KEY: Protein
24 LOCATION: 1..261
25 OTHER INFORMATION: /label= XLNA
26 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Query Match	58.6%;	Score 637.5;	DB 2;	Length 261;
Best Local Similarity	60.1%;	Pred. No. 1.4e-53;		
Matches 113; Conservative	27;	Mismatches 47;	Indels 1;	Gaps 1;

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QY      3  TPNSEGMHDEYXXYSWMSDGAQATYTNLEGGTYEISWGDGGLVCGKGMNPGLNARAIHF  62
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      30  TSSATGTHNGYXXYSFWTLDGQNI RFNLESGQYSVTWSGNGMVGKGMNPGTDNRVINY  89

QY      63  EGVYQPNGNSYLA VYGMTBNPLAVEYYIYENFGTYDPSSGATDLGTYECDSIYRLGKTR  122
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Db      90  TADYRPNGNSYLA VYGMTBNPLIEYYVESFGTYDPSTGATRMGSVTTDDGTYNIYRTR  149

QY      123  VNAPSIDGTQFDQYWSVRQDKRTSGTYQTGCHFDAMARAGILNNGDHYQYIVATEGYFS  182
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      150  VNAPSIEGTKTFYQYWSVRTSKRTGTVTMANHFNAWRQAQLQL-GSHDYQIVATEGYYS  208

QY      183  SGYARITV 190
      | | | : |
Db      209  SGSATVNV 216

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RESULT 14
US-08-044-621D-28
; Sequence 28, Application US/08044621D
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. Wakarchuk
; APPLICANT: Wing L. Sung
; APPLICANT: Makoto Yaguchi
; APPLICANT: Robert L. Campbell
; APPLICANT: David R. Rose
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gowling, Strachy & Henderson
; STREET: Suite 2600, 160 Elgin Street
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1P 1C3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS
;

```

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: SOFTWARE: wordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/044,621D
: FILING DATE: April 8, 1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Judy A. Erralt
: REGISTRATION NUMBER: 34,076
: REFERENCE/DOCKET NUMBER: 08-863796
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 613-786-0199
: TELEFAX: 613-563-9869
: TELEX:
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 190
: TYPE: Amino Acid
: STRANDEDNESS: No. 5405769 Relevant
: TOPOLOGY: linear
: MOLECULE TYPE:
: DESCRIPTION: protein
: HYPOTHETICAL: No
: ANTI-SENSE: No
: FRAGMENT TYPE: No
: ORIGINAL SOURCE:
: ORGANISM: Trichoderma harzianum
: STRAIN: Trichoderma harzianum, 20kd
: IMMEDIATE SOURCE:
: POSITION IN GENOME:
: FEATURE:
: PUBLICATION INFORMATION:
: AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
: AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler
: AUTHORS: J.N.
: TITLE:
: JOURNAL: Xylans and Xylanases
: VOLUME:
: ISSUE:
: PAGES: 435-438
: DATE: 1992
: DOCUMENT NUMBER:
: FILING DATE:
: PUBLICATION DATE:
: RELEVANT RESIDUES IN SEQ ID NO:
: US-08-044-621D-28

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Query Match          58.5%; Score 636.5; DB 1; Length 190;
Best Local Similarity 60.7%; Pred. No. 1.2e-53;
Matches 116; Conservative 27; Mismatches 47; Indels 1; Gaps 1;

QY      1 QTPNSEGWHDGYYSWSWSDGGAQATYTNLGGTVEISWGDGCLVGGKWNPGLNARAI 60
      || : : ||| : : || | ||| : : : || | ||| || : |
Db       1 QTIGPGTGYNSNGYYYSYWNDDHAGVTTYTNGGGSPFTVWMSNSGNFVGKGWQPGTKNKVI 60

QY      61 HFEGVYQPNNGNSYLA VYGMTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKT 120
      : | | | | | | | | : : : : | | | | | | | | : : : :
Db       61 NFSGSYNPNNGNSYLSIYGMSRNP LIEYIVENFGTYNPSTGATKLGEVTSDSGVYDIYRT 120

QY      121 TRVNAPSIDGTQTFDDOYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYIYQIVATEGY 180
      ||| ||| ||| : : ||| ||| : : ||| ||| : | | | | |
Db       121 QRVNQPSIIIGTATFYQYWSVRNRHRSSGSVNTANHNAMASHGLTL-GTMDYQIVAVEGY 179

QY      181 FSSGYARITVA 191
      ||| ||| :
Db       180 FSSGSASITVS 190

RESULT 15
US-08-709-912-14
; Sequence 14, Application US/08709912

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Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Thrichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
US-08-709-912-14

Query Match 58.5%; Score 636.5; DB 1; Length 190;
Best Local Similarity 60.7%; Pred. No. 1.2e-53;
Matches 116; Conservative 27; Mismatches 47; Indels 1; Gaps 1;

OY 1 QTPNSEGWHGYYYSWSDGGAQATYTNLEGGTYEISWGDGDLVGKGMNPGINARAI 60
DB 1 QTIPTGTYSNGYYYSYNDGAGVYTNNGGGGFTVNMNSNGNFVGGKMGPGTKNKVI 60
OY 61 HFEGVYQPNNGSYLAVYGTNRNPLVEYIYVENFGTYDPSSGATDLGTVBCDGSIRLGKT 120
DB 61 NFSGSYNPNNGSYLSIYGWSRNPLEIYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
OY 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTYQTGCHFDAWARAGLNVNGDHYQIYVATEGY 180
DB 121 QRVNQPSSIIGTATFYQYWSVRNRHRSRSGSVTANHFNAWASHGLTL-GTMDYQIYAVEGY 179

OY 181 FSSGYARITVA 191
DB 180 FSSGSASITVS 190
Search completed: February 10, 2006, 15:03:37
Job time : 33.8735 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 10, 2006, 15:17:55 ; Search time 113.437 Seconds
(without alignments)
714.573 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225
Perfect score: 1088
Sequence: 1 QTPNSEGMHDGYYSWMSD.....VATEGYFSSGYARITVADV 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1088	100.0	194	4	US-10-307-441-20 Sequence 20, Appl
2	1088	100.0	194	6	US-11-088-725A-46 Sequence 46, Appl
3	1088	100.0	225	3	US-09-467-368-2 Sequence 2, Appl
4	1088	100.0	225	4	US-10-237-386-24 Sequence 24, Appl
5	758	69.7	227	4	US-10-237-386-21 Sequence 21, Appl
6	742	68.2	221	4	US-10-237-386-20 Sequence 20, Appl
7	737	67.7	227	4	US-10-425-115-221836 Sequence 221836,
8	725	66.6	221	4	US-10-425-115-267585 Sequence 267585,
9	721	66.3	227	4	US-10-237-386-22 Sequence 22, Appl
10	712	65.4	234	4	US-10-425-115-361946 Sequence 361946,
11	663	60.9	197	4	US-10-307-441-9 Sequence 9, Appl
12	663	60.9	197	6	US-11-088-725A-36 Sequence 36, Appl
13	663	60.9	201	4	US-10-237-386-23 Sequence 23, Appl
14	656	60.3	219	4	US-10-237-386-29 Sequence 29, Appl
15	656	60.3	231	4	US-10-237-386-26 Sequence 26, Appl
16	648	59.6	231	4	US-10-237-386-25 Sequence 25, Appl
17	646	59.4	227	4	US-10-237-386-27 Sequence 27, Appl
18	642.5	59.1	241	4	US-10-237-386-35 Sequence 35, Appl
19	641	58.9	234	4	US-10-213-990-69 Sequence 69, Appl
20	636.5	58.5	190	4	US-10-307-441-14 Sequence 14, Appl
21	636.5	58.5	190	6	US-11-088-725A-41 Sequence 41, Appl
22	635.5	58.4	190	4	US-10-307-441-16 Sequence 16, Appl
23	635.5	58.4	222	4	US-10-237-386-32 Sequence 32, Appl
24	635.5	58.4	223	4	US-10-237-386-31 Sequence 31, Appl
25	633	58.2	189	4	US-10-307-441-19 Sequence 19, Appl
26	633	58.2	189	6	US-11-088-725A-28 Sequence 28, Appl
27	632.5	58.1	190	4	US-10-307-441-17 Sequence 17, Appl

28	632.5	58.1	190	6	US-11-088-725A-42	Sequence 42, Appl
29	630.5	58.0	190	4	US-10-237-386-33	Sequence 33, Appl
30	630	57.9	221	4	US-10-213-990-66	Sequence 66, Appl
31	624.5	57.4	190	6	US-11-088-725A-1	Sequence 1, Appl
32	623.5	57.3	223	4	US-10-237-386-30	Sequence 30, Appl
33	616	56.6	225	4	US-10-237-386-36	Sequence 36, Appl
34	609	56.0	233	4	US-10-237-386-28	Sequence 28, Appl
35	604	55.5	221	4	US-10-237-386-44	Sequence 44, Appl
36	585.5	53.8	223	4	US-10-237-386-34	Sequence 34, Appl
37	576	52.9	223	4	US-10-299-393-2	Sequence 2, Appl
38	576	52.9	223	6	US-11-154-793-2	Sequence 2, Appl
39	573	52.7	313	4	US-10-213-990-72	Sequence 72, Appl
40	571	52.5	240	4	US-10-237-386-42	Sequence 42, Appl
41	568	52.2	189	4	US-10-307-441-13	Sequence 13, Appl
42	568	52.2	189	6	US-11-088-725A-40	Sequence 40, Appl
43	562.5	51.7	191	4	US-10-307-441-10	Sequence 10, Appl
44	562.5	51.7	191	6	US-11-088-725A-38	Sequence 38, Appl
45	562.5	51.7	228	4	US-10-237-386-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-10-307-441-20
; Publication 20, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; TITLE OF INVENTION: and Alkalophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307, 441
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213, 803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 20
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
US-10-307-441-20

Query Match 100.0%; Score 1088; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.7e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTPNSEGMHDGYYSWMSDGAQATYTNLEGGTYEISWGDGNNLGGKGNPGLNARAI 60
DB 1 QTPNSEGMHDGYYSWMSDGAQATYTNLEGGTYEISWGDGNNLGGKGNPGLNARAI 60
QY 61 HREGVYQPNNGNSYLAAYGWTNRNPLVEYIYVENFGTYDPSSGATDLGTYECDGSIYRLGKT 120
DB 61 HREGVYQPNNGNSYLAAYGWTNRNPLVEYIYVENFGTYDPSSGATDLGTYECDGSIYRLGKT 120
QY 121 TRVNAPSIDGTQTFDQYSVRQDKRTSGTVQTCGFDAWARAGLNVDHYIQIVATEGY 180
DB 121 TRVNAPSIDGTQTFDQYSVRQDKRTSGTVQTCGFDAWARAGLNVDHYIQIVATEGY 180
QY 181 FSSGYARITVADV 194
DB 181 FSSGYARITVADV 194

RESULT 2
US-11-088-725A-46
; Sequence 46, Application US/11088725A
; Publication No. US20050214410A1
; GENERAL INFORMATION:

APPLICANT: Iogen Bio-Products Corporation
APPLICANT: White, Theresa C
APPLICANT: Giroux, Genevieve R
APPLICANT: Wallace, Katie E.A.
TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
FILE REFERENCE: Q80712
CURRENT APPLICATION NUMBER: US/11/088,725A
CURRENT FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/556,061
PRIOR FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.2
SEQ ID NO 46
LENGTH: 194
TYPE: PRT
ORGANISM: Thermomyces lanuginosus
US-11-088-725A-46

Query Match 100.0%; Score 1088; DB 6; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.7e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTPNSEGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGWNPGLNARAI 60
DB 1 QTPNSEGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGWNPGLNARAI 60
QY 61 HFEGVYQPNNGNSYLA VYGWTRNPLVEYIYVENFGTYDPSSGATDLGTVCECDGSYRLGKT 120
DB 61 HFEGVYQPNNGNSYLA VYGWTRNPLVEYIYVENFGTYDPSSGATDLGTVCECDGSYRLGKT 120
QY 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNNGDHYIQIVATEGY 180
DB 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNNGDHYIQIVATEGY 180
QY 181 FSSGYARITVADV 194
DB 181 FSSGYARITVADV 194

RESULT 3

US-09-467-368-2
Sequence 2, Application US/09467368
Patent No. US20020160080A1
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
Wagner, Peter
Mullertz, Anette
Knap, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20020160080A1o No. US20020160080A1disk of No. US200201600
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,368
FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324.204-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-467-368-2

Query Match 100.0%; Score 1088; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTPNSEGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGWNPGLNARAI 60
DB 32 QTPNSEGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGWNPGLNARAI 91
QY 61 HFEGVYQPNNGNSYLA VYGWTRNPLVEYIYVENFGTYDPSSGATDLGTVCECDGSYRLGKT 120
DB 92 HFEGVYQPNNGNSYLA VYGWTRNPLVEYIYVENFGTYDPSSGATDLGTVCECDGSYRLGKT 151
QY 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNNGDHYIQIVATEGY 180
DB 152 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNNGDHYIQIVATEGY 211
QY 181 FSSGYARITVADV 194
DB 212 FSSGYARITVADV 225

RESULT 4

US-10-237-386-24
Sequence 24, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
APPLICANT: Sidsesen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 225
TYPE: PRT
ORGANISM: T. lanuginosus
US-10-237-386-24

Query Match 100.0%; Score 1088; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTPNSEGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGWNPGLNARAI 60
DB 32 QTPNSEGMHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNNLVGKGWNPGLNARAI 91
QY 61 HFEGVYQPNNGNSYLA VYGWTRNPLVEYIYVENFGTYDPSSGATDLGTVCECDGSYRLGKT 120
DB 92 HFEGVYQPNNGNSYLA VYGWTRNPLVEYIYVENFGTYDPSSGATDLGTVCECDGSYRLGKT 151
QY 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNNGDHYIQIVATEGY 180

Db 152 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 211
QY 181 FSSGYARITVADVG 194
Db 212 FSSGYARITVADVG 225

RESULT 5

US-10-237-386-21
; Sequence 21, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 227
; TYPE: PRT
; ORGANISM: H. turcicum
US-10-237-386-21

Query Match 69.7%; Score 758; DB 4; Length 227;
Best Local Similarity 71.6%; Pred. No. 2.5e-65;
Matches 136; Conservative 20; Mismatches 32; Indels 2; Gaps 2;

QY 1 QTPNSEGWHHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGWNPGLNARAI 60
Db 37 QSTPNEGTHNGCFYSWMSDGGARATYTNAGAGSYSVSWGTGNTLVGKGWNPGLNARAI 95
QY 61 HPEGVYQPNNGNSYLAVYGTNRNPLVEYYIVENFGTYDPSSGATDLGTVGCGSIYRLGKT 120
Db 96 TVSGQYNPNNGNSYLAVYGTNRNPLVEYYIVENFGTYDPSSQAQNKGTVTSDDSSYKIAQS 155
QY 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 180
Db 156 TRTNQPSIDGTRTFQYQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 214
QY 181 FSSGYARITV 190
Db 215 FSSGSASITV 224

RESULT 6

US-10-237-386-20
; Sequence 20, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 221
; TYPE: PRT
; ORGANISM: C. carbonum
US-10-237-386-20

Query Match 68.2%; Score 742; DB 4; Length 221;
Best Local Similarity 70.0%; Pred. No. 8.5e-64;
Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 1 QTPNSEGWHHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGWNPGLNARAI 60
Db 31 QSTPNEGTHNGCFYSWMSDGGARATYTNAGAGSYSVSWGTGNTLVGKGWNPGLNARAI 89
QY 61 HPEGVYQPNNGNSYLAVYGTNRNPLVEYYIVENFGTYDPSSGATDLGTVGCGSIYRLGKT 120
Db 90 TVSGTYNPNNGNSYLAVYGTNRNPLVEYYIVENFGTYDPSSQAQNKGTVTSDDSSYKIAQS 149
QY 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 180
Db 150 TRTNQPSIDGTRTFQYQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 208
QY 181 FSSGYARITV 190
Db 209 FSTGNAQITV 218

RESULT 7

US-10-425-115-221836
; Sequence 221836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 221836
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133906C.1.pap
US-10-425-115-221836

Query Match 67.7%; Score 737; DB 4; Length 227;
Best Local Similarity 67.4%; Pred. No. 2.7e-63;
Matches 128; Conservative 28; Mismatches 32; Indels 2; Gaps 2;

QY 1 QTPNSEGWHHDGYYYSWMSDGAQATYTNLEGTYEISWGDGNTLVGKGWNPGLNARAI 60
Db 37 QSTPNEGTHNGCFYSWMTDGSKVTYTNAGAGSYSVNWSGNGFVGKGWNPGLNARAI 95
QY 61 HPEGVYQPNNGNSYLAVYGTNRNPLVEYYIVENFGTYDPSSGATDLGTVGCGSIYRLGKT 120
Db 96 TVSGSYNPNNGNSYLAVYGTNRNPLVEYYIVENFGTYDPSSQAQNKGTVTSDDSSYKIAQS 155
QY 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 180
Db 156 TRTNQPSIDGTRTFQYQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYQIVATEGY 214
QY 181 FSSGYARITV 190
Db 215 FSTGSASITV 224

RESULT 8

```

US-10-425-115-267585
; Sequence 267585, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 267585
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(221)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_175642C.1.pep
US-10-425-115-267585

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Query Match	66.6%;	Score 725;	DB 4;	Length 221;
Best Local Similarity	68.4%;	Pred. No. 3.8e-62;		
Matches 130;	Conservative 22;	Mismatches 36;	Indels 2;	Gaps 2;

[illegible]

RESULT 9
US-10-23

```

: Sequence 22, Application US/10237386
: Publication No. US20030180895A1
: GENERAL INFORMATION:
: APPLICANT: Danisco A/S
: APPLICANT: Sibbesen, Ole
: APPLICANT: Sorensen, Jens
: TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
: FILE REFERENCE: 674509-2046
: CURRENT APPLICATION NUMBER: US/10/237,386
: CURRENT FILING DATE: 2002-12-06
: PRIOR APPLICATION NUMBER: PCT/IB01/00426
: PRIOR FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: GB 0005585.5
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: GB 0015751.1
: PRIOR FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 22
: LENGTH: 227
: TYPE: PRT
: ORGANISM: A. pisi
US-10-237-386-22

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Query Match	66.3%	Score 721;	DB 4;	Length 227;
Best Local Similarity	69.1%	Pred. No. 9.7e-62;		
Matches 130; Conservative	22;	Mismatches 34;	Indels 2;	Gaps 2;

[illegible]

RESULT 10

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US-10-425-115-361946
; Sequence 361946, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 361946
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_93271C.1.pep
US-10-425-115-361946

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Query Match	65.4%	Score 712;	DB 4;	Length 234;
Best Local Similarity	67.6%	Pred. No. 7.5e-61;		
Matches 127; Conservative	24;	Mismatches 35;	Indels 2;	Gaps 22;

QY		3	TPNSEGWHIDGYYSWWSDDGAQAITYNLEGGCTYEISWGDCGNLVGGKGMNPGLNARAIHF	62
Dd		43	TPSSQGTHNGCFYSWMTDGAQAITYNEAGGKYSVNMKTGNNVGGKGWNPGA-ARTITTY	1011
QY		63	EGVYQPNGNSYLAIVYGWTRNPLVEYYIVENFGTYDPSSGATDLGVECDGSIRLGTKTR	1222
Dd		102	SGTYPQGNSTYLAIYGMTNRNPLVEYYIVENFGTYDPSSAASVKGSVTADSSSYKIAQTQR	1611
QY		123	VNAPSIDGTQTFDQYWSVRQDKRTSGTYQTGCHFDAWARAGLNVDHYIYQIVATEGYFS	1822
Dd		162	VNOPSIDGTKITFNQYWSVRQNKRSSGSVNMMKTHFDAMASKMQL-GQHNYQIVATEGYFS	2202
QY		183	SGYARITV	190
Dd		221	SGSSSITV	228

RESULT 11

US-10-307-441-9
; Sequence 9, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity


```

1  / TITLE OF INVENTION:  and Alkalophilicity
2  / FILE REFERENCE: 027367-5006US
3  / CURRENT APPLICATION NUMBER: US/10/307,44
4  / CURRENT FILING DATE: 2002-12-02
5  / PRIOR APPLICATION NUMBER: PCT/CA01/00769
6  / PRIOR FILING DATE: 2001-05-31
7  / PRIOR APPLICATION NUMBER: 60/213,803
8  / PRIOR FILING DATE: 2000-05-31
9  / NUMBER OF SEQ ID NOS: 51
10 / SOFTWARE: PatentIn Ver. 2.1
11 / SEQ ID NO 9
12 / LENGTH: 197
13 / TYPE: prt
14 / ORGANISM: Schizopyllum commune
15 / US-10-307-441-9

```

Query Match	60.9%;	Score 663;	DB 4;	Length 197;
Best Local Similarity	61.3%;	Pred. No. 3.5e-56;		
Matches 119; Conservative	26;	Mismatches 43;	Indels 6;	Gaps 2;

```
QY      3 TPNSEGMHDGYYYSWMSDGAQATYTNLGGCTYEISM-GDGNLVGKGWNPGLNAPRAIH 61
       ||| | | | | | | | | | | | | | : : : | | | | | | | | | | : : |
Db      3 TPSSTGTDDGYIYSWMTDGAGDATYQNNGGGSYTLTWSGNNGNLVGKGMNPGAASRIS 62
QY      62 FEGVYQPNGNSYLAIVGWTRNP LVEYYYIVENFGTYDPSSGATDLGTECDGISYRLGKT 121
       : | | | | | | | | | | | | : | | | | | | | | : | | : | : |
Db      63 YSGTYQPNGNSYLSVYGWTRSSLIEYYLVEYSYGSYDPSSAASHKGSVTGNGATYDILSTW 122
QY      122 RVNAPSIDGTQTDFDYWSVRQDKRT-----SGTVQTGFDMARAGLNVNGDHYYQIVA 176
       | | | | | | | | | | | | : | | | | | | | | : : : | | | | |
Db      123 RYNAPSIDGTQTDFEQFWSVRNPKAPGSGISGTVDVQCCHFDAMKGLGMNLGSEHNYQIVA 182
```

QY	177	TEGYFSSGYARITV	190
Db	183	TEGYQSSGTATITV	196

RESULT 12
US-11-088

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; Sequence 36, Application US/11088725A
; Publication No. US20050214410A1
; GENERAL INFORMATION:
; APPLICANT: Iogen Bio-Products Corporation
; APPLICANT: White, Theresa C
; APPLICANT: Giroux, Genevieve R
; APPLICANT: Wallace, Katie E.A.
; TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
; FILE REFERENCE: 080712
; CURRENT APPLICATION NUMBER: US/11/088,725A
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/556,061
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Schizophyllum commune
US-11-088-725A-36

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Query Match	60.9%	Score 663;	DB 6;	Length 197;
Best Local Similarity	61.3%	Pred. No. 3.5e-56;		
Matches 119; Conservative	26;	Mismatches 43;	Indels 6;	Gaps 2;

[illegible]

Db	123	RYNAPSIDGOTFEQFMVSVRNPKAPBGSSISGTVDVQCHFDAMKGLGMNLGSEHNQIVA	182
QY	177	TEGYFSSGYARITV	190
Db	183	TEGYOSSGTATITV	196

RESULT 13
US-10-237

```

; Sequence 23, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 201
; TYPE: PRT
; ORGANISM: S. commune
US-10-237-386-23

```

Query Match	60.9%;	Score 663;	DB 4;	Length 201;
Best Local Similarity	61.3%;	Pred. No. 3.6e-56;		
Matches 119; Conservative	26;	Mismatches 43;	Indels 6;	Gaps 2;

[illegible]

RESULT 14
US-10-237

```

; Sequence 29, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
; FILE REFERENCE: 6/74509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27

```

NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 29
LENGTH: 219
TYPE: PRT
ORGANISM: C. gracile
US-10-237-386-29

Query Match 60.3%; Score 656; DB 4; Length 219;
Best Local Similarity 61.9%; Pred. No. 1.9e-55;
Matches 117; Conservative 28; Mismatches 42; Indels 2; Gaps 2;

QY 3 TPNSEGWHDGYYYSWWSDDGAQATYTNLEGTYEISWGDGNLVGKGWNPGLNARAIHF 62
DB 33 TPGGTGTTNNGYFYFSFMTDGGGTIVYQNGAGGSYSVQWQNCNFGVGGKWNPGA-ARTINF 91
QY 63 EGVYQPNNGNSYLAVYGTWRNPLVEYYIVENFGTYDPSSGATDLGTECDGSYRLGKTR 122
DB 92 SGTFSPOGNGYLAIYGTQNPFLVEYYIVESFGTYDPSSQASKFGTIQDGSYTTIAKTR 151
QY 123 VNAPSIDGTOTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVDHYQIVATEGYFS 182
DB 152 VNQPSIEGTSTFDQFWSVRQNHRSQSVNVAHFNAQAQGLKL-GSHNYQIVATEGYQS 210
QY 183 SGYARITVA 191
DB 211 SGSSSITVS 219

RESULT 15
US-10-237-386-26
Sequence 26, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Slobesen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
LENGTH: 231
TYPE: PRT
ORGANISM: C. bativus
US-10-237-386-26

Query Match 60.3%; Score 656; DB 4; Length 231;
Best Local Similarity 61.1%; Pred. No. 2.1e-55;
Matches 116; Conservative 27; Mismatches 45; Indels 2; Gaps 2;

QY 1 QTPNSEGWHDGYYYSWWSDDGAQATYTNLEGTYEISWGDGNLVGKGWNPGLNARAI 60
DB 41 QSTPSSEGYHNGYFYFSFMTDGGGSAQYTMGEGRYSVTWRTGNFVGGKWNPGA-TGRVI 99
QY 61 HFEGVYQPNNGNSYLAVYGTWRNPLVEYYIVENFGTYDPSSGATDLGTECDGSYRLGKT 120
DB 100 NYGGAFFNPQNGYLAIVYGTWRNPLVEYYIVESYGTYNPSSGAQYKGSFQTDGGTYNVAVS 159
QY 121 TRVNAPSIDGTOTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVDHYQIVATEGY 180
DB 160 TRYNOPSIDGTTRTFQOYWSVRQOKRVGGSVNMQNHFNWMSRYGLNL-GQHYQIVATEGY 218
QY 181 FSSGYARITV 190

DB 219 QSSGSSDIYV 228

Search completed: February 10, 2006, 15:22:35
Job time : 113.437 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: February 10, 2006, 15:18:39 ; Search time 9.72315 Seconds
(without alignments)
261.826 Million cell updates/sec

Title: US-09-467-368-2_COPY_32_225
Perfect score: 1088
Sequence: 1 QTPNSEGWHGYYYSWSD.....VATEGYFSSGYARITVADVG 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1088	100.0	225	7	US-11-170-653-24 Sequence 24, Appl
2	758	69.7	227	7	US-11-170-653-21 Sequence 21, Appl
3	742	68.2	221	7	US-11-170-653-20 Sequence 20, Appl
4	721	66.3	227	7	US-11-170-653-22 Sequence 22, Appl
5	663	60.9	201	7	US-11-170-653-23 Sequence 23, Appl
6	656	60.3	219	7	US-11-170-653-29 Sequence 29, Appl
7	656	60.3	231	7	US-11-170-653-26 Sequence 26, Appl
8	648	59.6	231	7	US-11-170-653-25 Sequence 25, Appl
9	646	59.4	227	7	US-11-170-653-27 Sequence 27, Appl
10	642.5	59.1	241	7	US-11-170-653-35 Sequence 35, Appl
11	635.5	58.4	222	7	US-11-170-653-32 Sequence 32, Appl
12	635.5	58.4	223	7	US-11-170-653-31 Sequence 31, Appl
13	630.5	58.0	190	7	US-11-170-653-33 Sequence 33, Appl
14	623.5	57.3	223	7	US-11-170-653-30 Sequence 30, Appl
15	616	56.6	225	7	US-11-170-653-36 Sequence 36, Appl
16	609	56.0	233	7	US-11-170-653-28 Sequence 28, Appl
17	604	55.5	221	7	US-11-170-653-44 Sequence 44, Appl
18	598	55.0	432	6	US-10-517-939-178 Sequence 178, App
19	585.5	53.8	223	7	US-11-170-653-34 Sequence 34, Appl
20	571	52.5	240	7	US-11-170-653-42 Sequence 42, Appl
21	569.5	52.3	335	6	US-10-517-939-232 Sequence 232, App
22	564	51.8	348	6	US-10-517-939-166 Sequence 166, App
23	562.5	51.7	228	7	US-11-170-653-39 Sequence 39, Appl
24	560	51.5	193	7	US-11-108-163B-14 Sequence 14, Appl
25	560	51.5	217	7	US-11-108-163B-13 Sequence 13, Appl

26	560	51.5	220	7	US-11-108-163B-12	Sequence 12, Appl
27	560	51.5	301	7	US-11-108-163B-11	Sequence 11, Appl
28	560	51.5	344	7	US-11-108-163B-10	Sequence 10, Appl
29	555.5	51.1	221	7	US-11-170-653-37	Sequence 37, Appl
30	554	50.9	239	7	US-11-170-653-40	Sequence 40, Appl
31	554	50.9	242	7	US-11-170-653-41	Sequence 41, Appl
32	544	50.0	241	7	US-11-170-653-43	Sequence 43, Appl
33	543.5	50.0	240	7	US-11-170-653-38	Sequence 38, Appl
34	541	49.7	354	6	US-10-517-939-216	Sequence 216, App
35	537	49.4	358	6	US-10-517-939-182	Sequence 182, App
36	535	49.2	352	6	US-10-517-939-226	Sequence 226, App
37	533.5	49.0	542	6	US-10-517-939-262	Sequence 262, App
38	532.5	48.9	216	7	US-11-170-653-45	Sequence 45, Appl
39	531	48.8	303	6	US-10-517-939-214	Sequence 214, App
40	526.5	48.4	347	6	US-10-517-939-196	Sequence 196, App
41	524	48.2	445	6	US-10-517-939-368	Sequence 368, App
42	522.5	48.0	237	7	US-11-170-653-47	Sequence 47, Appl
43	521	47.9	225	6	US-10-517-939-172	Sequence 172, App
44	520.5	47.8	358	6	US-10-517-939-370	Sequence 370, App
45	512.5	47.1	346	6	US-10-517-939-160	Sequence 160, App

ALIGNMENTS

RESULT 1
US-11-170-653-24
; Sequence 24, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 225
; TYPE: PRT
; ORGANISM: T. lanuginosus
US-11-170-653-24

Query Match 100.0%; Score 1088; DB 7; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7e-93;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QTPNSEGWHGYYYSWSDGGAQATTNLEGGTYEISWGDGNLVGKGNPGLNARAI	60
DB	32	QTPNSEGWHGYYYSWSDGGAQATTNLEGGTYEISWGDGNLVGKGNPGLNARAI	91
QY	61	HFEGVYQPNNGNSYLAIVYGTNRNPLVEYYIYENFGTYDPPSSGATDLGTVCEGDSIYRLGKT	120
DB	92	HFEGVYQPNNGNSYLAIVYGTNRNPLVEYYIYENFGTYDPPSSGATDLGTVCEGDSIYRLGKT	151
QY	121	TRVNAPSIDGTQTFDQYMSVRQDKRTSGTVGTGCHFDAMARAGLNVNGDHYIQIVATEGY	180
DB	152	TRVNAPSIDGTQTFDQYMSVRQDKRTSGTVGTGCHFDAMARAGLNVNGDHYIQIVATEGY	211
QY	181	FSSGYARITVADVG 194	
DB	212	FSSGYARITVADVG 225	

```
RESULT 2
US-11-170-653-21
; Sequence 21, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 227
; TYPE: PRT
; ORGANISM: H. turcicum
US-11-170-653-21
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```
Query Match          69.7%; Score 758; DB 7; Length 227;
Best Local Similarity 71.6%; Pred. No. 4.7e-63;
Matches 136; Conservative 20; Mismatches 32; Indels 2; Gaps 2;
```

```
QY      1 QTPNSEGWHDDGYYSWWSDDGAQATYTNLEGTYEISWGDGNLVGGKGNPGLNARAI 60
      ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      37 QSTPNBEGTHNGCFYSWWSDDGARATYTNAGAGSYSVSWGTGNLVGGKGNPGLNARAI 95
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      61 HFEGVYQPNNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVGCDGSIYRLGKT 120
      : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      96 TYSGQYNPNNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSQAQNKGTVTSDDSSYKIAQS 155
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYVQIVATEGY 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      156 TRTNQPSIDGTRTFQQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYVQIVATEGY 214
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      181 FSSGYARITV 190
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      215 FSSGSASITV 224
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 3
US-11-170-653-20
; Sequence 20, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
```

```
; LENGTH: 221
; TYPE: PRT
; ORGANISM: C. carbonum
US-11-170-653-20
```

```
Query Match          68.2%; Score 742; DB 7; Length 221;
Best Local Similarity 70.0%; Pred. No. 1.4e-61;
Matches 133; Conservative 22; Mismatches 33; Indels 2; Gaps 2;
```

```
QY      1 QTPNSEGWHDDGYYSWWSDDGAQATYTNLEGTYEISWGDGNLVGGKGNPGLNARAI 60
      ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      31 QNTPNBEGTHNGCFYSWWSDDGARATYTNAGAGSYSVSWGSGNLVGGKGNPGLNARAI 89
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      61 HFEGVYQPNNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVGCDGSIYRLGKT 120
      : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      90 TYSGTYNNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSQAQNKGTVTSDDSSYKIAQS 149
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYVQIVATEGY 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      150 TRTNQPSIDGTRTFQQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYVQIVATEGY 208
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      181 FSSGYARITV 190
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      209 FSTGNAQITV 218
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 4
US-11-170-653-22
; Sequence 22, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 227
; TYPE: PRT
; ORGANISM: A. pisi
US-11-170-653-22

Query Match          66.3%; Score 721; DB 7; Length 227;
Best Local Similarity 69.1%; Pred. No. 1.2e-59;
Matches 130; Conservative 22; Mismatches 34; Indels 2; Gaps 2;
```

```
QY      3 TPNSEGWHDDGYYSWWSDDGAQATYTNLEGTYEISWGDGNLVGGKGNPGLNARAIHF 62
      ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      39 TPSSQGTGTHNGCFYSWWTDDGAQATYTNAGAGSYSVNMKTGNLVGGKGNPGLNARAIHF 97
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      63 EGVYQPNNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVGCDGSIYRLGKTTR 122
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      98 SGTYSPPSGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSQAQTKGSVTADSSYKIAQTOR 157
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      123 VNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYVQIVATEGYFS 182
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      158 TNQPSIDGTQTFQQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYVQIVATEGYFS 216
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      183 SGYARITV 190
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      217 SGSAQITV 224
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

RESULT 5
US-11-170-653-23
/ Sequence 23, Application US/11170653
/ Publication No. US20050271769A1
/ GENERAL INFORMATION:
/ APPLICANT: Danisco A/S
/ APPLICANT: Sibbesen, Ole
/ APPLICANT: Sorensen, Jens
/ TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
/ FILE REFERENCE: 674509-2046
/ CURRENT APPLICATION NUMBER: US/11/170,653
/ PRIOR FILING DATE: 2005-06-23
/ PRIOR APPLICATION NUMBER: US/10/237,386
/ PRIOR FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: PCT/IB01/00426
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: GB 0005585.5
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: GB 0015751.1
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 23
/ LENGTH: 201
/ TYPE: PRT
/ ORGANISM: S. commune
US-11-170-653-23

```

Query Match	60.9%	Score 663;	DB 7;	Length 201;
Best Local Similarity	61.3%	Pred. No. 2.3e-54;		
Matches 119, Conservative	26;	Mismatches 43;	Indels 6;	Gaps 2;

OY		3	TPNSEGHMDGYRYSWMSDGAQATYNLEGTYEISW-GDGGNLVGKGWNPGIAPRAIH	61
Dd		5	TPSSTGTGDGGYYTSWMTDAGADATYQNNGCGSYTLTWSGNNGNLVGKGMNPGLAASHSIS	64
OY		62	PBGVYOFPNGNSYLAVYGWTNRNPLVEYYIVENFGTYPDPSSGATDIGTVCEDSIYRLGKT	121
Dd		65	YSGTYQPNGNSYLSVYGWTRSSLIEYYIVESYGSYDPSASAHSKSVCNCATYDILSTW	124
OY		122	RVNAPSIDGTQTFFDYWSVRQDKRT-----SGTVOTGFHFDAMARAGLNVNGDHYYQIVA	176
Dd		125	RYNAPSIDGTQTFEQFWSVRNPKKAFGCSI SGTVDVOCHFDMXGLGMNLGSEHNHYQIVA	184
OY		177	TEGYFSSGIYARTV	190
Dd		185	TEGYOSSGTAITV	198

```

RESULT 6
US-11-170-653-29
/ Sequence 29, Application US/11170653
/ Publication No. US20050271769A1
/ GENERAL INFORMATION:
/ APPLICANT: Danisco A/S
/ APPLICANT: Stbensen, Ole
/ APPLICANT: Sorensen, Jens
/ TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
/ FILE REFERENCE: 674509-2046
/ CURRENT APPLICATION NUMBER: US/11/170,653
/ CURRENT FILING DATE: 2005-06-23
/ PRIOR APPLICATION NUMBER: US/10/237,386
/ PRIOR FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: PCT/IB01/00426
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: GB 0005585.5
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: GB 0015751.1
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 29
; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. gracile
US-11-170-653-29

```

Query Match	60.3%;	Score 656;	DB 7;	Length 219;
Best Local Similarity	61.9%;	Pred. No. 1.1e-53;		
Matches 117; Conservative	28;	Mismatches 42;	Indels 2;	Gaps 2;

```
OY      3 TPNSEGHWDGYTYSWMSDGAQATYTNLLEGCTYEISWGDDGNLVGKGMNPLNARAIHF   62
       || : | ::||:::|||          || : : | : ||||||| || : | 
Db     33 TPGSGTGNNNGIFYSFMTDGCGTVANYQNAGAGSYSISVQMNCNFVGKGKNPGA-ARTINF   91

OY      63 EGVYQPNGNSYLAVYGWTBNPLVEYYIYVENFGTYDPSSGATDLGTVECDSIYRLGKTTR  122
       | : | | |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     92 SGTFSPPQGNYLAIVGWTONPLVEYYIVESFPTYDPSSQAASKFTIIQQDGSYTIAKTTIR  151

OY     123 VNAPSIDGTQTFFDYWSVRQDKRTSGVTQTGFADAMARAGLNVNGDHYYQIVATEGYFS  182
       || |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    152 VNOPSIEGSTFPDQFWMSVRQRHRRSSGSYNVAAHFNMAWAQAGLKL-GSHNTYQIVATEGYQS  210

OY     183 SGYARITVA  191
       || : |||:
Db    211 GSSSSITVS  219
```

RESULT 7
US-11-170-653-26

; Sequence 26, Application US/11170653

GENERAL INFORMATION:

APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole

APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylase

FILE REFERENCE: 674509-2046

CURRENT FILING DATE: 2005-06-23

; PRIOR APPLICATION NUMBER: US/10/237,386
 ; PRIOR FILING DATE: 2002-09-09

;
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08

/ ENRON FILING DATE: 2000 03 06
 ; PRIOR APPLICATION NUMBER: GB 0015751.1
 PRIOR FILING DATE: 2000 06 27

; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66; SOFTWARE: Pa
; SEQ ID NO 26; LENGTH: 231
; TYPE: PRT

ORGANISM: C. sativus

US-11-170-653-26

Query Match	60.3%;	Score 656;	DB 7;	Length 231;
Best Local Similarity	61.1%;	Pred. No. 1.2e-53;		
Matches 116;	Conservative 27;	Mismatches 45;	Indels 2;	Gaps 2;

```

QY      1 QTPNSEGHMDGYYYSWSWDGGAQATYTNLEGGTYEISWGDDGNLVGGKGMNPGLNARAI 60
      ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      41 QSTPSSEGYHNGYFYFSWWTDDGGGSAQYTMWEGSRYSVTWRNTGNFVGKKGMNPG-TGRVI 99

QY      61 HFEGVYQPNGNSYLA VGMTRNPLVEYIYVENFGTYDPPSSGATDLGTVCECDGSIYRLGKT 120
      ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      100 NYGAFNPQNGCYLA VGMTRNPLVEYIYVIESGYTNPSSGAYKGSFQTDGGTYNVAVS 159

QY      121 TRVNAPSIDGTOTPDQYWSVRQDKRTSGTVQTGFADAWARAGLVNGDHYIYQIVATEGY 180
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      160 TRYNQPSIDGTRTFQYQYWSVRQQKRVGGSVNMQNHFNAWSRYGLNL-GQHYIYQIVATEGY 218

QY      181 FSSGYARITV 190
      |||:|:|:|

```



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      |:| | | | : |
Db 209 YSSGSATVNV 219

```

RESULT 11
MS-11-170

```

: Sequence 32, Application US/11170653
: Publication No. US20050271769A1
: GENERAL INFORMATION:
: APPLICANT: Danisco A/S
: APPLICANT: Slibesen, Ole
: APPLICANT: Sorensen, Jens
: TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
: FILE REFERENCE: 674509-2046
: CURRENT APPLICATION NUMBER: US/11/170,653
: CURRENT FILING DATE: 2005-06-23
: PRIOR APPLICATION NUMBER: US/10/237,386
: PRIOR FILING DATE: 2002-09-09
: PRIOR APPLICATION NUMBER: PCT/IB01/00426
: PRIOR FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: GB 0005585.5
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: GB 0015751.1
: PRIOR FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 32
: LENGTH: 222
: TYPE: PRT
: ORGANISM: T. reesei
US-11-170-653-32

```

Query Match	58.4%;	Score 635.5;	DB 7;	Length 222;
Best Local Similarity	60.2%;	Pred. No. 9e-52;		
Matches 115; Conservative	28;	Mismatches 47;	Indels 1;	Gaps 1;

[illegible]

RESULT 12

```

: Sequence 31, Application US/11170653
: Publication No. US20050271769A1
: GENERAL INFORMATION:
: APPLICANT: Danisco A/S
: APPLICANT: Sibbesen, Ole
: APPLICANT: Sorensen, Jens
: TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
: FILE REFERENCE: 674509-2046
: CURRENT APPLICATION NUMBER: US/11/170,653
: CURRENT FILING DATE: 2005-06-23
: PRIOR APPLICATION NUMBER: US/10/237,386
: PRIOR FILING DATE: 2002-09-09
: PRIOR APPLICATION NUMBER: PCT/IB01/00426
: PRIOR FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: GB 0005585.5
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: GB 0015751.1
: PRIOR FILING DATE: 2000-06-27

```

```

; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 223
; TYPE: PRF
; ORGANISM: T. reesei
US-11-170-653-31

```

Query Match	58.4%	Score 635.5;	DB 7;	Length 223;
Best Local Similarity	60.2%;	Pred. No. 9.1e-52;		
Matches 115; Conservative	28;	Mismatches 47;	Indels 1;	Gaps 1;

QY 1 QTTPNSEGHMDGYYSWSWSDGGAQAATYNLEGGCTYEISWGDGNLVGKGWNPLNARAI 60
DB 34 QTIPGTGTNNNGFYFSYMNDBGHGVITYTNGPGGQFSSVMMSNSGNFVGKGMQPCTKNKI 93
QY 61 HFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDICTVECDGSIRLGKT 120
DB 94 NFGSGYNPNGNSYLSVYGWSRNPILIEYYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRT 153
QY 121 TRVNAPSIDGQTQTFDQYWSVRQDKRTSGTQTGCHFDAMARAGLNVNGDHYIQIVATEGY 180
DB 154 QRVNQPSIIIGTATFYQYWSVRNRHRSSGSVNTANHFNAWAQQGLTL-GTMDYQIVAVEGY 212
QY 181 FSSGYARTYA 191
DB 213 FSSGSASTVS 223

RESULT 13

```

; Sequence 33, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sildesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 190
; TYPE: PRT
; ORGANISM: T. harzianum
US-11-170-33

```

Query Match	58.0%;	Score 630.5;	DB 7;	Length 190;
Best Local Similarity	60.2%;	Pred. No. 2.2e-51;		
Matches 115; Conservative	27;	Mismatches 48;	Indels 1;	Gaps 1;

```
QY      1 QTTPNSEGHMDGYIYSWSWSDGGAQATYTNNLEGGTYEISWGDDGNLVGGKWNPLNARAI   60
        || : : ||| : : | | | | : : : : | | | | | : |
Db      1 QTIGPGTIGSYNGYYIYSYNDGDHAGVTTYTGCGGGSFTVMWSNSGNFVAGKGWQPPTKKVI   60
QY      61 HFEGVYOENGSYLA VYGWTRNP LVEY IVENFGTYDPSSGATDICTVECDGSIYRLGKT   120
        : | | | | | | : : : : | | | | | | | | | | | | : : : :
Db      61 NFSGSYNBNGSYLSIYGMSRNP L EY IVENFGTYNPSTGATKLGEVTS DGSVYDIYRT   120
QY      121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCHEFDAMARA GLNVNGDHYYQIVATEGY   180
        ||| | | | | | : : : : | | : : | | | | : : | | | |
Db      121 QRVNQPSIIIGTATFYQYWSVRNRHHS SSVNTANHFNAWASHGLTL- GTMDYQIVAVEGY   179
```

Qy 181 FSSGYARITVA 191
| | | | | :
Db 180 FSSGSASITVS 190

RESULT 14

US-11-170-653-30
; Sequence 30, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-11-170-653-30

Query Match 57.3%; Score 623.5; DB 7; Length 223;
Best Local Similarity 59.2%; Pred. No. 1.2e-50;
Matches 113; Conservative 29; Mismatches 48; Indels 1; Gaps 1;

Qy 1 QTPNSEGMDGYYSWMSDGAQATYTNLEGTYEISWGDGNLVGGKGNPGLNARAI 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 34 QTIQPTGTGNNNGYFHSYWNDDHGGTYTNGPGGQFSVWMSNSGNFVGGKGNPGLNARAI 93
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 61 HFEGVYQPNNGNSYLAIVYGTWRNPLVEYYIVENFGTYDPSSGATDLGTVECDSIYRLGKT 120
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 94 NFSGSYNPNGNSYLSVYGWMSRNPLEIYYIVGNFGTYNPSTGATKLGTVSDGSVYDIYRT 153
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYIQIVATEGY 180
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 154 QRVNQPSIIGTATFYQYWSVRNRHSSGSVNTANHFNAWAQGLTL-GTMDYQIVAVEGY 212
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 181 FSSGYARITVA 191
| | | | | :
Db 213 FSSGSASITVS 223

RESULT 15

US-11-170-653-36
; Sequence 36, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 225
; TYPE: PRT
; ORGANISM: A. niger
US-11-170-653-36

Query Match 56.6%; Score 616; DB 7; Length 225;
Best Local Similarity 58.4%; Pred. No. 5.8e-50;
Matches 111; Conservative 30; Mismatches 47; Indels 2; Gaps 2;

Qy 1 QTPNSEGMDGYYSWMSDGAQATYTNLEGTYEISWGDGNLVGGKGNPGLNARAI 60
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 37 RSTPSSTGENNGFYSPWTDGGDVITYINGDAGAYTVEWSNVGNFVGGKGNPGLNARAI 95
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 61 HFEGVYQPNNGNSYLAIVYGTWRNPLVEYYIVENFGTYDPSSGATDLGTVECDSIYRLGKT 120
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 96 TYSGTFTPSGNGYLSVYGWTTDPLIEYIVESYGDYNPGSGGTYYKGTYSVYDIYTA 155
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 121 TRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYIQIVATEGY 180
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 156 TRTNAASIGTATFYQYWSVRQDKRTSGTVQTCGHPDAMARAGLNVNGDHYIQIVATEGY 214
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 181 FSSGYARITV 190
| | | | | :
Db 215 QSSGSSSITV 224

Search completed: February 10, 2006, 15:23:01
Job time : 9.72315 secs